

|    |        |       |      |    |                  |                   |
|----|--------|-------|------|----|------------------|-------------------|
| 1  | 3621   | 100.0 | 3621 | 12 | US-10-032-717-1  | Sequence 1, Appl  |
| 2  | 3621   | 100.0 | 4874 | 12 | US-10-032-717-27 | Sequence 27, Appl |
| 3  | 3151.8 | 87.0  | 3633 | 12 | US-10-032-717-3  | Sequence 3, Appl  |
| 4  | 3151.8 | 87.0  | 6613 | 12 | US-10-032-717-28 | Sequence 28, Appl |
| 5  | 2008.4 | 55.5  | 2010 | 12 | US-10-032-717-15 | Sequence 15, Appl |
| 6  | 2003   | 55.3  | 2003 | 12 | US-10-032-717-5  | Sequence 5, Appl  |
| 7  | 1987.4 | 54.9  | 2003 | 12 | US-10-032-717-23 | Sequence 23, Appl |
| 8  | 1986.4 | 54.9  | 2022 | 12 | US-10-032-717-11 | Sequence 11, Appl |
| 9  | 1986.4 | 54.9  | 2022 | 12 | US-10-032-717-21 | Sequence 21, Appl |
| 10 | 1986.4 | 54.9  | 2022 | 12 | US-10-032-717-39 | Sequence 39, Appl |
| 11 | 1985.8 | 54.8  | 2013 | 12 | US-10-032-717-43 | Sequence 43, Appl |
| 12 | 1848.4 | 51.0  | 1860 | 12 | US-10-032-717-19 | Sequence 19, Appl |
| 13 | 1827.4 | 50.5  | 1854 | 12 | US-10-032-717-33 | Sequence 33, Appl |
| 14 | 1826.4 | 50.4  | 1856 | 12 | US-10-032-717-29 | Sequence 29, Appl |
| 15 | 1825.8 | 50.4  | 1854 | 12 | US-10-032-717-45 | Sequence 45, Appl |
| 16 | 1824.8 | 50.4  | 1863 | 12 | US-10-032-717-31 | Sequence 31, Appl |
| 17 | 1821.6 | 50.3  | 1863 | 12 | US-10-032-717-41 | Sequence 41, Appl |
| 18 | 1539.2 | 42.5  | 2022 | 12 | US-10-032-717-17 | Sequence 17, Appl |
| 19 | 1531.8 | 42.0  | 2003 | 12 | US-10-032-717-7  | Sequence 7, Appl  |

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RESULT 2
US-10-032-717-27
; Sequence 27, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: Pesticidal Activity Against Coleopterans
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Genomic DNA 1218-1
; US-10-032-717-27

Query Match 100.0%; Score 3621; DB 12; Length 4874;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3131 TACACAGATATAGATTGAGGGGTTTTCGGAGCAGTCAAGGATTTGGAATTTTTCACA 3190  
QY 2461 ATTGCTCATCAACGAACCGAATTTGTAAAAAATGTACCGGATGATTTGCTGCCAGATGTA 2520



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Db 3191 ATTGGTCTCAAAAGCAACCGAATGTAATAAAGATGACCGGATGATTTGCTGCCAGATGTA 3250
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Qy 2581 CGTTTAGAGTAGAAAACCGTTCTGGTGAAGCGCATGAGTTCTCTATCTCTATTTGATACA 2640
Db 3311 CGTTTAGAGTAGAAAACCGTTCTGGTGAAGCGCATGAGTTCTCTATCTCTATTTGATACA 3370
Qy 2641 GGTGAATCCGATTACATGAATGAATGCAAGGATATGCGTTGCAATTTAGATTTACGGACCA 2700
Db 3371 GGTGAATCCGATTACATGAATGAATGCAAGGATATGCGTTGCAATTTAGATTTACGGACCA 3430
Qy 2701 GAGGGATATGCAACACTCGGAAACCTAGAAATTTGCTGCAAGGAGGACCTTTATCAGGAGAC 2760
Db 3431 GAGGGATATGCAACACTCGGAAACCTAGAAATTTGCTGCAAGGAGGACCTTTATCAGGAGAC 3490
Qy 2761 GCATTAGAACGCTTGCAGAGAGAAACAAACAGTGGAGATTCAAATGACAAAGACGTCGT 2820
Db 3491 GCATTAGAACGCTTGCAGAGAGAAACAAACAGTGGAGATTCAAATGACAAAGACGTCGT 3550
Qy 2821 GAGGAACAGATAGAGATATATGGCATCGAACAAGCGGTAGATCGTTTATATGCCGAT 2880
Db 3551 GAGGAACAGATAGAGATATATGGCATCGAACAAGCGGTAGATCGTTTATATGCCGAT 3610
Qy 2881 TATCAGGATCAGCAACTGGAATCTGATGTAGAGATTACAGATCTTACTGCGGCCCAAGAT 2940
Db 3611 TATCAGGATCAGCAACTGGAATCTGATGTAGAGATTACAGATCTTACTGCGGCCCAAGAT 3670
Qy 2941 CTGATACAGTCCATTCCTTACGTTATATAACGAAATGTTCCGAGAAATPACCAAGGATGAAC 3000
Db 3671 CTGATACAGTCCATTCCTTACGTTATATAACGAAATGTTCCGAGAAATPACCAAGGATGAAC 3730
Qy 3001 TATACAGATTTACAGAAATTAACAGATCGATCTCCAAACAGCGTGGAGTTGTATGATCAG 3060
Db 3731 TATACAGATTTACAGAAATTAACAGATCGATCTCCAAACAGCGTGGAGTTGTATGATCAG 3790
Qy 3061 CGAAATGCCATACCAATGGTGATTTTCGAAATGGGTTAAGTAAATTCGGAATGCAAGCCCT 3120
Db 3791 CGAAATGCCATACCAATGGTGATTTTCGAAATGGGTTAAGTAAATTCGGAATGCAAGCCCT 3850
Qy 3121 GCGGTAGAAGTACAAACAAATCAATCATACATCTCTCTCTGTTGATTCGAAATCGGATGAG 3180
Db 3851 GCGGTAGAAGTACAAACAAATCAATCATACATCTCTCTCTGTTGATTCGAAATCGGATGAG 3910
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Db 3911 CAAGTTTCGCAACAGTTTACAGTTTCAACCGGAATCAAGATATGTTTACGAGTTACTGCG 3970
Qy 3241 AGAAAGAGAGGGGTAGGAAATGATATGTAAGTATCGGTGATCGGTGGAATCAACAGAA 3300
Db 3971 AGAAAGAGAGGGGTAGGAAATGATATGTAAGTATCGGTGATCGGTGGAATCAACAGAA 4030
Qy 3301 ACCTTTACTTTTATAGTCAACGGATATGATATACAAATGGAATGATATAGCAAGTGTCC 3360
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Db 4151 TATAACGCAAAATATATGATATATACGCAAGCATCGATATCAACAAACGGAATACAAAT 4210
Qy 3481 AGTGTGTACAATGATCAAAACCGGTATATCACAAAACAGTGATCATTCATCCCGTATACA 3540
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Qy 3541 GATCAAAATGGAATGAGATGAGAGACAGAAAGGTCATTTCTATATAGAAAGTGTAGAA 3600
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Db 4331 TTGATTGTAGACGTAGAGTAA 4351

RESULT 3
US-10-032-717-3
; Sequence 3, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Peng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins with
; FILE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3633
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3633)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry12I8-2
US-10-032-717-3
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Query Match 87.0%; Score 3151.8; DB 12; Length 3633;

Best Local Similarity 92.1%; Pred. No. 0; Matches 3353; Conservative 0; Mismatches 262; Indels 24; Gaps 2;

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Db 1 ATGAGTCCAAATTAATCAAAATGAATGAATATGAATATAGATGCGACACCTTCTACTTCTGTA 60
Qy 61 TCCAAATGATTTTAAACAGATACCCCTTTTTCGAAATGAGCCCAACAAATGCGCTACAAATATG 120
Db 61 TCCAAATGATTTTAAACAGATACCCCTTTTTCGAAATGAGCCCAACAAATGCGCTACAAATATG 120
Qy 121 GATTATAAGATTTTAAATAATGCTCTCGGGGAAATGCTAGTGAATACCCCTGGTTCACCT 180
Db 121 GATTATAAGATTTTAAATAATGCTCTCGGGGAAATGCTAGTGAATACCCCTGGTTCACCT 180
Qy 181 GAAGTACTTTGTAGCGGACAAAGATGAGCTTAAGCGCGCAATTCGATATAGTAGTAAATTA 240
Db 181 GAAGTACTTTGTAGCGGACAAAGATGAGCTTAAGCGCGCAATTCGATATAGTAGTAAATTA 240
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Db 301 GATATTTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360
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Db 361 GAACCTCAATTAATCAAAAAATAGCAGAAATGCAAGGAATTAAGCGCTTTTCGGAAATAGAA 420
Qy 421 GGATTAGGTAATTAATTAACCAATTTATATCTAAGTCCGCTTTGAAGAAATGGGAAGAAATCCA 480
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Db 481 AATGGTTCAAGAGCCTTACGAGATGTCGGAATCATTTGAAATCCTGATAGTTATTT 540  
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Qy 601 GCAATGGCAGCAACCTTCAATTTACTGTATTTAAAGGACGGTCAATTTTGGAGAGAA 660  
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Qy 1723 AAGCAGGGAATAATCGTGTAAAGACTGAGATATCTACTGATGACGATATTTGTATTGCAT 1782  
Db 1741 TATAGTATGAGGATTCGGTATGCTTCCTCGCTAAATAATTAATTTTATATAAATCCCTCT 1800  
Qy 1783 GTAAACGATGCTCAGATTCAGATGCCAAAGAAATTAAGAACCCAGGTGAGGATCTGACATCT 1842  
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Qy 1843 AAAACTTTTAAAGTTGCAGATGCTATCAACATTTAAATTTTAGCAACAGATAGTTGCTA 1902  
Db 1861 AATAAATTTTAAATGCGACTTTGCCCCCTTATTAATTTTACGACACCGAACCTTTTCAT 1920  
Qy 1903 GCATTGAAACATAATTTAGGTGAAGACCCCTAAATTCACATTTCTGGTATATAGTTTACGTT 1962  
Db 1921 ACTCTAGGGCTATATTTGAAGCGGAAGACTTCTCTGGAAT-----TGAAGCTTATATA 1974  
Qy 1963 GACCGAATTCGAATTCATCCAGTAGATGAGACATATGAAGCGGAACAGATTTAGAAGCA 2022  
Db 1975 GACCGAATTCGAATTTATCCAGTAGATGAGACATATGAAGCGGAACAGATTTAGAAGCA 2034  
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QY 3523 ACATTCATCCCGTATACAGATCAAAATGTGGATTGAGATGAGTACAGAGGATACATTC 3582
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Db 3595 TATATAGAAGTGTAGAAATGATTGATGAGGTAGGTAGTAA 3633
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## RESULT 4

US-10-032-717-28  
; Sequence 28, Application US/10032717  
; Patent No. US20020151709A1

## GENERAL INFORMATION:

APPLICANT: Andre R. Abad  
APPLICANT: Nicholas B. Duck  
APPLICANT: Xiang Feng  
APPLICANT: Ronald D. Flannagan  
APPLICANT: Theodore W. Kahn  
APPLICANT: Lynn E. Sims  
TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
Pesticidal Activity Against Coleopterans  
FILE REFERENCE: 35718/237005  
CURRENT APPLICATION NUMBER: US/10/032,717  
CURRENT FILING DATE: 2001-10-23  
PRIOR APPLICATION NUMBER: 60/242,838  
PRIOR FILING DATE: 2000-10-24  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PastSeq for Windows Version 4.0  
SEQ ID NO 28  
LENGTH: 6613  
TYPE: DNA  
ORGANISM: Bacillus thuringiensis  
NAME/KEY: misc feature  
LOCATION: (0)...(0)  
OTHER INFORMATION: Genomic Cry12Ib-2  
US-10-032-717-28

Query Match 87.0%; Score 3151.8; DB 12; Length 6613;

Best Local Similarity 92.1%; Pred. No. 0; Mismatches 262; Indels 24; Gaps 2;

Matches 3353; Conservative 0;

QY 1 ATGAGTCCAAATAATCAAAATGAATATGAAATATATAGATCGCACACCTTCTTCTCTGTA 60

Db 1254 ATGAGTCCAAATAATCAAAATGAATATGAAATATATAGATCGCACACCTTCTTCTCTGTA 1313

QY 61 TCAATGATTTCAACAGATACCCCTTTTGGCAATAGCCAAACAAATGCGCTACAAATATG 120

Db 1314 TCAATGATTTCAACAGATACCCCTTTTGGCAATAGCCAAACAAATGCGCTACAAATATG 1373

QY 121 GATTATAAGATTTTAAATAATGTCGCGGAATGCTAGTGAATACCTGGTTCACTT 180

Db 1374 GATTATAAGATTTTAAATAATGTCGCGGAATGCTAGTGAATACCTGGTTCACTT 1433

QY 181 GAAGTACTTTAGCGCAACAGATGAGCTAAGCGCGCAATGATATAGTAAATTA 240

Db 1434 GAAGTACTTTAGCGCAACAGATGAGCTAAGCGCGCAATGATATAGTAAATTA 1493

QY 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTCAGTCTTTTATCTCAACTTAT 300

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QY 301 GATATTTCTGCGCTTCAGGGGAAAGAGTCAATGGGAATTTTATGGAACAAGTAGAA 360

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DB 1914 TGGGGATGGTCTACAAACCACTATTAAATAAATAATGATCGTCAAAATGAAATCTACTGCA 1973  
QY 721 GAATATCTGATCACTGTTGTAAGTGGTATGAAACTGGTTAGCAAAATTAAGAGGACG 780  
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## RESULT 5

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US-10-032-717-15
; Sequence 15, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Peng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; CURRENT APPLICATION NUMBER: US/10/032,717
; FILE REFERENCE: 35718/237005
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
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; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 1218-1A
US-10-032-717-15
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Query Match 55.5%; Score 2008.4; DB 12; Length 2010;
Best Local Similarity 100.0%; Pied. No. 0;
Matches 2009; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1381 AGTACAGAGATTCGGAAATTAAGATTAATCTCCAGAACTTCGATCAACCAATTTATGAG 1440  
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Qy 1981 CCAAGTAGATGAGACATATGAAGCGGAACAA 2010  
Db 1981 CCAAGTAGATGAGACATATGAAGCGGAATAA 2010

## RESULT 6

US-10-032-717-5  
; Sequence 5, Application US/10032717  
; Patent No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Peng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sing  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 50/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 2003  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis (truncated)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2001)  
; NAME/KEY: misc feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: 1218-1  
US-10-032-717-5

Query Match 55.3%; Score 2003; DB 12; Length 2003;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2003; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATCGACACCTTCTACTTCTGTA 60  
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QY 1801 CAGATGCCAAACCAATGAACCCAGGTGAGATCTGACATCTTAAACTTTTAAAGTTGCA 1860
Db 1801 CAGATGCCAAACCAATGAACCCAGGTGAGATCTGACATCTTAAACTTTTAAAGTTGCA 1860
QY 1861 GATGCTATCAACCAATTAATTTAGCAACAGATAGTTCCGCTAGCAATTAAGAAAATTTA 1920
Db 1861 GATGCTATCAACCAATTAATTTAGCAACAGATAGTTCCGCTAGCAATTAAGAAAATTTA 1920
QY 1921 GGTGAAGACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 1980
Db 1921 GGTGAAGACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 1980
QY 1981 CCAGTAGATGAGACATATGAAGC 2003
Db 1981 CCAGTAGATGAGACATATGAAGC 2003
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## RESULT 7

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US-10-032-717-23
; Sequence 23, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2013)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: LKMS.R1218-1
US-10-032-717-23
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Query Match 54.9%; Score 1987.4; DB 12; Length 2013;  
Best Local Similarity 99.6%; Pred. NO. 0;  
Matches 2004; Conservative 0; Mismatches 6; Indels 3; Gaps 1;



QY 1 ATGAGTCCAAATATCAAAATGAATATGAAATATAGATGCGACACCTTCTACTTCTGTA 60  
DB 1 ATGAGTCCAAATATCAAAATGAATATGAAATATAGATGCGACACCTTCTACTTCTGTA 60  
QY 61 TCCAAATGATTTCTAAACAGATACCTTTTGGCAATGAGCCAAACAAATGCGCTTCAAAATATG 120  
DB 61 TCCAAATGATTTCTAAACAGATACCTTTTGGCAATGAGCCAAACAAATGCGCTTCAAAATATG 120  
QY 121 GATTTATAAAGATTTATTTAAATGCTGCGGAAATGCTAGTGAATACCTGTTTCACTT 180  
DB 121 GATTTATAAAGATTTATTTAAATGCTGCGGAAATGCTAGTGAATACCTGTTTCACTT 180  
QY 181 GAAGTACTTGTAGCGGACAAAGATGACCTAAGGCGCAATTTGATATAGTAGTAAATTA 240  
DB 181 GAAGTACTTGTAGCGGACAAAGATGACCTAAGGCGCAATTTGATATAGTAGTAAATTA 240  
QY 241 CTATCAGGTTTGGGTCCTTCAAGGGAAGAGTCAATGGGAAATTTTATGGAACAAAGTAGAA 360  
DB 241 CTATCAGGTTTGGGTCCTTCAAGGGAAGAGTCAATGGGAAATTTTATGGAACAAAGTAGAA 360  
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DB 361 GAAGTACTTATCAAAATATGACGAAATATGCAAGGAAATAAGCGCTTTCGGAATTTAGAA 420  
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DB 541 TTTACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATTCCTTACTGTA 600  
QY 598 TATGCAATGGGAGGCAACCTTCTACTTCTGTTATTAAGGAGCGGTCAATTTTGGAGAA 657  
DB 601 TATGCAATGGGAGGCAACCTTCTACTTCTGTTATTAAGGAGCGGTCAATTTTGGAGAA 660  
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DB 661 GAATGGGAGTGGTCAACAACTACTTATTAATTAATGATGCTCAATGAACTTACT 720  
QY 718 GCAGAAATTTCTGATCACTGTGTAAGTGGTATGAACTGGTTTAGCAAAATTTAAAGGC 777  
DB 721 GCAGAAATTTCTGATCACTGTGTAAGTGGTATGAACTGGTTTAGCAAAATTTAAAGGC 780  
QY 778 ACGAGCGTAAACAAATGGGTTGACTATTAACCAATTCCTGAGAGAAATGACACTGGCGTT 837  
DB 781 ACGAGCGTAAACAAATGGGTTGACTATTAACCAATTCCTGAGAGAAATGACACTGGCGTT 840  
QY 838 TTAGATGTTGTTGATTTATTTCCCAATTTATGACACACCGCTACCCCAATGGAACGAAA 897  
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QY 898 GCACAACTAAACAGGAGTATATACAGATCCACTGGGCGGGTAAACGTCTTCAATT 957  
DB 901 GCACAACTAAACAGGAGTATATACAGATCCACTGGGCGGGTAAACGTCTTCAATT 960  
QY 958 GGTTCCTGGTATGACAAAGACCTTCTTTTGGAGTGAATGATCATCCGTTATTCGACCA 1017  
DB 961 GGTTCCTGGTATGACAAAGACCTTCTTTTGGAGTGAATGATCATCCGTTATTCGACCA 1020  
QY 1018 CCCCATGTTATTTGATTTATTAACCGGACTCAACAGTGTATACCAATCAAGAGCAATTTCT 1077  
DB 1021 CCCCATGTTATTTGATTTATTAACCGGACTCAACAGTGTATACCAATCAAGAGCAATTTCT 1080  
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DB 1081 TCCGCTCGCTATATAAGACATTTGGCTGGTCAATCAATAAGCTACCATCGTGTAGTAGG 1140  
QY 1138 GGTAGTAAATCTTCAACAAATGATGNACTAATCAAAATCTACACAGCACTAGTACCTTT 1197  
DB 1141 GGTAGTAAATCTTCAACAAATGATGNACTAATCAAAATCTACACAGCACTAGTACCTTT 1200  
QY 1198 GATTTTACGAATTTATGATATTTTCAAGACTCTATCAAGGATGCGTACTCTCTTGATTT 1257  
DB 1201 GATTTTACGAATTTATGATATTTTCAAGACTCTATCAAGGATGCGTACTCTCTTGATTT 1260  
QY 1258 GTTTTACCTCGTTTATACGTATATTTTGGAAATGCGAAGTTCGAGTTTTCATGGTA 1317  
DB 1261 GTTTTACCTCGTTTATACGTATATTTTGGAAATGCGAAGTTCGAGTTTTCATGGTA 1320  
QY 1318 AACCAATTTGAATTAATACCAAGAGCGTTAAAGTATTAATCCAGTTTCCAAAGATTTATA 1377  
DB 1321 AACCAATTTGAATTAATACCAAGAGCGTTAAAGTATTAATCCAGTTTCCAAAGATTTATA 1380  
QY 1378 GCGAGTACAAAGAGTTCCGAAATTTAGAAATTTACCTCCAGAAATCTCAGATCAACCAATTTAT 1437  
DB 1381 GCGAGTACAAAGAGTTCCGAAATTTAGAAATTTACCTCCAGAAATCTCAGATCAACCAATTTAT 1440  
QY 1438 GAGTCATPATAGCCATAGATTTATGTCATATCAAAAGTATTTCCCGGACGGGTAAACACTTACC 1497  
DB 1441 GAGTCATPATAGCCATAGATTTATGTCATATCAAAAGTATTTCCCGGACGGGTAAACACTTACC 1500  
QY 1498 GGATTTAGTACTGTATTTTCTTGGACACATCGAAGTGCAGATTTAAACAATCAATATAT 1557  
DB 1501 GGATTTAGTACTGTATTTTCTTGGACACATCGAAGTGCAGATTTAAACAATCAATATAT 1560  
QY 1558 TCAGATAAATCACTCAAAATTTCCGGCGTTTAAATTTGGGATTAATTTTACCGTTTGTCCA 1617  
DB 1561 TCAGATAAATCACTCAAAATTTCCGGCGTTTAAATTTGGGATTAATTTTACCGTTTGTCCA 1620  
QY 1618 GTGGTAAAGGACCCAGGACATACAGGAGGGGATTTTATACAGTATATATAGAACTACTGGT 1677  
DB 1621 GTGGTAAAGGACCCAGGACATACAGGAGGGGATTTTATACAGTATATATAGAACTACTGGT 1680  
QY 1678 TCTGTAGAACCTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAGCAGGGAATAT 1737  
DB 1681 TCTGTAGAACCTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAGCAGGGAATAT 1740  
QY 1738 CGTGTAGAACCTGAGATATGCTACTGATGACAGATTTGATTTGATGTAAACGATGCTCAG 1797  
DB 1741 CGTGTAGAACCTGAGATATGCTACTGATGACAGATTTGATTTGATGTAAACGATGCTCAG 1800  
QY 1798 ATTCAGATGCCAAAAACAATGAACCCAGGTGAGGATCTGACATCTTAAAACTTTTAAAGTT 1857  
DB 1801 ATTCAGATGCCAAAAACAATGAACCCAGGTGAGGATCTGACATCTTAAAACTTTTAAAGTT 1860  
QY 1858 GCAGATGCTATCAACCAATTTAAATTTAGCAACAGATAGTTTCGCTAGCATTTGAACATAT 1917  
DB 1861 GCAGATGCTATCAACCAATTTAAATTTAGCAACAGATAGTTTCGCTAGCATTTGAACATAT 1920  
QY 1918 TTAGTGTGAAGACCTTAATTTCAACATTTCTGTTATAGTTTACGTTGACCGAATCGAATTC 1977  
DB 1921 TTAGTGTGAAGACCTTAATTTCAACATTTCTGTTATAGTTTACGTTGACCGAATCGAATTC 1980  
QY 1978 ATCCAGTAGTAGACATATGAAGCGGAACAA 2010  
DB 1981 ATCCAGTAGTAGACATATGAAGCGGAATAA 2013

## RESULT 8

US-10-032-717-11  
; Sequence 11, Application US/10032717  
; Patent No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan





QY 1369 GATATTATAGCGAGTCAAGAGATTCCGAAATTAGAAATTAACCTCCAGAACTTCAGATCAA 1428  
DB 1381 GATATTATAGCGAGTCAAGAGATTCCGAAATTAGAAATTAACCTCCAGAACTTCAGATCAA 1440  
QY 1429 CCAAAATTATGAGTCATATAGCCATAGATTAATGTCATATCAACAGTATTCCCGGACGGGT 1488  
DB 1441 CCAAAATTATGAGTCATATAGCCATAGATTAATGTCATATCAACAGTATTCCCGGACGGGT 1500  
QY 1489 AACATACCGGATAGTACCTGTAATTTCTTGGACACATCGAAGTGCAGATTTTAAACAAT 1548  
DB 1501 AACATACCGGATAGTACCTGTAATTTCTTGGACACATCGAAGTGCAGATTTTAAACAAT 1560  
QY 1549 ACAATATATTAGATAAAATCACTCAATTCGGGCGGTAAATGTTGGATTAATTTACCG 1608  
DB 1561 ACAATATATTAGATAAAATCACTCAATTCGGGCGGTAAATGTTGGATTAATTTACCG 1620  
QY 1609 TTTGTTCCAGTGTAAAGACACAGGACATACAGAGGGGATTTTATACAGTATAATAGA 1668  
DB 1621 TTTGTTCCAGTGTAAAGACACAGGACATACAGAGGGGATTTTATACAGTATAATAGA 1680  
QY 1669 AGTACTGGTCTGTAGGAACCTTATTTCTAGCTCGATATGGCTAGCAATTTAGAAAAAGCA 1728  
DB 1681 AGTACTGGTCTGTAGGAACCTTATTTCTAGCTCGATATGGCTAGCAATTTAGAAAAAGCA 1740  
QY 1729 GCGAAATATCGTGTAGCACTGAGATATGCTACTGATGCAGATATTGTATGCAATGAAC 1788  
DB 1741 GCGAAATATCGTGTAGCACTGAGATATGCTACTGATGCAGATATTGTATGCAATGAAC 1800  
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DB 1801 GATGCTCAGATTCAGATGCGCAAAACAAATGAACCCAGCTGAGGATCTGACATCTAAACT 1860  
QY 1849 TTTAAAGTTGCGATGCTATCAACAACATTAATTTAGCAACAGATAGTTCGCTAGCATTG 1908  
DB 1861 TTTAAAGTTGCGATGCTATCAACAACATTAATTTAGCAACAGATAGTTCGCTAGCATTG 1920  
QY 1909 AATCAATATTTAGGTGAGACCCCTAATTTCAACATTTCTGGTATAGTTAGTTGACCGA 1968  
DB 1921 AATCAATATTTAGGTGAGACCCCTAATTTCAACATTTCTGGTATAGTTAGTTGACCGA 1980  
QY 1969 ATCGAATTCATCCAGTAGATGAGACATATGAGCGGAACAA 2010  
DB 1981 ATCGAATTCATCCAGTAGATGAGACATATGAGCGGAATAA 2022

## RESULT 10

US-10-032-717-39  
; Sequence 39, Application US/10032717  
; Patent No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins with  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; PRIORITY FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIORITY FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 39  
; LENGTH: 2022  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis (mutated)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2022)  
; NAME/KEY: misc\_feature

; LOCATION: (0)...(0)  
; OTHER INFORMATION: LRNS.N1218-1  
US-10-032-717-39

Query Match 54.9%; Score 1986.4; DB 12; Length 2022;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 2009; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY 1 ATGAGTCCAAATTAATCAAAATGAATATGAATATAGATGCGACACCTTCTACTTCTGTA 60  
DB 1 ATGAGTCCAAATTAATCAAAATGAATATGAATATAGATGCGACACCTTCTACTTCTGTA 60  
QY 61 TCAATGATTTCAACAGATACCTTTTGGCAATGAGCCAAACAAATGCGGTACAAAATATG 120  
DB 61 TCAATGATTTCAACAGATACCTTTTGGCAATGAGCCAAACAAATGCGGTACAAAATATG 120  
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DB 121 GATTATAAGATTTATTTAAATATGCTGCGGGAAATGCTAGTAGAATACCTGCTCACCT 180  
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DB 181 GAAGTACTTTGTAGCGGACAAAGATGAGCTAAGCGCGCAATGATATAGTAGTAAATTA 240  
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DB 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTAGTCTTTTATCTCAACTTATT 300  
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DB 301 GATATTTCTGGGCTTCAGGGGAAAGAGTCAATGCGAAATTTTATGAAACAGTAGAA 360  
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DB 361 GAACCTCATTTAATCAAAATATGAGCAATATGCAAGGAATAAAGCGCTTCGGAAATTAGAA 420  
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DB 601 CTCTAGTATATGCAATGCGACCAACCTTCAATTTACTGTTATTAAGGACGCGTCAATTT 660  
QY 649 TTTGGAGAAATGGGGATGGTCAACAACTACTATTAACTATTATGATCGTCAATG 708  
DB 661 TTTGGAGAAATGGGGATGGTCAACAACTACTATTAACTATTATGATCGTCAATG 720  
QY 709 AAATTTACTGCAAGATATTCTGATCACTCTGTGTAAAGTGTATGAACTGTTTAGCAAAA 768  
DB 721 AAATTTACTGCAAGATATTCTGATCACTCTGTGTAAAGTGTATGAACTGTTTAGCAAAA 780  
QY 769 TTAAGAGGACGAGCGCTAAACAAATGGGTTGACTATAACCAATTTCCGTAGAGAAATGACA 828  
DB 781 TTAAGAGGACGAGCGCTAAACAAATGGGTTGACTATAACCAATTTCCGTAGAGAAATGACA 840  
QY 829 CTGGCGGTTTATAGATGTTGTTGCAATTTATCCCAATTTATGACACGACGACCCCAATG 888  
DB 841 CTGGCGGTTTATAGATGTTGTTGCAATTTATCCCAATTTATGACACGACGACCCCAATG 900  
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DB 901 GAAACGAAAGCACTCAACAGGGAAGTATATACAGATCCACTGGCGCGGTAAACGTTG 960  
QY 949 TCTTCAATTTGGTTCTGTTGATGACAAAGCAACCTTCTTTTGGAGTGTATAGAAATCATCCGTT 1008

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Db 961 TCCTCAATGGTCTCGTATGACAAAGCACCTTCTTCGGAGTGAGTAATCATCGGTT 1020
Qy 1009 ATTCGACACCCCAATGATTTGATATATTAACGGGACTCAAGTGTATACAAATCAAGA 1068
Db 1021 ATTCGACACCCCAATGATTTGATATATTAACGGGACTCAAGTGTATACAAATCAAGA 1080
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Db 1081 AGCAATTTCTCCGCTCGTATATGAACATTTGGGCTGTCTATCAAAATGAAGTACCATCGT 1140
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Db 1141 GTCAAGTGGGAGTATATCTTCAACAAATGATGGAACATAATCAAAATCTACACGACCT 1200
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Qy 1249 CTTGATATTTGTTTACCTCGTATATGATATATTTTGGAAATGCCAAGATCGAGTTT 1308
Db 1261 CTTGATATTTGTTTACCTCGTATATGATATATTTTGGAAATGCCAAGATCGAGTTT 1320
Qy 1309 TTCAATGTTAAACCAATTAATTAACCAAGAAAGCGTTTAAAGTATATATPCCAGTTTCCAAA 1368
Db 1321 TTCAATGTTAAACCAATTAATTAACCAAGAAAGCGTTTAAAGTATATATPCCAGTTTCCAAA 1380
Qy 1369 GATATATAGGAGTACAAAGATTCGGAATTAGAATTTACCTCCAGAACTTCAGATCAA 1428
Db 1381 GATATATAGGAGTACAAAGATTCGGAATTAGAATTTACCTCCAGAACTTCAGATCAA 1440
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Qy 1729 GGGAAATATCGTGAAGACTGAGATATGCTACTGATGAGATATTTGATTTGATGTAATAC 1788
Db 1741 GGGAAATATCGTGAAGACTGAGATATGCTACTGATGAGATATTTGATTTGATGTAATAC 1800
Qy 1789 GATGCTCAGATTCAGATCCCAAAACATGACCCAGGTGAGGATCTGACATCTAAACT 1848
Db 1801 GATGCTCAGATTCAGATCCCAAAACATGACCCAGGTGAGGATCTGACATCTAAACT 1860
Qy 1849 TTTAAAGTTGAGATGCTATACAAACATTTAAATTTAGCAACAGATAGTTTCGTCAGATTTG 1908
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Qy 1909 AAACATAATTTAGGTGAAGACCTTAATCAACATTTATCTGGTATAGTTTACGTTGACCGA 1968
Db 1921 AAACATAATTTAGGTGAAGACCTTAATCAACATTTATCTGGTATAGTTTACGTTGACCGA 1980
Qy 1969 ATCGAATTCATCCAGTAGATGAGACATATGAGCGGACAA 2010
Db 1981 ATCGAATTCATCCAGTAGATGAGACATATGAGCGGACAA 2022
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RESULT 11

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US-10-032-717-43
; Sequence 43, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2013)
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: LRMS.R1218-1
US-10-032-717-43
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Query Match 54.8%; Score 1985.8; DB 12; Length 2013;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2003; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

Qy 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATGCGACACCTTCTTCTCTGTA 60
Db 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATGCGACACCTTCTTCTCTGTA 60
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Db 61 TCCAAATGATTTCAAGATACCCCTTTTGGCAATGAGCGCAACAAATGCGCTACAAAATATG 120
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Db 121 GATTTATAAGATTTATTTAAATAATGCTCGCGGAAATCTAGTGAATACCTGGTTCCACT 180
Qy 181 GAAGTACTTGTAGCGGACAAAGATGCAAGCTAAGGCCCGCAATTTGATATAGTAGGTAATTA 240
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Db 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTAGTCTTTTATCTCAACTTATT 300
Qy 301 GATATTCTGTGGCCTTCAGGSGAAAGAGTCAATGGGAAATTTTATGGCAACAGTAGAA 360
Db 301 GATATTCTGTGGCCTTCAGGSGAAAGAGTCAATGGGAAATTTTATGGCAACAGTAGAA 360
Qy 361 GAATCTATTATCAAAATAATAGCAGAAATATGCAAGGAATTAAGCGCTTTCGGAATTAGAA 420
Db 361 GAATCTATTATCAAAATAATAGCAGAAATATGCAAGGAATTAAGCGCTTTCGGAATTAGAA 420
Qy 421 GGATTAGTATAATTAACCAATTTATCTAACTCGGCTTGAAGATGGGAAGAAATCC- 479
Db 421 GGATTAGTATAATTAACCAATTTATCTAACTCGGCTTGAAGATGGGAAGAAATCC 480
Qy 480 --AAATGGTTCAAGGCTTACGAGATGTCGAAATCGATTTGAATTCCTGGATAGTTTA 537
Db 481 TTAAGAAATGCTAGAGCCTTACGAGATGTCGAAATCGATTTGAATTCCTGGATAGTTTA 540
Qy 538 TTTACGCAATATATGCCATCTTTTAGAGTGAACAAATTTTGAAGTACCAATTCCTTACTGTA 597
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QY 598 TATGCAATGCGAGCAACCTTCAITTTACTGTTATTAAGAGACGGGTCAAATTTTGGAGAA 657
Db 601 TATGCAATGCGAGCAACCTTCAITTTACTGTTATTAAGAGACGGGTCAAATTTTGGAGAA 660
QY 658 GAATGGGATGGTCAACACTATATTAATAAATTAATTAAGTATGATCGTCAAACTTACT 717
Db 661 GAATGGGATGGTCAACACTATATTAATAAATTAATTAAGTATGATCGTCAAACTTACT 720
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Db 721 GCAGATATTTCTGATCACTGTTAAAGTGTATGAAACTGGTTTACGAAATTAAGGC 780
QY 778 ACAGAGCGCTAAACAATGGGTTGACTATAAACAATTCGGTAGAGAAATGACACTGGCGGTT 837
Db 781 ACAGAGCGCTAAACAATGGGTTGACTATAAACAATTCGGTAGAGAAATGACACTGGCGGTT 840
QY 838 TTAGATGTTGTTGATATTTCCCAATATTAAGACACGCGTACCAATGGAAACGAAA 897
Db 841 TTAGATGTTGTTGATATTTCCCAATATTAAGACACGCGTACCAATGGAAACGAAA 900
QY 898 GCACAACTAACAGGAGATATATACAGATCCACTGGCGGGTAAACGTGCTTCAATT 957
Db 901 GCACAACTAACAGGAGATATATACAGATCCACTGGCGGGTAAACGTGCTTCAATT 960
QY 958 GGTTCCTGTTATGACAAAGCACCTTCTTTCGGAGTATAGAACTCATCGTTATTTCGACCA 1017
Db 961 GGTTCCTGTTATGACAAAGCACCTTCTTTCGGAGTATAGAACTCATCGTTATTTCGACCA 1020
QY 1018 CCCATGTTATTTGATATATAACGGGACTCACAGTGTATACAAATCAAGAAGCATTTCT 1077
Db 1021 CCCATGTTATTTGATATATAACGGGACTCACAGTGTATACAAATCAAGAAGCATTTCT 1080
QY 1078 TCCGCTCGCTATATAGACATTTGGCTGTCTCAATATAGCTTACCACTCTGTCTAGG 1137
Db 1081 TCCGCTCGCTATATAGACATTTGGCTGTCTCAATATAGCTTACCACTCTGTCTAGG 1140
QY 1138 GGTAGTAATCTTCAACAAATGTTAGAACTAATCAAAATCTACACAGCACTAGTACCTTT 1197
Db 1141 GGTAGTAATCTTCAACAAATGTTAGAACTAATCAAAATCTACACAGCACTAGTACCTTT 1200
QY 1198 GATTTTACGAATTTAGATATTAACAGACTCTATCAAGAGTACGACTCTCTTGTATTT 1257
Db 1201 GATTTTACGAATTTAGATATTAACAGACTCTATCAAGAGTACGACTCTCTTGTATTT 1260
QY 1258 GTTTACCTCGTTATACGTATATATTTTGGATGCCAGAGTCCAGTTTTCATGGTA 1317
Db 1261 GTTTACCTCGTTATACGTATATATTTTGGATGCCAGAGTCCAGTTTTCATGGTA 1320
QY 1318 AACCAATTTGAATTAATACCAAGAAAGCGTTAAAGTATATTAATCCAGTTTCCAAAGATATTATA 1377
Db 1321 AACCAATTTGAATTAATACCAAGAAAGCGTTAAAGTATATTAATCCAGTTTCCAAAGATATTATA 1380
QY 1378 GCGAGTACAGAGATTCGGAATTTAGAAATTAACCTCCAGAACTTTAGATCAACCAAAATAT 1437
Db 1381 GCGAGTACAGAGATTCGGAATTTAGAAATTAACCTCCAGAACTTTAGATCAACCAAAATAT 1440
QY 1438 GAGTCATATAGCCATAGATATGTCATATACAAAGTATTCGCGGAGCGGTAACTACCC 1497
Db 1441 GAGTCATATAGCCATAGATATGTCATATACAAAGTATTCGCGGAGCGGTAACTACCC 1500
QY 1498 GGATTTAGTACCTGTTATTTCTTGGACACATCGAAGTGCAGATTTAAACAATACAAATATAT 1557
Db 1501 GGATTTAGTACCTGTTATTTCTTGGACACATCGAAGTGCAGATTTAAACAATACAAATATAT 1560
QY 1558 TCAGATAAAATCACTCAAAATTCGCGCGGTTAAATGTTGGGATTAATTAACGTTTGTTC 1617
Db 1561 TCAGATAAAATCACTCAAAATTCGCGCGGTTAAATGTTGGGATTAATTAACGTTTGTTC 1620
QY 1618 GTGGTAAAGGACACAGACATACAGAGGGGATTTATTAAGTATTAAGAGTACTGGT 1677
Db 1621 GTGGTAAAGGACACAGACATACAGAGGGGATTTATTAAGTATTAAGAGTACTGGT 1680
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QY 1678 TCTGTAGGAACCTTTATTTCTAGCTCGATATGGCTTAGCATTTAGAAAAGCAGGGAATAT 1737
Db 1681 TCTGTAGGAACCTTTATTTCTAGCTCGATATGGCTTAGCATTTAGAAAAGCAGGGAATAT 1740
QY 1738 CGTGTAAAGTCTGAGATATGCTACTGATGACAGATATTTGTTATGATGTAACGATGCTCAG 1797
Db 1741 CGTGTAAAGTCTGAGATATGCTACTGATGACAGATATTTGTTATGATGTAACGATGCTCAG 1800
QY 1798 ATTCAAGTCCCAAAAACAATGAACCCAGGTGAGGATCTGACATCTAAACTTTTAAAGTT 1857
Db 1801 ATTCAAGTCCCAAAAACAATGAACCCAGGTGAGGATCTGACATCTAAACTTTTAAAGTT 1860
QY 1858 GCAGATGCTTATCAACATTTAAATTTAGCAACAGATAGTTTCGCTAGCATTTGAAACATAT 1917
Db 1861 GCAGATGCTTATCAACATTTAAATTTAGCAACAGATAGTTTCGCTAGCATTTGAAACATAT 1920
QY 1918 TTAGGTGAAGACCTTAATTTCAACATTTATCTGTTATAGTTTACGTTGACCGAATCGAATTC 1977
Db 1921 TTAGGTGAAGACCTTAATTTCAACATTTATCTGTTATAGTTTACGTTGACCGAATCGAATTC 1980
QY 1978 ATCCCAAGTATGAGACATATGAGCGGAACAA 2010
Db 1981 ATCCCAAGTATGAGACATATGAGCGGAATAA 2013
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## RESULT 12

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US-10-032-717-19
; Sequence 19, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins with
; PESTICIDAL ACTIVITY AGAINST COLEOPTERANS
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; TYPE: DNA
; LENGTH: 1860
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)...(1860)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 49PVD
US-10-032-717-19
```

Query Match 51.0%; Score 1848.4; DB 12; Length 1860;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1849; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 142 ATGCTCGCGGAAATGCTAGTGAATACCCCTGCTACCTGCTGAACTAGTCTTGTAGCGGACAA 201
Db 10 ATGCTCGCGGAAATGCTAGTGAATACCCCTGCTGAACTAGTCTTGTAGCGGACAA 69
QY 202 GATGCAAGCTAAAGCCCAATTTGATATAGTAGTAAATTAATCACTCAGGTTTAGGGGTCCCA 261
Db 70 GATGCAAGCTAAAGCCCAATTTGATATAGTAGTAAATTAATCACTCAGGTTTAGGGGTCCCA 129
QY 262 TTTGTTGGCCGAGTAGTGTCTTTTATCTACTCAACTTATTTGATATTTCTGTCGCTTCAGGG 321
Db 130 TTTGTTGGCCGAGTAGTGTCTTTTATCTACTCAACTTATTTGATATTTCTGTCGCTTCAGGG 189
```

|    |      |   |      |
|----|------|---|------|
| Qy | 322  | GAAAAGAGTCAATGGGAAATTTTATGGAACAAGTAGAAGAACTCATTTAATCAAAAAATA      | 381  |
|    |      |   |      |
|    |      |   |      |
| Db | 190  | GAAAAGAGTCAATGGGAAATTTTATGGAACAAGTAGAAGAACTCATTTAATCAAAAAATA      | 249  |
|    |      |   |      |
| Qy | 382  | GCAGATATGCAAGGAATTAAGCGCTTTCGGGAATTTAGAGGAGTTAGGTAAATAATTACCAA    | 441  |
|    |      |   |      |
| Db | 250  | GCAGATATGCAAGGAATTAAGCGCTTTCGGGAATTTAGAGGAGTTAGGTAAATAATTACCAA    | 309  |
|    |      |   |      |
| Qy | 442  | TTATATCTAACTCGCGCTTGGAAGATGGGAAGAAAAATCCAAATGGTTCAGAGCCCTTACGA    | 501  |
|    |      |   |      |
| Db | 310  | TTATATCTAACTCGCGCTTGGAAGATGGGAAGAAAAATCCAAATGGTTCAGAGCCCTTACGA    | 369  |
|    |      |   |      |
| Qy | 502  | GATGTGCGAAATCGATTTGAAATCCTGGGATAGTTTATTCGCAATATATGCCATCTTTT       | 561  |
|    |      |   |      |
| Db | 370  | GATGTGCGAAATCGATTTGAAATCCTGGGATAGTTTATTCGCAATATATGCCATCTTTT       | 429  |
|    |      |   |      |
| Qy | 562  | AGAGTGACAAATTTTGAAGTACCATTCCCTTACTGTATATGCAATGGCAGCCAACTCTCAT     | 621  |
|    |      |   |      |
| Db | 430  | AGAGTGACAAATTTTGAAGTACCATTCCCTTACTGTATATGCAATGGCAGCCAACTCTCAT     | 489  |
|    |      |   |      |
| Qy | 622  | TTACTGTATTATAAGGACGCGTCAATTTTGGAGGAAGATGGGGATGGTCAACAACACTACT     | 681  |
|    |      |   |      |
| Db | 490  | TTACTGTATTATAAGGACGCGTCAATTTTGGAGGAAGATGGGGATGGTCAACAACACTACT     | 549  |
|    |      |   |      |
| Qy | 682  | ATTTAATAACTATTATGATCGTCAAAATGAAACTTACTGCGAAGATATTTCTGATCAGTGTGA   | 741  |
|    |      |   |      |
| Db | 550  | ATTTAATAACTATTATGATCGTCAAAATGAAACTTACTGCGAAGATATTTCTGATCAGTGTGA   | 609  |
|    |      |   |      |
| Qy | 742  | AAGTGGTATCAAACTGGTTTATAGCAAAATTTAAAGGACGAGCGCTTAAACAATGGGTTGAC    | 801  |
|    |      |   |      |
| Db | 610  | AAGTGGTATCAAACTGGTTTATAGCAAAATTTAAAGGACGAGCGCTTAAACAATGGGTTGAC    | 669  |
|    |      |   |      |
| Qy | 802  | TATAACCAATTCGCTAGAGAAATGACACTGGCGGTTTATAGATGTTGTGTCATTAATCCCA     | 861  |
|    |      |   |      |
| Db | 670  | TATAACCAATTCGCTAGAGAAATGACACTGGCGGTTTATAGATGTTGTGTCATTAATCCCA     | 729  |
|    |      |   |      |
| Qy | 862  | AATATGACACACGACGTACCAATGGAAACGAAAGCAACTAACGAAGGAAGTATAT           | 921  |
|    |      |   |      |
| Db | 730  | AATATGACACACGACGTACCAATGGAAACGAAAGCAACTAACGAAGGAAGTATAT           | 789  |
|    |      |   |      |
| Qy | 922  | ACAGATCCACTGGCGCGGTAAACGCTGCTTCAATTTGGTTCCTGGGTATGACAAAGACACCT    | 981  |
|    |      |   |      |
| Db | 790  | ACAGATCCACTGGCGCGGTAAACGCTGCTTCAATTTGGTTCCTGGGTATGACAAAGACACCT    | 849  |
|    |      |   |      |
| Qy | 982  | TCCTTCGAGTGATAGAATCATCCGTTATTCGACACACCCCATGTAATTTGATATATAACG      | 1041 |
|    |      |   |      |
| Db | 850  | TCCTTCGAGTGATAGAATCATCCGTTATTCGACACACCCCATGTAATTTGATATATAACG      | 909  |
|    |      |   |      |
| Qy | 1042 | GGACTCAGCTGTATACAAATCAAGAAGCATTTCTTCGCTCGCTATATAAGACATTTGG        | 1101 |
|    |      |   |      |
| Db | 910  | GGACTCAGCTGTATACAAATCAAGAAGCATTTCTTCGCTCGCTATATAAGACATTTGG        | 969  |
|    |      |   |      |
| Qy | 1102 | GCTGGTCAATCAAAATTAAGCTACCACTCGTGTCACTAGGGGTAGTAACTCTTCAACAAATGTAT | 1161 |
|    |      |   |      |
| Db | 970  | GCTGGTCAATCAAAATTAAGCTACCACTCGTGTCACTAGGGGTAGTAACTCTTCAACAAATGTAT | 1029 |
|    |      |   |      |
| Qy | 1162 | GGAACTAAATCAAAATCTACACAGCACTAGTACTTTGATTTTTCGAAATATGATATTTAC      | 1221 |
|    |      |   |      |
| Db | 1030 | GGAACTAAATCAAAATCTACACAGCACTAGTACTTTGATTTTTCGAAATATGATATTTAC      | 1089 |
|    |      |   |      |
| Qy | 1222 | ARGACTCTATCAAGGATGAGTACTTCTTGATATTTGTTTACCTGGTGTATACGTATATA       | 1281 |
|    |      |   |      |
| Db | 1090 | ARGACTCTATCAAGGATGAGTACTTCTTGATATTTGTTTACCTGGTGTATACGTATATA       | 1149 |
|    |      |   |      |
| Qy | 1282 | TTTTTTTGGAAATGCCAAGTCGAGTTTTTTCATGGTAAACCAATTCGAAATAACACGAAGA     | 1341 |
|    |      |   |      |
| Db | 1150 | TTTTTTTGGAAATGCCAAGTCGAGTTTTTTCATGGTAAACCAATTCGAAATAACACGAAGA     | 1209 |
|    |      |   |      |
| Qy | 1342 | ACGTTAAAGTATAATCAAGTTTCCAAAGATATATATAGCGAGTACAAAGAGATTCGGAATTA    | 1401 |
|    |      |   |      |
| Db | 1210 | ACGTTAAAGTATAATCAAGTTTCCAAAGATATATATAGCGAGTACAAAGAGATTCGGAATTA    | 1269 |

|    |      |  |      |
|----|------|--|------|
| Qy | 1402 | GAATACCTCCAGAACTTCAGATCAACCAAAATTAAGTGCATATATAGCCATAGATTATGT       | 1461 |
| Db | 1270 | GAATACCTCCAGAACTTCAGATCAACCAAAATTAAGTGCATATATAGCCATAGATTATGT       | 1329 |
| Qy | 1462 | CATATACAAGTAGTATCCCGCGACGGTAACACTACCGAATTTAGTACCTGTATTTTCTTGG      | 1521 |
| Db | 1330 | CATATACAAGTAGTATCCCGCGACGGTAACACTACCGAATTTAGTACCTGTATTTTCTTGG      | 1389 |
| Qy | 1522 | ACACATCGAAGTCGAGATTTAAACAATACAATATATTCAGATAAAATCACTCAAATTCGG       | 1581 |
| Db | 1390 | ACACATCGAAGTCGAGATTTAAACAATACAATATATTCAGATAAAATCACTCAAATTCGG       | 1449 |
| Qy | 1582 | GCCGTTAAATGTGGGATAATTTACGGTTTGTTCAGTGGTAAAGGACCAAGGCATACA          | 1641 |
| Db | 1450 | GCCGTTAAATGTGGGATAATTTACGGTTTGTTCAGTGGTAAAGGACCAAGGCATACA          | 1509 |
| Qy | 1642 | GGAGGGGATTTATTACAGTATAATAGNAGTACTGTGTTCTGTAGGAACCTTATTTCTAGCT      | 1701 |
| Db | 1510 | GGAGGGGATTTATTACAGTATAATAGNAGTACTGTGTTCTGTAGGAACCTTATTTCTAGCT      | 1569 |
| Qy | 1702 | CGATATGGCCTAGCATTTAGAAAAAGCAGGGAATAATCGTGTAGAAGCTGAGATATGCTACT     | 1761 |
| Db | 1570 | CGATATGGCCTAGCATTTAGAAAAAGCAGGGAATAATCGTGTAGAAGCTGAGATATGCTACT     | 1629 |
| Qy | 1762 | GATGCGAGATTTGTTATGTCATGTAAACGATGCTCAGATTCAGATGCCAAAAACAATGAAC      | 1821 |
| Db | 1630 | GATGCGAGATTTGTTATGTCATGTAAACGATGCTCAGATTCAGATGCCAAAAACAATGAAC      | 1689 |
| Qy | 1822 | CCAGTGGAGGATCTGACATCTAAACTTTTAAAGTTGCAGATGCTATCACAACAATTAAT        | 1881 |
| Db | 1690 | CCAGTGGAGGATCTGACATCTAAACTTTTAAAGTTGCAGATGCTATCACAACAATTAAT        | 1749 |
| Qy | 1882 | TTAGCAACAGATAGTTTCGCTAGCATTTGAAACAATAATTTTAGGTGAAGACCCCTAAATTCACCA | 1941 |
| Db | 1750 | TTAGCAACAGATAGTTTCGCTAGCATTTGAAACAATAATTTTAGGTGAAGACCCCTAAATTCACCA | 1809 |
| Qy | 1942 | TTATCTGGTATAGTTTACGTTTGACCGAATCGAAATTCATCCCGAGTAGATGA              | 1991 |
| Db | 1810 | TTATCTGGTATAGTTTACGTTTGACCGAATCGAAATTCATCCCGAGTAGATTA              | 1859 |

RESULT 13  
US-10-032-717-33



Query Match 50.5%; Score 1827.4; DB 12; Length 1854;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1844; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

|    |      |   |      |
|----|------|---|------|
| QY | 142  | ATGCTCTGCGGGAATGCTAGTGAATACCCCTGGTTCACCTGAAGTACTTGTAGCGGCA      | 201  |
| DB | 1    | ATGCTCTGCGGGAATGCTAGTGAATACCCCTGGTTCACCTGAAGTACTTGTAGCGGCA      | 60   |
| QY | 202  | GATGCACTAAGCGCGCAATTTGATATAGTATAGTAAATTTACTATCAGGTTTAGGGTCCCA   | 261  |
| DB | 61   | GATGCACTAAGCGCGCAATTTGATATAGTATAGTAAATTTACTATCAGGTTTAGGGTCCCA   | 120  |
| QY | 262  | TTTGTGCGGCGGATAGTGAATCTTTTATACCTCAACTTATGATATCTGTGGCCCTTCAGGG   | 321  |
| DB | 121  | TTTGTGCGGCGGATAGTGAATCTTTTATACCTCAACTTATGATATCTGTGGCCCTTCAGGG   | 180  |
| QY | 322  | GAAGAAGTCAATGGGGAATTTTATGGAACAGTAGAAGACTCATTAATCAAAAATA         | 381  |
| DB | 181  | GAAGAAGTCAATGGGGAATTTTATGGAACAGTAGAAGACTCATTAATCAAAAATA         | 240  |
| QY | 382  | GCAGAATATCAAGGAATAAAGCGCTTTCGGAATTAGAAGATTAGGTAAATTAACCAA       | 441  |
| DB | 241  | GCAGAATATCAAGGAATAAAGCGCTTTCGGAATTAGAAGATTAGGTAAATTAACCAA       | 300  |
| QY | 442  | TTATATCTAACTCGCTTGAAGATGGAAGAAATCC---AAATGGTTCAAGAGCCTTA        | 498  |
| DB | 301  | TTATATCTAACTCGCTTGAAGATGGAAGAAATCC---AAATGGTTCAAGAGCCTTA        | 360  |
| QY | 499  | CGAGATGTGCGGAATCGAATTTGAAATCCTGGATAGTTTATTTAGCGAATATATGCCATCT   | 558  |
| DB | 361  | CGAGATGTGCGGAATCGAATTTGAAATCCTGGATAGTTTATTTAGCGAATATATGCCATCT   | 420  |
| QY | 559  | TTTATAGTATCAAAATTTGAAGTACCAATCTCTACTGTATATGCAATGGCGCAACCTT      | 618  |
| DB | 421  | TTTATAGTATCAAAATTTGAAGTACCAATCTCTACTGTATATGCAATGGCGCAACCTT      | 480  |
| QY | 619  | CAATTTACTGTTATTAAGGACGCGTCAATTTTGGAGAAGATGGGATGGTCAACAAT        | 678  |
| DB | 481  | CAATTTACTGTTATTAAGGACGCGTCAATTTTGGAGAAGATGGGATGGTCAACAAT        | 540  |
| QY | 679  | ACTATTAATTAACCTATTAATGATCGTCAAAATGAACCTTACTGCAAGATATCTGATCACTGT | 738  |
| DB | 541  | ACTATTAATTAACCTATTAATGATCGTCAAAATGAACCTTACTGCAAGATATCTGATCACTGT | 600  |
| QY | 739  | GTAAAGTGGTATGAAATCTGGTTAGCAAAATTAAGAGCGACGCGCTAAACAAATGGT       | 798  |
| DB | 601  | GTAAAGTGGTATGAAATCTGGTTAGCAAAATTAAGAGCGACGCGCTAAACAAATGGT       | 660  |
| QY | 799  | GACTATAACCAATTCGGTAGAGAAATGACACTGGCGGTTTATGATGTTTGTGCAATTATC    | 858  |
| DB | 661  | GACTATAACCAATTCGGTAGAGAAATGACACTGGCGGTTTATGATGTTTGTGCAATTATC    | 720  |
| QY | 859  | CCAATTTATGACACGACGCTACCCATGGAACGAAAGCAACACTAACAGGGAAGTA         | 918  |
| DB | 721  | CCAATTTATGACACGACGCTACCCATGGAACGAAAGCAACACTAACAGGGAAGTA         | 780  |
| QY | 919  | TATACAGATCCACTGGCGCGGTAAAGTGTCTTCAATTTGGTTCTCGTATGACAAAGCA      | 978  |
| DB | 781  | TATACAGATCCACTGGCGCGGTAAAGTGTCTTCAATTTGGTTCTCGTATGACAAAGCA      | 840  |
| QY | 979  | CTTCTTTTGGAGTATAGAAATCATCGGTTATTCGACACCCCATGTTATTTGATATATA      | 1038 |
| DB | 841  | CTTCTTTTGGAGTATAGAAATCATCGGTTATTCGACACCCCATGTTATTTGATATATA      | 900  |
| QY | 1039 | ACGGACTCAAGTGTATACAAATCAAGAGCAATTTCTCCGCTCGCTATATAAGACAT        | 1098 |
| DB | 901  | ACGGACTCAAGTGTATACAAATCAAGAGCAATTTCTCCGCTCGCTATATAAGACAT        | 960  |
| QY | 1099 | TGGGCTGGTCAATCAATTAAGTACCATCGTCTAGTAGGGGTAGTATCTTCAACAATG       | 1158 |
| DB | 961  | TGGGCTGGTCAATCAATTAAGTACCATCGTCTAGTAGGGGTAGTATCTTCAACAATG       | 1020 |
| QY | 1159 | TATGGAACCTAATCAAAATCTACACGCACTAGTACCTTTTGATTTTACGAATTTATGATATT  | 1218 |

|    |      |   |      |
|----|------|---|------|
| DB | 1021 | TATGGAACCTAATCAAAATCTACACGCACTAGTACCTTTGATTTTACGAATTTATGATATT   | 1080 |
| QY | 1219 | TACAGACTCTATCAAGAGTACGAGTACTCCTTGATATTGTTTACCTGGTTATAGTAT       | 1278 |
| DB | 1081 | TACAGACTCTATCAAGAGTACGAGTACTCCTTGATATTGTTTACCTGGTTATAGTAT       | 1140 |
| QY | 1279 | ATATTTTGGGAATGCGAGAAGTCGAGTCTTTTTCATGGTAAACCAATTTGAATATACAGA    | 1338 |
| DB | 1141 | ATATTTTGGGAATGCGAGAAGTCGAGTCTTTTTCATGGTAAACCAATTTGAATATACAGA    | 1200 |
| QY | 1339 | AGACGTTTAAAGTATTAATCCAGTTTCCAAAGATATTTATAGCGAGTACAAGAGATTCCGAA  | 1398 |
| DB | 1201 | AGACGTTTAAAGTATTAATCCAGTTTCCAAAGATATTTATAGCGAGTACAAGAGATTCCGAA  | 1260 |
| QY | 1399 | TTAGATTAACCTCCAGAAACTTCAGATCAACCAAAATTTATGAGTCATATAGCCATAGATTA  | 1458 |
| DB | 1261 | TTAGATTAACCTCCAGAAACTTCAGATCAACCAAAATTTATGAGTCATATAGCCATAGATTA  | 1320 |
| QY | 1459 | TGTCATATCACAAGTATTTCCCGCGACGGGTAACACTTACCGGATTAGTACTGTATTTTCT   | 1518 |
| DB | 1321 | TGTCATATCACAAGTATTTCCCGCGACGGGTAACACTTACCGGATTAGTACTGTATTTTCT   | 1380 |
| QY | 1519 | TGACACATCGAAGTGCAGATTTTAAACAATAACAATATTTTCAGATAAAATCACTCAAAAT   | 1578 |
| DB | 1381 | TGACACATCGAAGTGCAGATTTTAAACAATAACAATATTTTCAGATAAAATCACTCAAAAT   | 1440 |
| QY | 1579 | CGGCGGTTAAATTTGGGATTAATTTACCGTTTGTTCAGTGGTAAAGGACCGAGCAT        | 1638 |
| DB | 1441 | CGGCGGTTAAATTTGGGATTAATTTACCGTTTGTTCAGTGGTAAAGGACCGAGCAT        | 1500 |
| QY | 1639 | ACAGGAGGGGATTTTATACAGTATATAGAGTACTTGGTTCTGTAGGAACCTTATTTCTA     | 1698 |
| DB | 1501 | ACAGGAGGGGATTTTATACAGTATATAGAGTACTTGGTTCTGTAGGAACCTTATTTCTA     | 1560 |
| QY | 1699 | GCTCGATATGGCTAGCATTAGAAAAAGCAGGGAATATCGTGTAAAGCTGAGATATGCT      | 1758 |
| DB | 1561 | GCTCGATATGGCTAGCATTAGAAAAAGCAGGGAATATCGTGTAAAGCTGAGATATGCT      | 1620 |
| QY | 1759 | ACTGATGCAAGTATTTGATTTGATGCTTAAAGCATGCTCAGATTCAGATCCCAAAACAATG   | 1818 |
| DB | 1621 | ACTGATGCAAGTATTTGATTTGATGCTTAAAGCATGCTCAGATTCAGATCCCAAAACAATG   | 1680 |
| QY | 1819 | AACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCGAGATGCTATCAACAATTA    | 1878 |
| DB | 1681 | AACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCGAGATGCTATCAACAATTA    | 1740 |
| QY | 1879 | AATTTAGCAACAGATAGTTCGCTAGCAATTTGAAACATAAATTTAGGTGAAGACCCCTAATTC | 1938 |
| DB | 1741 | AATTTAGCAACAGATAGTTCGCTAGCAATTTGAAACATAAATTTAGGTGAAGACCCCTAATTC | 1800 |
| QY | 1939 | ACATTTATCTGTATAGTTCAGTTTACGTTGACCGAATCGAATTCATCCCACTAGATGA      | 1991 |
| DB | 1801 | ACATTTATCTGTATAGTTCAGTTTACGTTGACCGAATCGAATTCATCCCACTAGATGA      | 1853 |

RESULT 14

US-10-032-717-29  
; Sequence 29, Application US/10032717  
; Patent No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins with  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838

;; PRIOR FILING DATE: 2000-10-24  
;; NUMBER OF SEQ ID NOS: 48  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 29  
;; LENGTH: 1863  
;; TYPE: DNA  
;; ORGANISM: Bacillus thuringiensis (mutated)  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (1)...(1863)  
;; NAME/KEY: misc\_feature  
;; LOCATION: (0)...(0)  
;; OTHER INFORMATION: NGSF.N49PVD  
US-10-032-717-29

Query Match 50.4%; Score 1826.4; DB 12; Length 1863;

Best Local Similarity 99.3%; Pred. No. 0;  
Matches 1849; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 142 | ATGTCGCGGAAATGCTAGTGAATACCCCTGGTTCACCTGGAAGTACTTGTAGCGGACAA    | 201 |
| Db | 1   | ATGTCGCGGAAATGCTAGTGAATACCCCTGGTTCACCTGGAAGTACTTGTAGCGGACAA    | 60  |
| Qy | 202 | GATCAGCTAAGCGCGCAATTTGATATAGTAGTGAATTAATTAATTAATTAATTAATTAAT   | 261 |
| Db | 61  | GATCAGCTAAGCGCGCAATTTGATATAGTAGTGAATTAATTAATTAATTAATTAATTAAT   | 120 |
| Qy | 262 | TTTGTGGCGCGATAGTGAGTCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT | 321 |
| Db | 121 | TTTGTGGCGCGATAGTGAGTCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT | 180 |
| Qy | 322 | GAAAGAGTCAATCGGAAATTTTATGAAACAAAGTAGAAGAACTCATTAATCAAAAATA     | 381 |
| Db | 181 | GAAAGAGTCAATCGGAAATTTTATGAAACAAAGTAGAAGAACTCATTAATCAAAAATA     | 240 |
| Qy | 382 | GCAGATATGCAAGGAATAAAGCGCTTTCCGAAATTTAGAGGATAGTGAATTAATTAATTAAT | 441 |
| Db | 241 | GCAGATATGCAAGGAATAAAGCGCTTTCCGAAATTTAGAGGATAGTGAATTAATTAATTAAT | 300 |
| Qy | 442 | TTATATCTAACTGCGCTTGAAGATGGAAGAAATCCAAATGTTCAAGA-----           | 492 |
| Db | 301 | TTATATCTAACTGCGCTTGAAGATGGAAGAAATCCAAATGTTCAAGA-----           | 360 |
| Qy | 493 | ---GCCTTACAGATGTCGGAATCGATTTGAAATCCTGGATAGTTTATTAATCAAGCAATAT  | 549 |
| Db | 361 | CGGCGCTTACAGATGTCGGAATCGATTTGAAATCCTGGATAGTTTATTAATCAAGCAATAT  | 420 |
| Qy | 550 | ATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTTCTTACTGTATATGCAATGCCA   | 609 |
| Db | 421 | ATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTTCTTACTGTATATGCAATGCCA   | 480 |
| Qy | 610 | GCCAACTTCAATTTACTGTTATTAAGGACGCGTCAATTTTGGAGAGAAATGGGGATGG     | 669 |
| Db | 481 | GCCAACTTCAATTTACTGTTATTAAGGACGCGTCAATTTTGGAGAGAAATGGGGATGG     | 540 |
| Qy | 670 | TCAACAACTACTATTAACTATTTATGATCGTCAATGAAATTTACTTGCAAGATATTCT     | 729 |
| Db | 541 | TCAACAACTACTATTAACTATTTATGATCGTCAATGAAATTTACTTGCAAGATATTCT     | 600 |
| Qy | 730 | GATCACTGTGTAAGTGTATGAACTGGTTTGTAGCAAAATTTAAAGGACGACGCGCTAAA    | 789 |
| Db | 601 | GATCACTGTGTAAGTGTATGAACTGGTTTGTAGCAAAATTTAAAGGACGACGCGCTAAA    | 660 |
| Qy | 790 | CAATGGGTTGACTATAACCAATTCGTTAGAGAAATGACACTGGCGGTTTATAGTCTGCT    | 849 |
| Db | 661 | CAATGGGTTGACTATAACCAATTCGTTAGAGAAATGACACTGGCGGTTTATAGTCTGCT    | 720 |
| Qy | 850 | GCATTATTTCCAAATTTATGACACGACGACGACGACGACGACGACGACGACGACGACGAC   | 909 |
| Db | 721 | GCATTATTTCCAAATTTATGACACGACGACGACGACGACGACGACGACGACGACGACGAC   | 780 |
| Qy | 910 | AGGGAAGTATATACAGATCCACTGGCGCGGTAAACGTCCTTCAATTTGGTTTCTTGGTAT   | 969 |

|    |      |  |      |
|----|------|--|------|
| Db | 781  | AGGGAAGTATATACAGATCCACTGGCGCGGTAAACGTCCTTCAATTTGGTTTCTTGGTAT       | 840  |
| Qy | 970  | GACAAAGCACCTTCTTTTCGAGTGATAGATCATCCGTTATTCGACCAACCCCATGTATTT       | 1029 |
| Db | 841  | GACAAAGCACCTTCTTTTCGAGTGATAGATCATCCGTTATTCGACCAACCCCATGTATTT       | 900  |
| Qy | 1030 | GATTATATAACGGGACTCACAGTGATACAAATCAAGAAAGCATTTTCTCGCTCGCTAT         | 1089 |
| Db | 901  | GATTATATAACGGGACTCACAGTGATACAAATCAAGAAAGCATTTTCTCGCTCGCTAT         | 960  |
| Qy | 1090 | ATAAGACATTTGGGCTGTCTATCAAAATGAAGTACCATCGTGTAGTGGGGTAGTAATCTT       | 1149 |
| Db | 961  | ATAAGACATTTGGGCTGTCTATCAAAATGAAGTACCATCGTGTAGTGGGGTAGTAATCTT       | 1020 |
| Qy | 1150 | CAACAAATGATGGAATCAAAATCTACACAGCACTAGTACCTTTGATTTTAAACGAAT          | 1209 |
| Db | 1021 | CAACAAATGATGGAATCAAAATCTACACAGCACTAGTACCTTTGATTTTAAACGAAT          | 1080 |
| Qy | 1210 | TATGATATTTTACAGACTCTATCAAAAGGATGCGAGTACTCTCTTGATATTTTACCTGGT       | 1269 |
| Db | 1081 | TATGATATTTTACAGACTCTATCAAAAGGATGCGAGTACTCTCTTGATATTTTACCTGGT       | 1140 |
| Qy | 1270 | TATAGGTATATATTTTGGGATGCCAGAGTGCAGTGTTCATGCTGCTGCTGCTGCTGCTGCT      | 1329 |
| Db | 1141 | TATAGGTATATATTTTGGGATGCCAGAGTGCAGTGTTCATGCTGCTGCTGCTGCTGCTGCT      | 1200 |
| Qy | 1330 | ATAACCAAGAAAGCGTTAAAGTATATCCAGTTTCCAAAGTATTTATAGCGAGTACAAAGA       | 1389 |
| Db | 1201 | ATAACCAAGAAAGCGTTAAAGTATATCCAGTTTCCAAAGTATTTATAGCGAGTACAAAGA       | 1260 |
| Qy | 1390 | GATTTCGGAATTTAGAAATTAACCTCCAGAAATTTCCAGATCAACCAAAATTTATGATCATATAGC | 1449 |
| Db | 1261 | GATTTCGGAATTTAGAAATTAACCTCCAGAAATTTCCAGATCAACCAAAATTTATGATCATATAGC | 1320 |
| Qy | 1450 | CATAGATTTATGTCATATCAAGTATTTCCCGGACGGGTAACTACCGGATAGTACCT           | 1509 |
| Db | 1321 | CATAGATTTATGTCATATCAAGTATTTCCCGGACGGGTAACTACCGGATAGTACCT           | 1380 |
| Qy | 1510 | GTATTTTCTTGGACACATCGAAGTGCAGATTTTAAACAAATCAATATATTCAGATATAAATC     | 1569 |
| Db | 1381 | GTATTTTCTTGGACACATCGAAGTGCAGATTTTAAACAAATCAATATATTCAGATATAAATC     | 1440 |
| Qy | 1570 | ACTCAAAATTTCCGCGGTTAAATGTTGGGATAAATTTACCGTTTGTTCAGTGGTAAAGGA       | 1629 |
| Db | 1441 | ACTCAAAATTTCCGCGGTTAAATGTTGGGATAAATTTACCGTTTGTTCAGTGGTAAAGGA       | 1500 |
| Qy | 1630 | CCAGGACATACAGGAGGGGATTTATTAAGATTAATTAAGAGTACTGTTCTGTAGGAACC        | 1689 |
| Db | 1501 | CCAGGACATACAGGAGGGGATTTATTAAGATTAATTAAGAGTACTGTTCTGTAGGAACC        | 1560 |
| Qy | 1690 | TTATTTCTAGCTCGATATGGCTAGCATTTAGTATGCAATGATAAAGCAGGAAATATCGTGAAGCTG | 1749 |
| Db | 1561 | TTATTTCTAGCTCGATATGGCTAGCATTTAGTATGCAATGATAAAGCAGGAAATATCGTGAAGCTG | 1620 |
| Qy | 1750 | AGATATGCTACTGATGAGATTTGTTATGCAATGATAAAGCAGTCAAGATTCAGATGCCA        | 1809 |
| Db | 1621 | AGATATGCTACTGATGAGATTTGTTATGCAATGATAAAGCAGTCAAGATTCAGATGCCA        | 1680 |
| Qy | 1810 | AAAAAATGAAACCCAGGTGAGGATCTGACATCTTAAATCTTTAAAGTTGCGAGATGCTATC      | 1869 |
| Db | 1681 | AAAAAATGAAACCCAGGTGAGGATCTGACATCTTAAATCTTTAAAGTTGCGAGATGCTATC      | 1740 |
| Qy | 1870 | ACAAATTAATTTAGCAACAGATGTTCCGTAGCATTTGAAACATTAATTTAGGTGAAGAC        | 1929 |
| Db | 1741 | ACAAATTAATTTAGCAACAGATGTTCCGTAGCATTTGAAACATTAATTTAGGTGAAGAC        | 1800 |
| Qy | 1930 | CCTAATTTCAACATTTATCTGGTATAGTTTACGTCACGGAATTCGAATTCATCCCAAGTAGAT    | 1989 |
| Db | 1801 | CCTAATTTCAACATTTATCTGGTATAGTTTACGTCACGGAATTCGAATTCATCCCAAGTAGAT    | 1860 |
| Qy | 1990 | GA 1991  |      |
| Db | 1861 | TA 1862  |      |

RESULT 15  
US-10-032-717-45  
; Sequence 45, Application US/10032717  
; Patent No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Protein With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 1854  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis (mutated).  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1854)  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: LRMS.R49PVD  
US-10-032-717-45

Query Match 50.4%; Score 1825.8; DB 12; Length 1854;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1843; Conservative 0; Mismatches 7; Indels 3; Gaps 1;  
QY 142 ATGCTGCGGGAAATGCTAGTGAATACCTGGTTCACCTGAAGTACTTGTAGCGGACAA 201  
DB 1 ATGCTGCGGGAAATGCTAGTGAATACCTGGTTCACCTGAAGTACTTGTAGCGGACAA 60  
QY 202 GATGAGCTAAGCGCGCAATGATAGTAGTAAATTAATCACTAGGTTTGGGGTCCCA 261  
DB 61 GATGAGCTAAGCGCGCAATGATAGTAGTAAATTAATCACTAGGTTTGGGGTCCCA 120  
QY 262 TTTGTTGGCCGATAGTACTTATATCTCACTTATGATTTCTGTCGCTTCAGGG 321  
DB 121 TTTGTTGGCCGATAGTACTTATATCTCACTTATGATTTCTGTCGCTTCAGGG 180  
QY 322 GAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAAGAACTCATTAATCAAAAATA 381  
DB 181 GAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAAGAACTCATTAATCAAAAATA 240  
QY 382 GCAGATATGCAAGGAATAAGCGCTTTTCGGAAATTAGAGGATAGGTAAATTAACCA 441  
DB 241 GCAGATATGCAAGGAATAAGCGCTTTTCGGAAATTAGAGGATAGGTAAATTAACCA 300  
QY 442 TTATATCTAATCTCGCTTGAAGATGGGAAGAAATCC---AAATGGTTCAAGAGCTTA 498  
DB 301 TTATATCTAATCTCGCTTGAAGATGGGAAGAAATCCATTAAGAATGTCTAGAGCTTA 360  
QY 499 CGAGATGTCGGAATCGATTTGAAATCCCTGGATAGTTTATTTAGCNAATATAGCCATCT 558  
DB 361 CGAGATGTCGGAATCGATTTGAAATCCCTGGATAGTTTATTTAGCNAATATAGCCATCT 420  
QY 559 TTTAGAGTGCAAAATTTGAAGTACCAATCTCTTACTGTATATGCAATGGCAGCCCACTT 618  
DB 421 TTTAGAGTGCAAAATTTGAAGTACCAATCTCTTACTGTATATGCAATGGCAGCCCACTT 480  
QY 619 CATTTACTGTATTAAGGACGCGTCAATTTTGGAGAGAAATGGGATGGTCAACAAT 678  
DB 481 CATTTACTGTATTAAGGACGCGTCAATTTTGGAGAGAAATGGGATGGTCAACAAT 540

QY 679 ACTATTAAATACTATTATGATCGTCAAAATGAAACTTACTGCGAATATTCTGATCACTGT 738  
DB 541 ACTATTAAATACTATTATGATCGTCAAAATGAAACTTACTGCGAATATTCTGATCACTGT 600  
QY 739 GTAAAGTGGTATGAAACTGGTTTGTAGCAAAATTTAAAGAGCACGAGCGCTAAACAATGGTT 798  
DB 601 GTAAAGTGGTATGAAACTGGTTTGTAGCAAAATTTAAAGAGCACGAGCGCTAAACAATGGTT 660  
QY 799 GACTATAACCAATTCGTTAGAGAAATGACATCGGCGGTTTGTAGATGTTGTGATTTATTC 858  
DB 661 GACTATAACCAATTCGTTAGAGAAATGACATCGGCGGTTTGTAGATGTTGTGATTTATTC 720  
QY 859 CCAAAATTTATGACACGACGCTACCAATGGAACCAAGAGCAACCTAAACAAGGAAGTA 918  
DB 721 CCAAAATTTATGACACGACGCTACCAATGGAACCAAGAGCAACCTAAACAAGGAAGTA 780  
QY 919 TATACAGATCCACTGGGCGCGGTAAACGTTCTTCAATTTGGTTTCTGGTATGACAAAGCA 978  
DB 781 TATACAGATCCACTGGGCGCGGTAAACGTTCTTCAATTTGGTTTCTGGTATGACAAAGCA 840  
QY 979 CTTTCTTTCGGAGTATAGAAATCATCCGTTATTCGACCAACCCCATGTTTGTATATATA 1038  
DB 841 CTTTCTTTCGGAGTATAGAAATCATCCGTTATTCGACCAACCCCATGTTTGTATATATA 900  
QY 1039 ACGGGAATCCACTGATGATACCAATCAAGAGCAATTTCTTCCGCTCGCTATATAAGCAT 1098  
DB 901 ACGGGAATCCACTGATGATACCAATCAAGAGCAATTTCTTCCGCTCGCTATATAAGCAT 960  
QY 1099 TGGGCTGGTCAATCAATAAGCTACCATCGTGTAGTGGGTAGTAAATCTTCAACAATG 1158  
DB 961 TGGGCTGGTCAATCAATAAGCTACCATCGTGTAGTGGGTAGTAAATCTTCAACAATG 1020  
QY 1159 TATGGAATCAATAAATCTACACAGCACTAGTACCTTTGATTTTACGAATTTATGATAT 1218  
DB 1021 TATGGAATCAATAAATCTACACAGCACTAGTACCTTTGATTTTACGAATTTATGATAT 1080  
QY 1219 TACAAGACTCTATCAAGGATGAGTACTCTTGTATTTTACCTGGTTTATAGTAT 1278  
DB 1081 TACAAGACTCTATCAAGGATGAGTACTCTTGTATTTTACCTGGTTTATAGTAT 1140  
QY 1279 ATATTTTGGAAATGCCAGAGTCCGAGTTTTCATGGTAAACCAATTTGAATTAATACAGA 1338  
DB 1141 ATATTTTGGAAATGCCAGAGTCCGAGTTTTCATGGTAAACCAATTTGAATTAATACAGA 1200  
QY 1339 AAGAGCTTAAAGTATTAATCCAGTTTCCAAAGATATATAGCGAGTACAAGAGTTCCGAA 1398  
DB 1201 AAGAGCTTAAAGTATTAATCCAGTTTCCAAAGATATATATAGCGAGTACAAGAGTTCCGAA 1260  
QY 1399 TTAGAAATTAACCTCCAGAAATTTTACAGATCAACCAATTTATGATCATATAGCCATAGATTA 1458  
DB 1261 TTAGAAATTAACCTCCAGAAATTTTACAGATCAACCAATTTATGATCATATAGCCATAGATTA 1320  
QY 1459 TGTATATCAAGATATTCCTCGGAGCGGTAAACACTACCGGATTAGTACTGTATTTCT 1518  
DB 1321 TGTATATCAAGATATTCCTCGGAGCGGTAAACACTACCGGATTAGTACTGTATTTCT 1380  
QY 1519 TGGACACATCGAAGTGCAGATTTTAAACAATATATATTTAGATTAATAATCATCTCAAT 1578  
DB 1381 TGGACACATCGAAGTGCAGATTTTAAACAATATATATTTAGATTAATAATCATCTCAAT 1440  
QY 1579 CCGGCGGTTAAATGTTGGGATTAATTTACCGTTTGTTCAGTGGTAAAGGACCGACAT 1638  
DB 1441 CCGGCGGTTAAATGTTGGGATTAATTTACCGTTTGTTCAGTGGTAAAGGACCGACAT 1500  
QY 1639 ACAGAGGGGATTTTATACAGTATTAATAAGAGTACTGGTTCTGTAGGAACTTTATTTCTA 1698  
DB 1501 ACAGAGGGGATTTTATACAGTATTAATAAGAGTACTGGTTCTGTAGGAACTTTATTTCTA 1560  
QY 1699 GCTCATATGCGCTAGCATTTAGAAAAGCAGGGAATATCGGTGTAAGACTGATATGCT 1758  
DB 1561 GCTCATATGCGCTAGCATTTAGAAAAGCAGGGAATATCGGTGTAAGACTGATATGCT 1620



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 7, 2003, 05:11:04 ; Search time 45 Seconds

(without alignments)

2576.403 Million cell updates/sec

Title: US-10-032-717-2

Perfect score: 6332

Sequence: 1 MSPNNQNEVEIIDATPSTSV.....MSTETGTFYIESVELIVDVE 1206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------|
| 1          | 3066   | 48.4        | 1160   | 2  | 140589      |
| 2          | 2595.5 | 41.0        | 1157   | 1  | S49247      |
| 3          | 2440   | 38.5        | 1154   | 2  | S39536      |
| 4          | 2348   | 37.1        | 1138   | 2  | A48944      |
| 5          | 2340   | 37.0        | 1228   | 2  | S00873      |
| 6          | 2174.5 | 34.3        | 1189   | 2  | S00944      |
| 7          | 2150.5 | 34.0        | 1156   | 2  | S19306      |
| 8          | 2145   | 33.9        | 1176   | 2  | A48970      |
| 9          | 2115.5 | 33.4        | 1172   | 2  | S32689      |
| 10         | 2078.5 | 32.8        | 1165   | 2  | S11446      |
| 11         | 2073.5 | 32.7        | 1176   | 2  | JC0241      |
| 12         | 2070.5 | 32.7        | 1176   | 2  | JC2219      |
| 13         | 2069   | 32.7        | 1166   | 2  | S32645      |
| 14         | 2065   | 32.6        | 1160   | 2  | S32647      |
| 15         | 2063.5 | 32.6        | 1176   | 2  | S02215      |
| 16         | 2062.5 | 32.6        | 1176   | 2  | A22617      |
| 17         | 2058   | 32.5        | 1181   | 2  | A41052      |
| 18         | 2053   | 32.4        | 1155   | 2  | JD0052      |
| 19         | 2048.5 | 32.4        | 1171   | 2  | A40572      |
| 20         | 2045   | 32.3        | 1155   | 2  | S02134      |
| 21         | 2042   | 32.2        | 1155   | 2  | A26513      |
| 22         | 2034.5 | 32.1        | 1156   | 2  | A29125      |
| 23         | 2034.5 | 32.1        | 1171   | 2  | A37829      |
| 24         | 2027   | 32.0        | 1177   | 2  | A49785      |
| 25         | 2025   | 32.0        | 1155   | 2  | S19838      |
| 26         | 2033.5 | 32.0        | 1178   | 1  | USBSXH      |
| 27         | 2020   | 31.9        | 1174   | 2  | A42459      |
| 28         | 2005   | 31.7        | 1174   | 2  | S32649      |
| 29         | 1995.5 | 31.5        | 1156   | 2  | A29838      |

RESULT 1  
I40589  
parasporal crystal protein cry8Cal - Bacillus thuringiensis  
N;Alternate names: parasporal crystal protein cryiii  
C;Species: Bacillus thuringiensis  
C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 01-Dec-2000  
C;Accession: I40589  
R;Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asa  
Curr. Microbiol. 28, 15-19, 1994  
A;Title: Cloning, heterologous expression, and localization of a novel crystal protein  
A;Reference number: I40589; MUID:94100786; PMID:7764305  
A;Accession: I40589  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-1160 <RES>  
A;Cross-references: EMBL:U04366; NID:G532523; PIDN:AAA21119.1; PID:G532524  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 48.4%; Score 3066; DB 2; Length 1160;  
Best Local Similarity 50.3%; Pred. No. 5.4e-169;  
Matches 632; Conservative 180; Mismatches 298; Indels 146; Gaps 23;

QY 1 MSPNNQNEVEIIDATPSTSVSDNSRYPFANETPALQNNMDYKDYKQNSAGNASEYPCSP 60  
DB 1 MSPNNQNEVEIIDALPSTSVSDNSIRYPLANDQTNTLQNNYKDYKNTSTWAEISRP 60  
QY 61 EVLVSGQDAAKAAIDIVGKLLSGLVFPVGPVIVSLYTLQIDILPWSGKESQWEIFMQVE 120  
DB 61 GTFTSAQDAVGTGIDIVSTIISGLGIPVLGEVFSILGSLGLLPWSNNVNVQIFMNRVE 120  
QY 121 ELNQKTAEVARKALSEGLGNQYLYTALBEWENPNSGRALDVNRREILDSLF 180  
DB 121 ELIDQKILDSVRSRAIALANSRIAYEYQVALEDWRKPNHSTRSAALVRFEGNAEAIL 180  
QY 181 TQYMPSPRVNFEVPFTVTYVAMAANLHLLKDKASIFGEWGWSTTTNNYIDROMKLT 240  
DB 181 RTNMGSPQNYETPLPTTQAASLHLLVNRDVIYKREWGPQNDIDLFYKEQVSYTA 240  
QY 241 EYSDHCVKYETGLAKLKGTSKQWVDYNOFREMTLAVLDVVVALFPNYDTRYPMETKA 300  
DB 241 RYSDHCQWYNAGLNKLRGTGAQWVDYNNFRREMNVMVLDLVALFPNYDARYPLETNA 300  
QY 301 QLTREVTYDPLGAV---NVSSIGSWD---KAPSGVIESSVIRPHVFDYITGLTVYT 353  
DB 301 ELTREIFTPGVSVYTGQSSTLISWYDMIPALPSTLE-NLLRKDFFTLLQEIIRMT 359  
QY 354 QSRSSISARVIRWAGHOISYHRVSRGNSNQWYGTGNLHNS-----TSTFDFTNYDIY 407  
DB 360 SFKQNGTIEYINWGGORLT-----LSYIGSSFNKGYSGLVAGAEIDIIPVGQNDIY 410  
QY 408 KTLKQAVLLDIVPG-YTYIFFGMEPEVFFMWVQLNTRKTLKYNPVSVDIIASTRDS 466

#### ALIGNMENTS

Db 411 RVV-----WTYIGRYTNSLLGVNPTVF-----SNTQKTY-S-KPKQAGGKITDSG 458  
QY 467 LELPETSOPNYESYSHRLCHITS--IPATGNTT-GLVPFVSWTHSADNNTIYSDKI 523  
Db 459 EELTYE-----NQYSHRVSYSITSFEIKSTGGTVLGVVPIFGTHSSASRNPIYATKI 513  
QY 524 TQIPAVKVC-----WDNLFFV-----PVYKGPCHTGGDLQVNRSTGSGVTGLFLARYGL 571  
Db 514 SQIPINKASRTSGGAVNFOEGLYNGVPMKLSG-SGSQVINLRVATDKGA-----564  
QY 572 ALKAGKIRVRLRYATDADIVLHV-----DAQIOMPKTMNPGEBOLTSKTFKAD 621  
Db 565 ----SQYRIRIRYASDRAGKFTISSRSPENPATYSIAIYNTMTNSTNASITSTFYAYE 620  
QY 622 AITTLNLTDS-----LALKHNLGEPDNSTLSGIVVVDRIEPIVDTEAEQDLBAK 676  
Db 621 S-GPINLIGSGSRTFDISITKAG-----AANLYIDRIEPIVNTLFEASEDLQVAK 672  
QY 677 KAVNALFTNTKGLRPGVTDYEVNQAAANLVECLSDDLYPNEKRLFLDAVREAKRLSEARN 736  
Db 673 KAVNGLFTNEKDALQTSVTDYQVNAANLIECLSDLYPNEKRLMDAVREAKELVQARN 732  
QY 737 LLODPPOEINGENGWTAAGTIEVIEGDALFKGRLPLPGAREIDTETPTLYLYQKVEEG 796  
Db 733 LLODTGFNRINGENGWGTSGTIEVVEGDVLFKORSLRLTSAREIDTETPTLYLYQKIDES 792  
QY 797 VLKPYTRYLRGFGVSSQGLIEFTIRHOTNRIKVNQVDDLLPDVSPVNSDGSINRCSQK 856  
Db 793 LLKPYTRYKLKGFISQDLIEILIRHANQIVKQVDPNLLPDVSPVNSCGGVDRCSQK 852  
QY 857 YVNSRLEVENR-----SGBAHPISIPIDTGEIDYENENAGIWWGFKITDPEGVATLGNLE 910  
Db 853 YVDANLALENNGENGNSSSHAFSHFDITGEIDLNTGNTGIWVFKIPTTNGATLGNLE 912  
QY 911 LVEEGLSGDALERLQREOQWKIQMTRREEDRRYVMAKQAVDRLYADYQDQQLNPV 970  
Db 913 FVEEGLSGTLEWAQOQOQWQKMARKAASEKTYAAKQADRLFPADYQDQKLSGV 972  
QY 971 EITDLTAADLIQSIPIVYNEMPEIPIGMNTKETELTDRLQAAWLYDQARNATPNGDGR 1030  
Db 973 EMSDLLAAQNLVOSIPVYNDALPEIPIGMNTSTFELTNRLQAAWLYDQARNATPNGDGR 1032  
QY 1031 NGLSNWATPGVEVQIINHSTSVLIPNWDQVSOFTVQPNQRYVLRVLTARKEGVNGYV 1090  
Db 1033 NGLSNWATSDVNVQQLSDTSVLPVNNWSQVSOFTVQPNRYVLRVLTARKEGVNGYV 1092  
QY 1091 SIRGGQNTETLTPSASDYDTNGMYNTQVSNNGYNTNNAYNTOASSTNGYNNANMNTQ 1150  
Db 1093 IIRGDAQNTETLTPNICDDDT-GVLST-----1118  
QY 1151 ASNTNGYNTSVYNDOTGYLTKTTFPIPYTDOMIEMSETGTFYIESVELVDVE 1206  
Db 1119 -----DQTSYITKTFEFTPTPEQVWIDMSETGVNIESVELVLLEE 1160

RESULT 2  
S49247  
parasporal crystal protein cry9Cal [validated] - Bacillus thuringiensis  
N;Alternate names: parasporal crystal protein cryIIH  
C;Species: Bacillus thuringiensis  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000  
C;Accession: A59350; S49247  
R;Lambert, B.; Buysse, L.; Decock, C.; Janssens, S.; Piens, C.; Saey, B.; Seurinck, J.; V  
Appl. Environ. Microbiol. 62, 80-86, 1996  
A;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity aga  
A;Reference number: A59350; PMID:96141404; PMID:8572715  
A;Accession: A59350  
A;Molecule type: DNA  
A;Residues: 1-1157 <LAM>  
A;Cross-references: EMBL:Z37527; NID:g547554; PIDN:CAA85764.1; PID:g547556  
A;Experimental source: serovar tolworthi  
C;Comment: This parasporal crystal protein, active against corn borer and other insects,

C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin  
Query Match 41.0%; Score 2595.5; DB 1; Length 1157;  
Best Local Similarity 44.1%; Pred. No. 8.e-142; Indels 157; Gaps 22;  
Matches 554; Conservative 197; Mismatches 348;  
QY 1 MSPNNQNEYEIIDATPSTSVNSDNRYPPANPTNALQNDYKYLKMSAGNASEYPGSP 6C  
Db 1 MNRNNQNEYEIIDAPHCPCSDDDVRYPLASDPNAALQNMNYKYLOMTDEDYTDYINP 6C  
QY 61 EVLVSQDAAKAALDIVKGLSLGVPFVGPVIVSLYTLQIDILWPSGEKSKOWEIPMEOVE 120  
Db 61 SLISGRDVAQTALTAVGRILGALGVPPFSGQIVSPYQFLNLTLPVNDTAIMEAFRQVE 120  
QY 121 ELINQIKAEYARKALSELEGGNNYOLVLTALAEWENPNGRALRDVNRREIILDSLF 180  
Db 121 ELVNOQITFARNQALRQLGDSFNVQSLQNLWADNRNLSVVRQAQIALDLDF 180  
QY 181 TQMPSPFRVTNPEVPLTVYMAAANLHLLKLDASIFGEGWGSMTTNNYIDROMKLT 240  
Db 181 VNAIPLFVNGQVPLSVYQAANLHLLKLDASIFGEGWGSMTTNNYIDROMKLT 240  
QY 241 EYSDHCWKVETGLAKLGTSAKQWVDYQFREMFLAVLVVVALPNDITRYPMETKA 300  
Db 241 KYTNYCETWYNTGLDLRGNTTESMLRHYQFREMFLAVLVVVALPNDITRYPMETKA 300  
QY 301 QLTREYVYVPL---GAVNVSSISG---YDKAPSGVIESSVIRPHVDPYITGLTYVT 353  
Db 301 QLTREYVYVPL---GAVNVSSISG---YDKAPSGVIESSVIRPHVDPYITGLTYVT 353  
QY 354 QSRISISARYIRHWAGHOISYHRVSRGSLQOYMG-----TNQNLHSTSTFDTNYD 405  
Db 357 SNRPVSSNFMDFYSGHTLRRSLVNDASVQEDSYGLITTRATINPGVDGTRIESTAVD 416  
QY 406 IYKTLKQAVLLDIVPGYTYIFFGMPVEVEFFMVNQLNTRKTLKYNPVSKDIIASTRDS 465  
Db 417 FRBALIG-----IYGVNRASFVPGGLFNGT--TSPANGGCRDLY---DT 455  
QY - 466 ELALPETSOPNYESYSHRLCHITSIPATGN-----TTGLVPFVSWTHSADNNTIY 519  
Db 456 NDELPPDEST-----GSHRLSHVTFPSFQTNQAGSIANAGSVPTVYVTRDVLNNTIT 511  
QY 520 SDRITQIPAVKWDNLFPFVNVKPGHGTGDLQVNRSTGSGVTGLFLARYGLALEKAGY 579  
Db 512 PNRITQLPLVKAAPVSGTIVLKGPGTGGILR-RTNGTGTGL---RVTVNSPLTQQY 567  
QY 580 RVLRYATDADIVLH-----VNDQIOMPKTMNPGEBOLTSK-----TF 617  
Db 568 RLVRVFASTGNFIRVLRGGVSGIDVRLAGSTNNRGOELTYESFTRFTTGTGPFNPPFTF 627  
QY 618 KVADAITTLNLTDSIALKHNLDGPNSTLSGIVVVDRIEPIVDTEAEQDLBAK 677  
Db 628 TQAOELITVNAEGVST-----GGEYIDRIEPIVNPAREAEDELEAKK 672  
QY 678 AVNALFTNTKGLRPGVTDYEVNQAAANLVECLSDDLYPNEKRLFLDAVREAKRLSEARN 737  
Db 673 AVASLFTREDFGLQVNTDYQVQAAANLVSCLSDQYGHDKWMLLEAVRAAKLSRENL 732  
QY 738 LQDPDFQOEING--ENGWTAAGTIEVIEGDALFKGRLPLPGAREIDTETPTLYLYQKVEE 795  
Db 733 LQDPDFNTINSTENGWKAAGVNTISSEGGPFPKGRALQALASAR---ENYPTIYQKVA 788  
QY 796 GVLKPYTRYLRGFGVSSQGLIEFTIRHOTNRIKVNQVDDLLPDVSPVNSDGS---LNRC 852  
Db 789 SVLKPYTRYLRGFGVSSQGLIEFTIRHOTNRIKVNQVDDLLPDVSPVNSDGS---LNRC 845  
QY 853 SEQKYVNSRLEVEN-----RSGEAHFSIPIDTGEIDYENENAGIWWGFKITDPEGVATL 906  
Db 846 DEQHQVDMQLDAEHPMDCCAAQTHFFSYINTGDLNASVQDGIWVVKVTRTDGATL 905  
QY 907 GNLELVEEGLSGDALERLQREOQWKIQMTRREEDRRYVMAKQAVDRLYADYQDQQL 966

Db 906 GNLELVVGPISGESLEREQORDNAKNALGRKRAEIDRVYLAQAQANHLFVYDQOOL 965  
Qy 967 NPDVEITDLTAQADLIQSIPIVYVNEFPEIPGMNTYTKFTLDRLQQAWSLYDORNAIPN 1026  
Db 966 NPEIGLABINEASNLVESISGVYSDTLQIQPINEYIETELSDRLQQAASLYTSRNVQN 1025  
Qy 1027 GDFRNLGNWATPGVFVQCIQNHSTSVLVI PNWDEQVSQOFTVQPNQRYLVRVTAKEGVG 1086  
Db 1026 GDFNSGLSDSWNTWDASVQODGNHFLVLSHWDAQVSQQLRVNPNCKVYLVRTARKVGG 1085  
Qy 1087 NGYVSIIRGGNCTETLTPSASDYDNGMYNTQVSTNGYNTNANTQASSTNGYNNNM 1146  
Db 1086 DGYVIRGAGHQETLTINACDYVNGY----- 1114  
Qy 1147 YNTQASNTNGYNTSVYNDQTYITKTVTFIPYTDQMIEMSETEGTFVIESVELI 1202  
Db 1115 -----VNDNS-----YITEVVFYPTKMWVSESGSYIDSIEFI 1153

RESULT 3  
S39536  
parasporal crystal protein cry3Ba1 - Bacillus thuringiensis  
N;Alternate names: delta-endotoxin-related protein; parasporal crystal protein cryX  
C;Species: Bacillus thuringiensis  
C;Date: 07-Oct-1994 #sequence\_revision 01-Dec-1995 #text\_change 01-Dec-2000  
C;Accession: S39536  
R;Shevelev, A.B.; Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; Stepan  
FEBS Lett. 336, 79-82, 1993  
A;Title: Primary structure of the cryX, the novel delta-endotoxin-related gene from Bac  
A;Reference number: S39536; MUID:9408596; PMID:8262221  
A;Accession: S39536  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1154 <SHE>  
A;Cross-references: EMBL:X75019  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 38.5%; Score 2440; DB 2; Length 1154;  
Best Local Similarity 44.0%; Pred. No. 8.6e-133;  
Matches 534; Conservative 177; Mismatches 357; Indels 146; Gaps 25;

Qy 42 KYDLKMSAGNASHYPSGSEVLVSGQDAKAAIDIVGKLKSLGVPFVGPVIVSLYQLID 101  
Db 30 KYDLKMSAGNASHYPSGSEVLVSGQDAKAAIDIVGKLKSLGVPFVGPVIVSLYQLID 101  
Qy 102 ILWPSGKSEWEIPEQVEELINQIAEYARKALSELEGNGNYQLYLTALKEWENPN 161  
Db 87 FLWPSDQAVWEAFIEQVEELINQIAEYARKALSELEGNGNYQLYLTALKEWENPN 146  
Qy 162 GSRALDRVRNFEILDSLTQYMPSP-----RVTVPEVFLTVYAMAANHLHLKLDASIP 217  
Db 147 GVRA-NLVLRFEILHALFVSSMPSFGSGPSQRFQALLVYQAQANHLHLLDAAKY 205  
Qy 218 GEWGWSTTINNYDRMKL-TAEYSDHCWKVYETGLAKLGTSAKOWDYNDQFRREMT 276  
Db 206 GARGWGLRESQIGLYFNELOTRTDYTHCNVYNNGLAGLGRGSAESWLKYHQFRREAT 265  
Qy 277 LAVLDVVALFENYDTRTYPMETKQLTREVTDPDGVAVVSS-----IGSWD-KAPS 328  
Db 266 LMAVDLALFPYNNRYPIAVNPQLTREVTDPDGVAVVSS-----IGSWD-KAPS 325  
Qy 329 FGVISSVIRPPHFDYDTGLTVVTSRIS-SARYIRHMAHQIYXHVRSRGSN--LQQ 385  
Db 326 FSNLENALISSPHLFDYDTGLTVVTSRIS-SARYIRHMAHQIYXHVRSRGSN--LQQ 385  
Qy 386 MYGTNQLHSTSTFDYNTYDIYKTLK-----DAVLLDIV-----YPGTYIFFGMP 433  
Db 386 NYGTTSTI--VNYPSFENDRVVQINRSHRGLGFGNAFLFGITRAQFPYPGTY----- 436  
Qy 434 VEPFWNQLNTRKYLKYNFVSKDIIASTRSELELPETSDQPNYESYHRLCHITS-- 491  
Db 437 ----SVTQRNALTCEQNYNSID-----ELPSLDPNPEITSYHRLSHITSYL 480

Qy 492 -----IPATGNTTGLVPFVSWTHRSADLNNTIYSDKITQIPAVKWDNLFPVPVVKGPQH 546  
Db 481 HRVLTIDGINIYSGNLTYVWTHRDVLTNTITADRITQPLVASFEPAGTIVRGPGF 540  
Qy 547 TGGDLLQVNRSTGSGTFLIARYGLALEKAKYRVRLEYA--TDADIVLHVNDQAI---Q 601  
Db 541 TGGDIL---RRTG-VGTFGTIRVTTAPLQYRIRFRFASTTNLFIGIRVGDQVNYFD 596  
Qy 602 MPKTMNPGEDLTSTPKVADAITLNLATDSSL-----ALKENLGEDPNSTLSGVIYVDRI 657  
Db 597 FGRTMNRGDELRYESFATREFTTDFNFRQPELISVFANAFSAQOE-----VYFDRI 648  
Qy 658 EPIFVDETYEAOBLEAAKAVNALFNTKDGIRPGVTDYEVNOAANLVECLSDDLVENE 717  
Db 649 EIIIPVNPAREAKEDLEAAKAVASLFRTRDGLQVNVKDYQVDOAANLVSCLSEQGYD 708  
Qy 718 KRLLFDAVRAKRLSEARNLLQDDPQEIENG--ENGWASTAGTIEVIEGDAALFKGYRLRLP 775  
Db 709 KMLLEAVRAAKRLSRERLLQDDPNTINSTENGKASGVNTISEGPPFYKGRALQLA 768  
Qy 776 GAREIDTETVYLYOKVSEGVLPKPYTRYLRGPGVSSQGLEIFTRHQTNRIYVNPDD 835  
Db 769 SAR-----ENPTYIYQKVDASELKPTRYRSDGPFVSSQGLEIDLIHHKVKHLVKNVDPN 824  
Qy 836 LLPDVPSPVSDGSINRCSEOKYVNSRLVEN-----RSGEAHEFSIPIDTGEIDYEN 888  
Db 825 LVSTYDPPDSCSGINRCQEQWVNAQLETHHHHPMDCEAAQTHFSSYIDTGLNLSVD 884  
Qy 889 AGIWVGPKITDPEGYATLGNLELVSEGLSGDALERLQREEQQWKIQWTRRRETDRIYM 948  
Db 885 QGIWAIKPVRTDGTATLGNLELVSEGLSEREDONTKWSAELGRKRAETDRVYQ 944  
Qy 949 ASKQAVDLVADYDQOQLNPDPVEITDLTAQADLIQSIPIVYVNEFPEIPGMNTYTKFTLT 1008  
Db 945 DAKOSINHLFVYDQOQLNPEIGNADIMDAQNLSVSDVSAVLQIPGINYIETLS 1004  
Qy 1009 DRLOQASLYDORNAIPNGDFRNLGNLSNNATPGVEVQCIQNHSTSVLVI PNWDEQVSQOFTV 1068  
Db 1005 NRLOQASLYTSRNVAVQNGDFNGLDSWNAITAGASVQODGNTHFLVLSHWDAQVSQFPRV 1064  
Qy 1069 QPNORYLVRTARKEGVNGVSIIRDGNQOTETLTPSASDYDNGMYNTQVSTNGYNTN 1128  
Db 1065 QPNCKYLVRTARKEGVNGVSIIRDGNQOTETLTPSASDYDNGMYNTQVSTNGYNTN 1113  
Qy 1129 NAYNTQASSTNGYNNMYNTQASNTNGYNTSVYNDQTYITKTVTFIPYTDQMIEMSE 1188  
Db 1114 -----DNT-YLTKEVIFYSHTHEMWEV 1136  
Qy 1189 ETEGTFVIESVELI 1202  
Db 1137 ETEGAFHIDSIEFV 1150

RESULT 4  
A48944  
parasporal crystal protein cry7Aa1 - Bacillus thuringiensis  
N;Alternate names: parasporal crystal protein cryIIIC  
C;Species: Bacillus thuringiensis  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 01-Dec-2000  
C;Accession: A48944  
R;Lambert, B.; Hofte, H.; Amnys, K.; Jansena, S.; Soetaert, P.; Peferoen, M.  
Appl. Environ. Microbiol. 58, 2536-2542, 1992  
A;Title: Novel Bacillus thuringiensis insecticidal crystal protein with a silent activ  
A;Reference number: A48944; MUID:92384571; PMID:1514800  
A;Contents: BTL3137  
A;Accession: A48944  
A;Status: preliminary  
A;Molecule type: DNA; protein  
A;Residues: 1-1138 <LAW>  
A;Cross-references: GB:M64478; NID:gl42760; PIDN:AAA22351.1; PID:gl42761  
A;Note: sequence extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)  
C;Superfamily: parasporal crystal protein



C;Keywords: delta-endotoxin

Query Match 37.1%; Score 2348; DB 2; Length 1138;  
Best Local Similarity 41.1%; Pred. No. 1.8e-127;  
Matches 512; Conservative 211; Mismatches 385; Indels 120; Gaps 27;

QY 1 MSPNNQVEIIDATPSTSVNSDNRYPFANEPTNALQNNQNDYKDYLKWSAGNASEYGPSP 60  
DB 1 MNLNLDGVE-----DSNRPLNNSLNYPTOKALSPSLKNNYQDFLSITERE-----QP 49

QY 61 EVLVSGQDAKAAIDIVGKLLSGLVGPFVGVIVSLYTLQIDILWPSGEKSWEIFMEQVE 120  
DB 50 EALASGNATNTVTVSGATLSALGPGCAFITNFYKLAGLLWPENGKI-WDEFMTEVE 108

QY 121 ELINOKIAEYARNKALSELGKGNVYQLYLTALBEEWENPNPNSPALRDVNRREILDSLF 180  
DB 109 ALIDOKIEEYVRNKAIAELDGLSALDKYOKALADWLGKQDDPEAILSVATEFRIDSLF 168

QY 181 TQWPSFRVTNFPVPLTVYMAANLHLLKQASIFGEWGWSTTTINNYDROMKLT 240  
DB 169 EPSKPSFKVTGYRPLTVVAQAANLHLLRUSTLYGDKWGFQNNIENYNRQKRIS 228

QY 241 EYSDHCVKVYETGLAKLKGTSAKQWYDYNQFRREMTLAVDVVALFPNYDTRTPMETKA 300  
DB 229 EYSDHCTKYNKSLRSLNGSTYEQWYINFRFRREMLMALDLVAVFPFDPFRYMETST 288

QY 301 OLTRVYVTDPLGAVNVSIGSWDKAPSGVIESVIRPHEVDYITGLTVYTSRIS 360  
DB 289 OLTRVYVTDV-SLUSIN----PDGSPSQMENTAIRTHLVLDYDELXYITSKYKAFS 343

QY 361 ARY---IRHWAGHOISVHRVSRGNSLQ--MYGTNQLHSTSTPFTNYDIYKTLSDAV 415  
DB 344 HETQPDLFYSAHKVSPK-SEQNLTYTGYLGTSGYISSGAYSFHGNDIYRLAASP 402

QY 416 LLDIVPGYTYIFGMEVEBFWMVNLNTRKTLKYNPVSKDIIASTRDSLELELPETSD 475  
DB 403 ---VYVP-YTQ-NYGVQEVGFYKGVHVRGDKYD-----LAYDSIDQLPPD--G 447

QY 476 QPNYESYSHRLCHTSTI-----PATGNTTGLVPVPSWTHRSADLNNTIYSOKITQIPAVK 531  
DB 448 EPIHEKYTHRLCHATAIFKSTPDYDNAT--IPIFSWTHRSAYTNRYPNKTIKIPAVK 505

QY 532 WDNLFPVVPVPGHGTGDDLQVNRSTSGVGTFLFARYGLALEKAGYRVLRYATD--A 589  
DB 506 YKLLDPSTVVGFGFTGDLVK-RGSTGYIGDI-KATVNSPLSQ--KYRVRVRYATVSG 561

QY 590 DIVLVNDAQIOMP-K-----TMNPGBDLTSKTPKVAADAITLNLATDSSLAKHNGED 643  
DB 562 QFNVYINDKITLQTKFQNTVETIGEGKDLTYGSGFYIEYSTTIQFPDEHPKTLHLSDLS 621

QY 644 PNSTLSGIVVDRIEFTPDVETAEQDLEAKKAVNALFTNTKXGLRPGVTDYEVNQAA 703  
DB 622 NNSSF-----YVDSLEFPVDVNYAEKLEKAKAVNTLFEGRNALQKQVTDYKVDQS 677

QY 704 NLVECLSDLLYPNEKRLIFDAVREAKLSERNLQDPDFOEING--ENGWTAAGTGEVI 761  
DB 678 ILVDCISGDIYPNEKRELQNLVKAKLSYRNLLOPFDTSINSSENGWYSGNGVIG 737

QY 762 EGDALFKGYRLPAGREIDTETPTVYLYQKVEGVILKPYTRYRLRFGVSSQGLEIFTI 821  
DB 738 NGDFVFKGNLYLFSGTN--DTQ-YPTVLYQKIDESKLEKAVNTLFEGRNALQKQVTDYKVDQS 794

QY 822 RHQTRIVKVPDLDLDPVSPVNSDGSINRCSEKYNVSRLEVENRS-----GEAEHFS 875  
DB 795 RYDAKHRTLDVSNLDDLPILPENTCGPNRCAAOYLNDENPSPCSSWQDGLSDSHFS 854

QY 876 IPIDTGIDYNENAGIWWGFKITDPEGATLGNLEVEEGLSGDALERLQREQWQKIQ 935  
DB 855 LNIYDTSIGNHNNENGIWVLFKISTLEGYAKEGNLEVEDGPGVIGEARLVKQRTKRWK 914

QY 936 MTRREEDTRYMASKQAVDRLYADYQDQQLNPDPVEITDLTAAQDLIQSIPVYVNEFPE 995  
DB 915 LAQLTTTQATYTRAKQALDNLFANAQDHLKRDVTFPAEIAAARKIVQSIREAYMSWLSV 974

QY 996 IPGMNYTKFTELTDRLOQAWSLYDORNAIPNGDFRNLGNMWNATPGVYQOINHTEVLVI 1055  
DB 975 VPGVNHPIFETELSGRVQRAFQLYDVNRVNRGRFLNGLSDWIVTSVKVQBEENGVLVL 1034

QY 1056 PNWDEQVSQOFTVQPNQRVYLRVARTARKEGVNGYVSIIRGNGQTETLTTPFSASDYDNGMY 1115  
DB 1035 NNWDAQVLNVKLYQDRGYILHVTARKIGIGEGYITITDEEGHTDQLRFTACE----- 1087

QY 1116 NTQVSNYNGYNTNAYNTQASSTNGYNNMNYNTQASNTNGYNTNSVYNDQGYITKVT 1175  
DB 1088 --EIDASNAF-----ISGYITKELE 1105

QY 1176 FIYTDOMIEMSETEGTFVIRSVELIV 1203  
DB 1106 FPDTEKRVHIEGETEGIFLVESIELFL 1133

RESULT 5  
S00873  
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
N;Alternate names: parasporal crystal protein cryA4  
C;Species: Bacillus thuringiensis subsp. thuringiensis  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 01-Dec-2000  
C;Accession: S00873  
R;Brizzard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus  
C;Reference number: S00873; MUID:88203216; PMID:3362680  
A;Accession: S00873  
A;Molecule type: DNA  
A;Residues: 1-1228 <BRI>  
A;Cross-references: EMBL:X06711; NID:940264; PIDN:CAA29898.1; PID:g580949  
C;Genetics:  
A;Gene: cryA4  
A;Start codon: TTG  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 37.0%; Score 2340; DB 2; Length 1228;  
Best Local Similarity 42.1%; Pred. No. 5.8e-127;  
Matches 533; Conservative 193; Mismatches 435; Indels 106; Gaps 26;

QY 1 MSPNNQVEIIDATPSTSVNSDNRYPFANEPTNALQNNQNDYKDYLKWSAGNASEYGPSP 60  
DB 1 MTSNRKNEIINA-----VSNHSAQ-----MDLLPARIEDSLCIAEGNID----P 44

QY 61 EVLVSGQDAKAAIDIVGKLLSGLVGPFVGVIVSLYTLQIDILWPSGEKSWEIFMEQVE 120  
DB 45 FVSAS---TVQTGINTAGILGVLPVFPAGQLASFVSLVGLMWRPG-RDQWEIFLEHVE 100

QY 121 ELINOKIAEYARNKALSELGKGNVYQLYLTALBEEWENPNPNSPALRDVNRREILDSLF 180  
DB 101 OLINQOITENARTALARLQGLGDSFRAYQQSLDLEWLNRRDARTSRVLYTQYIALELDF 160

QY 181 TQWPSFRVTNFPVPLTVYMAANLHLLKQASIFGEWGWSTTTINNYDROMKLT 240  
DB 161 LNAMPFLPAINQVEPLMVAQAANLHLLRDLASLFGSEFGLTSQRIQRYERQVETR 220

QY 241 EYSDHCVKVYETGLAKLKGTSAKQWYDYNQFRREMTLAVDVVALFPNYDTRTPMETKA 300  
DB 221 DYSYCVWNTGLNSLGRNTAASWRYNQFRDLTLGLVLDLVALFPSTVTRTPINTSA 280

QY 301 OLTRVYVTDPLG--VNVSSIGSWY-DKAPSGVIESVIRPHEVDYITGLTVYTSRIS 357  
DB 281 OLTRVYVTDGATGAVNMAW-NWYNNAPSAIEAAAIRSPHLLDFLEQLTFPSASSR 339

QY 358 ISSARVIRHWAGHOISVHRVSRGNSLQWYGTNQLHSTSTPFTNYDIYKTLSDAVLL 417  
DB 340 WSTRWTWYRGTIISRPIGGGLNTSTGANTNTSINPV-TLFPASRDVTRTESYAGVLL 398

QY 418 DIVPGYTYIFFGMEVEBFWMVNLN-NTRKTLKYNPVSKDIIASTRDSLELELPETSDQ 476

Db 399 ---WGIVLEPHGVETVAFNFTPNQINSDRGNTANYSQPYSEGLQKDSSELPETTER 455  
Qy 477 PNYESYHRLCHITSIPTATNTGLVPFVSWTHRSADLNNTIYSKTIQIPAVKWDNLP 536  
Db 456 PNYESYHRLSHIGILOSRYN---VPYISWTHRSADRTNTIGPNRIQIPNVKASELPQ 512  
Qy 537 FVPVVGKPGHTGDLQVNRSTGSGVTLFLARYGLALBKAGKYRVLRYATDADIVLHVN 596  
Db 513 GTTVRGSGFTGGDILR-RTNKGSGPIRVTVNGPLTQ---RYRIGFRYASTVDPDFVS 568  
Qy 597 DA-----QIQMPKTNPGEDITSKTFKADATITLNLATDSSLAKHNL-GE DPNSTLSG 650  
Db 569 RGGTVNFRRLTNWSDELKYNP-VRRAPFTPTFTQIIDIIRTSIGLSGN---G 623  
Qy 651 IVYVDRIFIPVDETYAEQDLAAKAVNALFTNTKD-GLRPGVTDYEVNQAANLVECL 709  
Db 624 EVIDIKISIIPTATFEAYDLERAQEAVALFTWNPRRLKTDVTDHIDOVSNLVAEL 683  
Qy 710 SDDLVPNEKRLFDVAREAKLSEARNLLQDPDFQIN-----GE 749  
Db 684 SDEFCLDEKRELLKVKYAKLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSHEQSE 743  
Qy 750 NGWTASTGIEVIGDALPKGYRLRPGAREIDTETPTVYLQKVEGVLPKPYRRLRGP 809  
Db 744 HGWGSENITIQEGNDVFKENYVTLPGT---FNECYPTLYQKIGESLKAATRYQLRGY 800  
Qy 810 VGSQGLFIPTIRHQTNRIVKNVP--DDLPL--DVSPVNSDGSINRCSEQKYNSRLVE 865  
Db 801 IEDSQDLBIYLIRYNAKHETLDVPTGESLWPLSVESPIGRCEPNRCAPHFEPWPDPCS 860  
Qy 866 NRSGE-----AHEFSIPIDTGEIDYNENAGIWWGPKITDPEGYATLGNLELVEEGLSGD 920  
Db 861 CRDGEKCAHSHHFSLDIDVGCTDLHENLGVVWPKITQEGHARLGNLEPFEKPLLGE 920  
Qy 921 ALERLOREQQWQMTORRREBDRRYMASQAVDLVADYQDQQLNPDVEITDLTAQD 980  
Db 921 ALSRVKAEKWRDKREKLOLETKRYVTEAKEAVDALFVDSQYDRLOADTNGIMHAADK 980  
Qy 981 LIQSIPIVYNEMFPIPGMYNTKFTLDRLOQWMSLDORNAIPNGDPNGLSNWATP 1040  
Db 981 LVHRIEAYLSELPIVPGVNAEIFELSGHITALSIDARVNVKNGDFNGLTCCWNVK 1040  
Qy 1041 GVEVQOINHTSVLPIPNDEQVSQOFTVPQNRQYVLRVATKEGVNGVSVIRDGNGOTE 1100  
Db 1041 HVDVQSHRSDLVPIPEAEVQAVRCPGCGYILRVATYKEGYGEGCVTHIEENTD 1100  
Qy 1101 TLTSASDYDNGMYNTQVSWNTGNTNAYNTQASSTNGYNNMYTQASNTGNTN 1160  
Db 1101 ELKP--KNREBEVYPTDTGTCDNYTAHQGTAGCADACNSRNAGYEDAYEDVDTASVNYK 1158  
Qy 1161 SVYNDQ-----GYITKTVTFIYTDQMIEMSETEGTFVI 1196  
Db 1159 PTYBEETVDRDNHCYDRGVNYPVPAGYVTKLEYFPEPDTVWIEIGETGKIV 1218  
Qy 1197 ESVELIV 1203  
Db 1219 DSVELL 1225

RESULT 6  
S00944  
parasporal crystal protein cryiCal - Bacillus thuringiensis (strain entomocidus 60.5)  
C;Species: Bacillus thuringiensis  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 01-Dec-2000  
C;Accession: S00944  
R;Honee, G.; van der Salm, T.; Visser, B.  
Nucleic Acids Res. 16, 6240, 1988  
A;Title: Nucleotide sequence of crystal protein gene isolated from B. thuringiensis subs  
A;Reference number: S00944; MUID:88289380; PMID:3399402  
A;Accession: S00944  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-1189 <HON>

A;Cross-references: EMBL:X07518; NID:g40293; PIDN:CAA30396.1; PID:g40294  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 34.3%; Score 2174.5; DB 2; Length 1189;  
Best Local Similarity 40.0%; Pred. No. 2.1e-117;  
Matches 504; Conservative 189; Mismatches 437; Indels 129; Gaps 31;

Qy 1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTNLQNMDYKDYLKMSAGNASEYPGSP 60  
Db 1 MEENQNC-----IPNCLSNPE----- 19  
Qy 61 EVLVSGQ--DAAKAIDIVGKLGLGVFPVGPITVSYLTQIDILMPSEKSOEIMFEQ 118  
Db 20 EVLLDGERISITGNSIDISLSLVQFLVSNFV-PGGGFLVGLIDFVWGVGVSQMDAFLVQ 78  
Qy 119 VRELINQIAIYARANKALSEGLEGNRYQLYLTALFEWENPNGRALRDVNRFEILD 178  
Db 79 IEQLINERIAAFARNAAIANLEGLGNFNITYVEAFKEEEDPNPNPRTTRTRVIDRFLDG 138  
Qy 179 LFTQVMPSTVTFNEVPEPLTVYMAANLHLLKLDASI FGEWGWSTTTINNYIDROMKL 238  
Db 139 LLEDIPSTFISGGEVPLSVYAOANLHLALRDSVIFGRWGLTTINNVNENRLIRH 198  
Qy 239 TAESDHCVKWYETGLAKLGTSAKQWVDYNQFRREMTLAVLDVVALFPNPDYDTRPYMET 298  
Db 199 IDEYADHCANTYRGLNLPKSTYQDMITYNLRRLDTLTVLDIAAFPNPDYDTRPYPIQ 258  
Qy 299 KAQITREYVTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVVTOGRSI 358  
Db 259 VGQLTREYVTDPL--INFNPQLQSVAPLPTFNVMESRIRNPFLFDILNNLTITFTDFSV 316  
Qy 359 SSARYIRHWAGHQLSYHRVSRGSLNQMYGTQNLHSTSTFDTNYDIYKTLSDAV-LL 417  
Db 317 GRNYF---WGHRVSISSIGGNITSPYIGREANQEPSPFT-NGPVFTLSNPTLRL 372  
Qy 418 DIVPGYTYIPFGMEPEVEFFMVNQLNNTKTKYNPVSKOIIASTRSELELPETSQD 477  
Db 373 QQPWAPPENLRGVEGVF-----STPNSFTYRG-----RGTVDSLTELPEDSNP 420  
Qy 478 NYESYHRLCHITSIPTATN---TTGLVPFVSWTHRSADLNNTIYSKTIQIPAVKWDN 534  
Db 421 PREGYSHRLCHATFVQSRGTPFLTGV--VFSWTDRAATLTIDPERINOIPLVKGRV 478  
Qy 535 LPFPVVKPGHTGDLQVNRSTGSGVTLFLARYGLALEKAGKYRVLRYAT--DADIV 592  
Db 479 WGTSTVITGPGFTGEDIIRN---TFGDVSVLQVNSPITQRYRLFRVASSRDARVI 534  
Qy 593 LHVND-----QIQMP--KTNPGEDLTSKTFKADATITLNLATDSSLAKHNLGE 642  
Db 535 VLTGAASVGVGGQSVNMPKTKMEIGENLTSRTFRTDFSNPFSFRANPDII--GISE 591  
Qy 643 DP-----NSTLSGIVVDRIEIPVDETYAEQDLAAKAVNALFTNTKD-GLRPGVTDY 697  
Db 592 QPLFGAGSISSGELYIDKIEIILADATFEASDLERAQAVNALFTSNQIGLKTVDY 651  
Qy 698 EVNQAANLVECLSDLYPNKRLFDVAREAKLSEARNLLQDPDFQIN--GENGWTS 755  
Db 652 HIDQVSNLVDCLSDFCLEKREKSEKVKHARLUSDERNLLQDPNFRGINQPDGRWGRS 711  
Qy 756 TGEIVIGDALFKGYRLRPGAREIDTETPTVYLQKVEGVLPKPYRRLRFGVSSQG 815  
Db 712 TDITIQGDDVFKENYVTLPGT--VD-ECYPTLYQKIDESKLKAYTFELRGYIEDSQD 768  
Qy 816 LEITIRHQTNRIVKNVPD-----LLPDVSPVNSDGSINRCSEQKYNSRLREVENRSE- 870  
Db 769 LEIYLIRYNAKHETVNVPGTGLPPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEK 828  
Qy 871 ----AHEFSIPIDTGEIDYNENAGIWWGPKITDPEGYATLGNLELVEEGLSGDLERLQ 926  
Db 829 CAHSHHFTLDIDVGCTDLNEDLGVWVIFKIQDQGHARLGNLEPFEKPLLGSALARK 888  
Qy 927 REEQWQMTORRREBDRRYMASQAVDLVADYQDQQLNPDVEITDLTAQDILQISIP 986

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Db 889 RAEKWRDREKLEQETNIVYKEAKESVDALFVNSQYDRLOQVDTNAMIHAADKRVHRIR 948
Qy 987 YVYNEFPEIPGNNYTKFTELTDRLQOANSLYDQRIAPNGDFRNGLSNWNATPGVEV-Q 1045
Db 949 EAYLPESLVIPIGNAIAFELEGRIITFAYSLSYDARNVIRKNGDFNGLLWNVKGHDVVEE 1008
Qy 1046 QINHTSVLPINWDEQVSOFTVQPNORYVLRVTAKEGVNGVYSIRDCGNTOTELTFS 1105
Db 1009 QNNHRSVLVPEWAEVSOEVRVCPGRGILRLVTAYKEGEGECVTHIEIEDNTDELKFS 1068
Qy 1106 ASDYDNGMYNTQVSNNGYNTNNAY-NTQASSTNGYN---ANN-----MYN----- 1148
Db 1069 -NCVEBEVPPNNTVTCNNYTGTOBEYEGYTSRNOGYDEAYGNNPSPADYASVYEKSY 1127
Qy 1149 TOASNTNGYNTSVNDOT---GYLTKVTFTFYTDQWMIEMSETEGTFYIESVELIV 1203
Db 1128 TDGRRENPCESNKGYGDYPLPAGYVTKDLEYFPETDKWVIEIGETGTFIVDSVELLL 1186

RESULT 7
S19306
parasporal crystal protein cry9Aa1 - Bacillus thuringiensis
N:Alternate names: delta-endotoxin; insecticidal crystal protein; parasporal crystal pro
C:Species: Bacillus thuringiensis
C:Date: 04-Dec-1992 #sequence revision 04-Dec-1992 #text_change 01-Dec-2000
C:Accession: S19306; S23588; A44847; S14602; S14837
R:Smulevitch, S.V.; Osterman, A.L.; Shevelev, A.B.; Kaluger, S.V.; Karasin, A.I.; Kadyro
FBBS Lett. 293, 25-28, 1991
A:Title: Nucleotide sequence of a novel delta-endotoxin gene cryIg of Bacillus thuringie
A:Reference number: S19306; MUID:92070568; PMID:1660003
A:Accession: S19306
A:Molecule type: DNA
A:Residues: 1-1156 <SMU>
A:Cross-references: EMBL:X58120; NID:9870929; PIDN:CAA41122.1; PID:940271
A:Experimental source: subsp. galleriae
A:Accession: S23588
A:Molecule type: protein
A:Residues: 24-34 <SMUI>
A:Experimental source: subsp. galleriae
R:Gleave, A.P.; Hedges, R.J.; Broadwell, A.H.
J. Gen. Microbiol. 138, 55-62, 1992
A:Title: Identification of an insecticidal crystal protein from Bacillus thuringiensis B
A:Reference number: A44847; MUID:92211329; PMID:1556556
A:Accession: A44847
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1151 <GLE>
A:Cross-references: EMBL:X58534; NID:948879; PIDN:CAA41425.1; PID:948880
A:Experimental source: isolate DSIR517
A:Note: sequence extracted from NCBI backbone (NCBIN:92865, NCBIPI:92867)
C:Genetics:
A:Gene: cryIg
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 34.0%; Score 2150.5; DB 2; Length 1156;
Best Local Similarity 40.0%; Pred. No. 4.8e-116;
Matches 500; Conservative 203; Mismatches 396; Indels 151; Gaps 28;

Qy 5 NONEVEIIDATSTSVNSNRPANEP-----TNALQNMIDKYLKMSAGNASEYFG 58
Db 2 NQNGHGIIGASNGCASDDVAKYPLANNPYSSALNLSNCSNLSLNNIIG----- 53
Qy 59 SPEVLVSGDAAKAADIVGKLLSGLVGPVGPVLSYLTQLI-DILWPSEKSKQWEIFME 117
Db 54 -----DAAKEAVSIGTIVSLITAPSLTGLISIVYDLIGKVLGGSGGSDLSIC 104
Qy 118 QVEELINQIAEYARNKALSELGLGNNYQLYLTALTEENENPNGRALRDVNRFEILD 177
Db 105 DILLSIIDLRVSQVLNDGIADFNGLVLLRYNLEADSNWKNFNSASA-BELTRFRIAD 163
Qy 178 SLFTQYMPFSRVT-----NPEVPFLTVYAMAANLHLLLLKDAISFGEWG-WSTTTI 228
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Db 164 SEFDRILTRGSLNGSLARQNAQILLPSPASAAFFHLLLLRDLATRYCTNNGLYNATPF 223
Qy 229 NNYDYROMKLTAEYSDHCYKVTETGLAKL--KGTSAKQWVDYNQFRREMTLAVLDVVALP 286
Db 224 INYQKLELIELYDYCVHWTNRGNFELRQRTSATALEFHYRREMTLAVLDIVASF 283
Qy 287 PNVDRTYMETKAOLTREBYTDPGLGAVNVSSI--GSWYD--KAPSGVIESSVIRPPHV 342
Db 284 SLDITNPIETDFQLSRVYITDPIGFVHRSSLRGESFVFNANFSDLENAIPNPRS 343
Qy 343 FDIITGLTVYTSRSI---SSARYIRHWAGHOISYHRVSRGSLNQOMYCTNQNLHSTSTF 399
Db 344 W-FLANMIISTGLTLPVSPSTDRARVMYG---SRDRIS-PANSQFITEISSQHTTATQ 398
Qy 400 DTNVDIYKLSKDAVLIDIVPGTYTFFGMEPEVEFFMNVQNLNTRKTLKNFVSKDII 459
Db 399 TILGRNIFRVDISOACNLNDTTY-----GYNRAVFYHDASEGSRQ-----VYEGY 444
Qy 460 AST-----RDSLELPPETSDQPNYESYSHRLCHITSIPATG-----NTTGLVPVP 505
Db 445 RTGIDNPRVQNTLYLPGENSIDIPTEDYTHLS--TTINLTGGLRQVASHRRSLVMY 502
Qy 506 SWTHRSADLNNITYSKITQIPAVKQNDNLFPVVPVKGEGHTGGDLLQVNRSTGSGVTLP 565
Db 503 GWTXKSLARNNTINPRITQIPLTKVDTRGTGVSYVNDPFGICGALLQ-RTDHGSLGVL- 560
Qy 566 LARYGLALEKAGKYRVLRYADADIVLHVND----QIQMPTKWNPGEDLTKPKFVAD 621
Db 561 --RVQFPLHLRQYRIRVYASTTIRLSVNGSFGTISQNLPTMRLGEDLYRGSPAIR 618
Qy 622 AITLNLATDSSLALKHNLGEPNLTSGIVVYVDRIEPIPDVETYEAEODLEAAKAVNA 681
Db 619 FWTSTRPASPD---QIRLTIEP-SFIQEVYVDRIEPIPNPTREKEDLEAAKAVAS 674
Qy 682 LFTNTKQGLRPGVTDYEVNQAANLVECLSDLLYPNEKLLPDAVREAKLSBARNLLQDP 741
Db 675 LFTTRDGLQVNVKDYQVQDQANLVSLSDQYGYDKKWLLEAVRAAKLSERNLLQDP 734
Qy 742 DROEING--ENGWTAETGIEVEGDLAKGRVRLPGAREIDETETPTVLYOKVBEGLVK 799
Db 735 DNTNTNSTEENGWAKSNGVTISEGGPFYKGRAIQLASAR-----ENYPTIYOKVASELK 790
Qy 800 PYTRVLRGFGVSSQGLFTTIRHOTNRIVKNVDPDILLPDPVSPVNSDGSINCSQKQYN 859
Db 791 PYTRVLDGFWKSSQDLLEIDLHKKHVLKXNVPNLVSDTTPDDSCSINRCQEQQWN 850
Qy 860 SLEVEN-----RSGEAPEFSIPDTGEIDYNNAGIWGFKITDPEGYATLGNLELV 912
Db 851 AQLETEHHHPMDCCCAAQTHEPFSVIDTGLNSVDQGIWAFKVRTTDTGYATLGNLELV 910
Qy 913 EGGPLSGDALERLQREOQWKIQTMRREETDRRYWAKQAVDRLYADYQDQQLNPDVEI 972
Db 911 EVGPLSGSLERERQDNTKWSAELGRKGAETDRVYQDAKQSNHLLFVDYQDQQLNPEIG 970
Qy 973 TDLTAAQDLIOLISIPVYVYNNEMFPEIPGMNYTKFTELTDRLQOANSLYDQRIAPNGDFRNG 1032
Db 971 ADIMDAQNLVASISDVSDAVLQIPIGINVEIYTELNRLQOASLYLTSRNAVQNGDFRNG 1030
Qy 1033 LSNWATPGVEVQQINHYSVLVPIPNWDBQVSOQFTVQPNQRYLVRTAKEGVNGYVSI 1092
Db 1031 LDSMNATAGASVQDQGNTHFLVLSHWDQAQVSOQFVQPNCKYVLRVTAEBKVGGDGYVTI 1090
Qy 1093 RGGGNOTELTFESADYDNGMYNTQVSNNGYNTNNAYNTQASSTNGYNNANNMYNTQAS 1152
Db 1091 RDAHHTTETLTFNACDYDINGTYVT----- 1115
Qy 1153 NTNGYNTSVNDQGYITKVTFTFYTDQWMIEMSETGTFYIESVELI 1202
Db 1116 -----DNT-YLTKEVVFPEIQTMMVVEVNEGAFHDSIEPV 1152

RESULT 8
```



Db 207 DHCAQNFNRLDNFGVSAR---YLDQREVITSLVDIVALPNYDIRTYPISTQSOQT 262  
QY 304 REYVTPPLGAVNVSSIGSWDKAPSFVIESSVIRPHVFDYITGLTVYTSRSISARY 363  
Db 263 REYTSFPA-----EPGASLANIQLNREPLHMDFLRLVIYT---GVQSGIY 308  
QY 364 IRWAGHOISYHRVSR--GSLQ-QMYGT-----NONLHSTSTPFTNVYIKTSLKD 413  
Db 309 --HWAGHISRTGNLSSNQPLGYTAASADRAFNNHSHSET-----YRTLS-- 357  
QY 414 AVLLDI---VPGYTYIFGMPVEFPFVWQNLNTRKLYKNVPSKDIIASTRDSSELEP 470  
Db 358 APIYSVSGGISPNRTRVEG---VRFLIARDNNLDSLPFLYRK-----EGTLDSPTELP 408  
QY 471 PETSDQPNYESYHRLCHI-----TSIPATGNTTGLVPSVSWTHRSADLNNTIYSDKITOI 526  
Db 409 PEDESTPPYIGYHRLCHAFARSPVILEPSNFARLVPFVSWTHRSASPTNEVSPSRTQI 468  
QY 527 PAVKCDNLFPFVVPVKGPGHGTGDLLOYNR-STGSGVTGLFLARYGLALEKAGKYRVRRLY 585  
Db 469 PWYKAHTLASCASVIGKPGFTGGDIWTRNNILGDLGLAVTVYTGRLPQ---SYIIRLY 525  
QY 586 ATDAD---IVLVHNDQ--IQMPKTMNPGEDLTSTKTFKVADAITTLNLTATDSSLALKHNL 640  
Db 526 ASVANGSGVFRHLPPQPSYGISFPRTMGTDPLTSRSPALTLFTPIFLT-----RA 576  
QY 641 GEDPNSTLSIGVVDRIEFTPVDETYEABQDLEAKKAVNALFTNTKD-GLRPGVTDYEV 699  
Db 577 QEEFNLTIPRGVYDRIEFYFVDATPEAGYDLERAQAVNALEFTSTNQRGLKTDITDI 636  
QY 700 NOANLVECLSDDLYPNEKELLFDVAREAKRLSEARNLLODPOFQING--ENGWASTG 757  
Db 637 DQVSNLVECLSDFECLDEKELSEKVKHAKRLSDGRNLLQORNFISINGLLDRGWRGSTD 696  
QY 758 IEVIEDGALFKRYLRPLPGAREIDTPTYLYKQVEEGLKPYTRYRLRGFVSSQGLE 817  
Db 697 ITIQSGDDVFENKVTLPQTFD--ECPTYLYKIDESKLYATRYOLRGYIEDSDLE 753  
QY 818 IFTIRQTNRIKVNVP---DOLLPOVSPVNS---DGSINRSCQKYNSRLSEVENRSE-- 870  
Db 754 IYLIRNAKHEIVNVPGTSLWP--LSVENSIGPGCESNRCAHLEWNPNDLDCRDEK 812  
QY 871 ---AHBFSIPIDTGEIDYNENAGIWWGFKITDPEGYATLGNLELVEGSLSGDALERLQ 927  
Db 813 AHSHHFSLDIDVGTDLNEDLGWVLFKIKTDQGHARI GNLEPLEKPLVGEALARVK 872  
QY 928 EEOWKIQMTRREEDRRYMAKQAVDLRYADYQDOOLNPDEITDLTAQDLIQSIPI 987  
Db 873 AEKKWRDKRKLFEFTNI VYKEAKESVDALFVNSQYDKLADTNIAHAAADKRVHIRE 932  
QY 988 VYNEMPEIISGMNYYKFTLTDLRLOQAWSLYDORNAIPNGDFRNLGNNAWATPGVEV-QQ 1046  
Db 933 AYLPELSVPGVADIFEELEGRIFTAYSIDARNVTKNGDFNGLLCWAKVKGHVDEEQ 992  
QY 1047 INHTSVLIVNWBEOVSQOFTVOPNORYLRVTKARKEGVNGVYSIRDGNOTETLTF 1105  
Db 993 NHRSLVLPWENAEVSEVRCVCGYILRVYAKGYEGCVTHIEIDNDELKFSN 1052  
QY 1106 -----ASDYDTN--GMYNQVNTNGYNTNNAINTQASSTNGYNANNMNTQ 1150  
Db 1053 CVBEEVPSNTVTCNDYTAQNEEYGTYSRNOGY--DEAVESNSSVPANY--ASVYEK 1108  
QY 1151 ASWTNGYNTSV-----YNDQT-----GYIKTVTFIPIYTOQMIMSETGTFTFIESVEL 1201  
Db 1109 A-YTDRRENSCFNRGRYDTPLPAGYVTKLEYLFPFGTAKWIEIGETEGTFTIVDSVEL 1167  
QY 1202 IV 1203  
Db 1168 LL 1169

RESULT 10

S11446  
parasporal crystal cryo1dal - Bacillus thuringiensis  
N:Alternate names: parasporal crystal protein cryID  
C:Species: bacillus thuringiensis  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 01-Dec-2000  
C:Accession: S11446  
R:Hoefte, H.; Soetaert, P.; Janssens, S.; Peferoen, M.  
Nucleic Acids Res. 18, 5545, 1990  
A:Title: Nucleotide sequence and deduced amino acid sequence of a new Lepidoptera-specific  
A:Reference number: S11446; MUID:91016842; PMID:2216728  
A:Accession: S11446  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1165 <HOE>  
A:Cross-references: EMBL:X54160; NID:940279; PIDN:CAA38099.1; PID:g40280  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 32.8%; Score 2078.5; DB 2; Length 1165;  
Best Local Similarity 39.4%; Pred. No. 7.1e-112;  
Matches 499; Conservative 175; Mismatches 426; Indels 165; Gaps 33;

QY 1 MSPNNQVEYIIDATSTSVSDNSNRYPPFANEPTNALQNDYKDKYKMSAGNASEYVPGSP 6C  
Db 1 MEINNQNC-----VPYNCL-----SNPKETILGE 25  
QY 61 EVLVSGDAAKAIDIVGKLLSGLVPPVGVPIVSLYTQILIDILWPSGEKSKOWEIPMEOVE 120  
Db 26 ERLETGNTVADISLGLINFLYNSF-VPGGGFVIG-----LLELWFGIFGSPQMDIFLAQIE 80  
QY 121 ELINQIAEVARKKALSELGNNYOLYLTLAEEWENPNSGRALDRVNRREILDSLF 180  
Db 81 QLISQRIEFANQALSRLEGSLNLYKVYVAFSDWEKDPNTPALREEMRIQDNANSL 140  
QY 181 TOTMPSFRVNPVEPPLTVYMAANLHLLKLDASIFGEWGSTTTINNYDROKMLTA 240  
Db 141 ITAIPLRVQNVQVALLSVVQAANLHLILRSDVSFVGERWGYDTATINNRYSDLTSLIH 200  
QY 241 EYSDHCVKVEYELAKLKTSAQWVDYVQFREMVLAVLDVVALPNVDYTRYPMETKA 300  
Db 201 VYTNHCVDYTNQGLRLEGRFLSDMIVNFRRLQFTISVLDIVAFPPNYDIRTYPIQTAT 260  
QY 301 QLTRYVYT-PLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTSRSIS 359  
Db 261 QLTRYVYLDLPFINENLSPAASY---PTFSAESAIIIRSHPLVDPLNSFTIYTD---S 312  
QY 360 SARYIRHWAHQISYHRVSRGNL--QMYGNQNLHSTSTFDT-NYDIYKTLSDAVL 416  
Db 313 LARY-AYWGGHLVNSPRTGTTNLRSPLYGREGNTERPVTITASPSVPIFTLS----- 366  
QY 417 LDIVYPGTYI-----PFGMPVEVEFPWVQNLNTRKLYKNVPSKDIIASTR--DSE 466  
Db 367 -----YITGLDMSNPVAGIEGVEP-----QNTISRSIYKSGPIDSF 403  
QY 467 LELPETSQPNYESYHRLCHITSIPATGNTTGLVPFVSWTHRSADLNNTIYSDKITOI 526  
Db 404 SELPPQDASVSPAIGYSHRLCHATFLERISGPRIAGTVFSWTHRSASPTNEVSPSRTQI 463  
QY 527 PAVKCDNLFPFVVPVKGPGHGTGDLLOYNRSTGSGVTGLFLARYGLALEKAGKYRVRRLY 586  
Db 464 PWYKAHTLASCASVIGKPGFTGGDILTRN-SMGLGTLAVTFTGRLPQ---SYIIRFVYA 519  
QY 587 TDADIVLVHNDQ-----IQMPKTMNPGEDLTSTKTFKVADAITTLNLTATDSSLALKHNL 641  
Db 520 SVANRSCTFRYQPPSYGISFPKTMADAGEPLTSRSP-----AHTLFTPTTFSRA-----Q 570  
QY 642 EDPNSTLSIGVVDRIEFTPVDETYEABQDLEAKKAVNALFTNTKD-GLRPGVTDYEVN 700  
Db 571 EEPDLVIGSVYDRIEFTPVATFEAYDLERAQVNALEFTSTNQLGLKTDVTDYHID 630  
QY 701 QAANLVECLSDDLYPNEKELLFDVAREAKRLSEARNLLODPOFQIN--GENGWASTGTI 758  
Db 631 QVSNLVACLSDBECLDEKELSEKVKHAKRLSDERNLLODPPNFRGIRNRPDRGWRGSTD 690

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QY 759 EVIEGDALFKGRLRLPGAREIDTETPTLYLYQKVEGVLPYTRYRLRGFGVSSQGLEI 818
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
691 TIQGGDDVFKENYVTLPGTFD---ECYPTLYQKIDESKLKAYTRYQLRGYIEDSQDLEI 747
QY 819 FTIRHQTNRIVNVP---DDLIP-----DVSPVNSDGSINRCSEQKYNSRLEVENRSGE- 870
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
748 YLIRYNAKHETVNVPGTSLWPLSVENOIGFC---GEPNRCAPHEWNPDLHCSRDGCK 804
QY 871 ----AHEFSPIDTGEIDYNENAGIWWGPKITDPEGYATLGNLELVERGSLGDALERLQ 926
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
805 CAHSHHPSLIDVGCTDLNEDLGWVLFKIQDGHARLGNLEFLEKPLLEGEALARKV 864
QY 927 REBOCKIQMTRREBETDRRYMASHQAQVDRLYADYQDQQLPNDVEITDLTAAQDLIQSIP 986
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
865 RAEEKWRDKRETLQLETTIVYKEAKESVDALFVNSQYDRLQADTWIAMIHAADKEVHRIR 924
QY 987 YVYNEMPEIIGMNYTKETELTDLRLOQAWSLYDQNALPNDGFRNGLSNWATPGVEY-Q 1045
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
925 EAYLPELSVIPGVNAAIPEELEERIFTAFSLYDARNIIKNGDFNGLLCWNVKGHVEVEE 984
QY 1046 QINHTSVLIVPNWDEQVSQQTVOBNORYLVRVLTARKEGVNGVYSIRDGNOTETLTF- 1104
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
985 QNHRSLVIVPEWEAEVSQEVRCGRGYILRVYAKYEGYEGGCVTIHEIENNTDELAFN 1044
QY 1105 -----SASDYDTNGMYNTQVSNNGYNTNNAINTQASSTNGYNANNM 1146
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1045 NCVEEYVPPNNTVTCINYTATQEBYEGY---TSNRGY---DEAYGNPVPADY---ASV 1097
QY 1147 YN-----TQASSTNGYNTSVNDQT-----GYITKTVPITPYDQMWIEMSETEGFYIES 1198
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1098 YEEKSYDRRENPCESNRGYDGYTLPAGYVTKLEYFPETDKWIBIGETEGTFIVDS 1157
QY 1199 VELIV 1203
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1158 VELL 1162

RESULT 11
JT0241
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
N;Alternate names: 135K insecticidal protein
C;Species: Bacillus thuringiensis
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 01-Dec-2000
C;Accession: JT0241
R;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
A;Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein
A;Reference number: JT0241
A;Accession: JT0241
A;Molecule type: DNA
A;Residues: 1-1176 <SH1>
A;Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein
C;Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae
C;Superfamily: parasporal crystal protein
C;Keywords: Delta-endotoxin

Query Match 32.7%; Score 2073.5; DB 2; Length 1176;
Best Local Similarity 39.6%; Pred. No. 1.4e-111;
Matches 493; Conservative 176; Mismatches 439; Indels 137; Gaps 33;

QY 23 DSNRYPPANE--PTNALQNDYKDYLRKMSAGNASBPGSPYLVSGQDAAKAA---IDIV 77
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2 DNN--PNINECIPYCNLSN-----PEVEVLGGERIETGYTPIDIS 39
QY 78 GKLSGLGVPPFGPIVSVLYTOLIDLWPSGEKSQWEIPEQVEELINQKIAYARKALS 137
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
40 LSLAQFLLSSEFV-PCAGPVLGLVDIIWGIFGFSQMDAPLVQIEQLINQRIEFARNQAIS 98
QY 138 ELEGNNYQLYLTALEWEENPNPSRALRDVNRNFEILDSLFTQYMPSPFRVTFEVPFL 197
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
99 RLEGLSNLYQIYABSFREWEADPTNPALRBEEMRIQFNDMSALTAIPLFAVQNYQVPLL 158
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QY 198 TVYMAAANLHLLLKDASIFGEEWGWSTTTNNYVDQMKLTABYSCHVKWYETGLAKL 257
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
159 SVYVQAANLHLVLRLDVSFGQWGPDAATINSRYNDLTRIGNYTDVAVRWYNTGLERV 218
QY 258 KGTSAKWVDYNQPRREKTLALVDVALFPNYDTRTPMETKAQLTREVIYTDPLGAVNVS 317
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
219 WGPDSRDWRVYNQPRRELTITLVDIVALFNSYDSRRYPIRTVSQLTREIYTNP---VLEN 275
QY 318 SIGSWYDKAPSGFVIESSVIRPPHVFYITGLTVYITQSRSSISSARYIRHWAGHOISYHRV 377
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
276 PDGSPRGMAQR---IEQN-IRQPHLMDILANSIYITDVH-----RGFNWMSGHOITASPV 326
QY 378 --SRGSLQOQMYGNQNLHSTSTFDTNYDIYKTLSDKAVLLDIVPGYTYIFFG----- 430
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
327 GFSGPEFAFLFGNAGNAAPPVLVSLTGLGIFRTLSS-----PLYRRIILLGSGPNN 377
QY 431 -----MEVEFFVMVQNLNTRKTLKYNPVSKDIIASTDSELELPPETSDOPNYESYSHR 485
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
378 QELFVLDTGTEBFSFASLTNTLPSTI-YEQ-----RGTVDSLVDVIPPQDONSVPFRAGFSHR 430
QY 486 LCHITSIPTAGTNT--TGLVPVSWTHRSADLNNTIYSDKITQIPAVKCDNMLPFVPVVKG 543
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
431 LSHVTMLSQAGAVYTLRAPTFSSHQHSASFNNIIPSSQITQIPLTKSTNLGSGTSVVKG 490
QY 544 PGHTGDLQLQNRSTGSGVTFLFARYGLALEKAKGYRVRLYATDADIVLHVN-DA----- 598
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
491 PGFTGGDILR-RTSPGQISTL---RVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPIN 546
QY 599 QIQPKPTNMGEDLTSTKPKVADAITLNLATDSSL-----ALKHNLGEDPNSTLSGIYVV 654
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
547 QGNFSATMSGNSGSLQSGSPRTVGTTPFNSGSSVFTLSAHVFNSGNE-----VYI 598
QY 655 DRIEFIPVDETYEAEODLEAAKAVNALFTNTKD-GLRPGVTDYEVNOAANLVECLSDDL 713
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
599 DRIEFVPAEVTFEAYDLEAQAVALNELFTSSQIGLTKTDVTDHIDQVSNLVECLSEDF 658
QY 714 YPNEKRLFDVAERAKRLSEARNLLQDPDFQIEING--ENGWTAETGIEVIEGDALFKGRY 771
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
659 CLDEKQELSEKVKHAKLSDBERNLLQDPNFRGINRQLDRGWRGSTDTITIQGDDVFKENY 718
QY 772 LRLPGAREIDTETPTLYLYQKVEGVLPYTRYRLRGFGVSSQGLEIFTIRHQTNRIVKN 831
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
719 VTLIGTFD---ECYPTLYQKIDESKLKAYTRYQLRGYIEDSQDLEIYLIIRYNAKHETVN 775
QY 832 VPDD-----LLPDPVSPVNSDGSINRCSEQKYNSRLEVENRSGE-----AHEFSPIDTGE 882
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
776 VPGTGSIMPLSAQSPIGKCGEPNRCAPHEWNPDLDCSRDGECAHSHHFSLIDIDVGC 835
QY 883 IDYNENAGIWWGPKITDPEGYATLGNLELVEEGLSGDALERLQREBOCKIQMTRREE 942
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
836 TDLNEDLGWVVIKIKTQDGHARLGNLEFLEKPLVGEALARVKRAEKKWRDKREKLEWE 895
QY 943 TDRYMAKQAVDRLYADYQDQQLNPQVEITDLTAAQDLQSIPIPVYNEMPEIPEGMNVT 1002
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
896 TNIVYKEAKESVDALFVNSQYDQQLQADTNAMIHAADKRVHSIREAYLPELSVIPGVNAA 955
QY 1003 KFTBLTDLRLOQAWSLYDQNALPNDGFRNGLSNWNAATPGVEV-QQINHTSVLVIIPNWDQ 1061
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
956 IFEELEGRIPTAFSLYDARNVINKGDFNGLSCWNVKGVHDVVEEQNQRSVLVVPWEAE 1015
QY 1062 VSQQTFTQPNQRYVLRVYARKEGVNGVYSIRDGNOTETLTFPS-----AS 1107
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1016 VSQVRVCPGRGYILRVYAKYEGYEGGCVTIHEIENNTDELKFSNCVBEIYPNNVTVCN 1075
QY 1108 DYDTN-----GMYTQVSNNGYNTNNAINTQASSTNGYNANNMVNTQASNTNGYNTNSV 1162
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1076 DYTNOBEYGGAY---TSNRGY---NEAPSVPADYASYEEKSY--TDGRENPCFEFNRG 1128
QY 1163 YNDOT-----GYITKTVPITPYDQMWIEMSETEGFYIESVELIV 1203
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1129 YRDYTPLFVGVTKELEYFPETDKWIBIGETEGTFIVDSVELLL 1173
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RESULT 12  
JC2219  
parasporal crystal protein cryIAa - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 01-Dec-2000  
C:Accession: JC2219  
R:Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.  
Biosci. Biotechnol. Biochem. 58, 830-835, 1994  
A:Title: Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain FU-2-7 and an  
A:Reference number: JC2219, MUID:94289859; PMID:7764972  
A:Accession: JC2219  
A:Molecule type: DNA  
A:Residues: 1-1176 <UDA>  
A:Cross-references: DDBJ:D17518; NID:G506190; PIDN:BAA04468.1; PID:G535781  
C:Genetics:  
A:Gene: cryIA(a)  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 32.7%; Score 2070.5; DB 2; Length 1176;  
Best Local Similarity 39.5%; Pred. No. 2.1e-111;  
Matches 492; Conservative 176; Mismatches 440; Indels 137; Gaps 33;

QY 23 DSNRYFANE--PTNALQNDYKDYLMKSNAGNASEYPGSEVLVSGQDAKAA---IDIV 77  
DB 2 DNN--PNINECPYCNLSN-----PEVEVLGGERIETGYTPDIS 39

QY 78 GKLLSLGLVFPVGVISLYTQLDILWPSCGKSEWEIFMEQVEELINOKIAEYARNKALS 137  
DB 40 LSLTQFLLESEF-PGAGFVLGLVDIIWIGFPGSQWDAFLVQIEQLINQRIEFAFNQALS 98

QY 138 ELEGNNYQLYLTALAEWEENPGSRALDRVNRREIFLDSLTQYMPSPRVNFEVPEL 197  
DB 99 RLEGSLNLYQIAESPREWEADPTNPALREEMRIQFNMDMSALTTPALPLAVQNYQVPEL 158

QY 198 TVYMAANLHLLKDAFEGEWSGHTTTINNYDROMKLTAEYSDHCKVKTETGLAKL 257  
DB 159 SVYVQAANLHLSVLKDVSVFGQWGFDAATINSRYNDLTGLIGNYTDYAVRWNTGLERV 218

QY 258 KGTSAKQWYDYNQFREMTLAVLDVVALLPNDYTRYVPMETKALREVYTDPLGAVNVVS 317  
DB 219 WGFSDSDWRYNQFRELNLTVLDIVALSNDYRSRYPIRTVSQLREIYNP---VLEN 275

QY 318 STGSWYDKAPSGVIRPPEVDFYITGLTVYTSQSRSSISSARYIRHWAGHQISYHRV 377  
DB 276 FQGSFRGMAQR---IQON-IRQPHLMDILNISIYITDVH-----RGFNYSWGHIITASPV 326

QY 378 --SRGSNLQOMYGTQNLHSTSTFDFTNDYIYKLSKDAVLLDIVPGYIYIPFG----- 430  
DB 327 GFSGPEFAPPLFGNAGNAAPPVLVSLTGLGIFRTLS-----PLVRRITLGSPPNN 377

QY 431 ----MPEVEFFMVNQLNTRKTLKYNPVSKDIIASTRDSLELPPETSQPNYESYSR 485  
DB 378 QELFVLVDGTEFEFASLTNLPSTI-YRQ-----RGTVDLSDVIPPQDMSVPPRAGFSR 430

QY 486 LCHITSIPATGNT--TGLVPFVSWTHRSADLNTIYSDKITQIPAVKCDNLPFPVWVK 543  
DB 431 LSHVTMLSOAGAVYTLRAPTFSQWHSRAEFNIIIPSSQITQIPLKSTNLGSGTSVVK 490

QY 544 PCHTGGDLLOYNRSTGVCUTFLARYGLALEKAKYRVLRYATDADIVLHN-DA----- 598  
DB 491 PFGTGGDLIR-RTSPQGISLT---RVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPIN 546

QY 599 QIQMPTKMNPGDLTSKTPKVAADAITLNLATDSSL---ALKHNLGDPNSTLSGIVVV 654  
DB 547 QGNFATMSSGSLNLSGSRFTVGTFTFPNFGSSSVFTLSAHVFNNGNE-----VVI 598

QY 655 DRIEIPVDETYEAEODLEAKKAVNALFTNTKD-GLRFGVTDYEVNQANLVCELSDDL 713  
DB 599 DRIEFPVAEVTAEAYDLERAKAVNELFTSSNQIGLKTDDVDYHDQVSNLVECLSDSF 658

QY 714 YPNEKRLFLDAVREAKRLSEARNLQDDPQFQING--ENGWTASTGIEVIEGDLPKGRY 771

DB 659 CLDEKQELSEKVKHAKRLSDERNLQDPNFRGINRQLDRGWRGSTDITIQGGDDVPKENY 718

QY 772 LRPGAREIDTETYPYLYQKVEEGLVPYRVRLRGLFVSSQGLFIFTRHQTNRIVKN 831

DB 719 VTULGTFD---ECYPYLYQKIDESKLYATRYQLRGYIEDSODLEIYLIRYNAKHETVN 775

QY 832 VPDD----LLPDVSPVNSDGSINRSEQKYVNSRLSEVENRSGE-----AHEFSIPIDTGE 882

DB 776 VPQTGSLWPLSAGSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLDIDVGC 835

QY 883 IDYENAGIIVGFKITDPGYATLGNLELVSEGPLSGDALERLQREEQOQKIOMTTRREE 942

DB 836 TDINEDLGWVIFKIKTQDGHARLGNLEPLEBKPLVGEALARKVRAEKKWRDKRELEWE 895

QY 943 TDRRYWASKOAVDRLVADYQDQQLNPDVEITDLTAQODLIQSIPIYVYNEMFPEIPGNYT 1002

DB 896 TNIVYKEAKESVDALFVNSQYDQLOQADTNIAHAAADKRVHSIREAYLPSELSVIPGVNAA 955

QY 1003 KFTELTDRLQOAWSLYDQRNAIPNGDFRNLGNLNMNATPGVEV--QQINHTSVLVI PNWDEQ 1061

DB 956 IPFEELEGRISTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQSRSLVVPWEAE 1015

QY 1062 VSOQFTVQNRQYLVLTARKGNGVYVSIIRDGNGQTETLTFSS-----AS 1107

DB 1016 VSGEVRVCPGRGYILRTAYKEGYGEGCVTHIEINNTDELKPSNCVBEIYPNNTVTCN 1075

QY 1108 DYDTN-----GMVNTQVSNYNGVYTNNAVTOASTNGYNNANNMYTQASNTGYNTNSV 1162

DB 1076 DYTVNOEEYGGAY---TSNRGY--NEAPSVADYASVYEEKSY--TDQRRENPCBFNRG 1128

QY 1163 YNDQT---GYITKTFTPIFYTDQMIEMSETEGTFYIESVELIV 1203

DB 1129 YRDYPLPVGYVTKLEYPETDKWVIEIGETEGTFIVDSVELLL 1173

RESULT 13  
S32645  
parasporal crystal protein cryIgal - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S32645  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32645  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1166 <LAM>  
A:Cross-references: EMBL:Z22510; NID:G295861; PIDN:CAA80233.1; PID:G295862  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 32.7%; Score 2069; DB 2; Length 1166;  
Best Local Similarity 38.4%; Pred. No. 2.5e-111;  
Matches 481; Conservative 193; Mismatches 415; Indels 164; Gaps 32;

QY 22 NDSNRYFANEPTNALQNDYKDYLMKSNAGNASEYPGSEVLVSGQDAKAAIDIVKLL 81

DB 4 SQNQY---IPYCNLNPSEIPIF-----NARNSNFGLVSQVS 37

QY 82 SGL-----GVFPVGVISLYTQLDILWPSCGKSEWEIFMEQVEELINOKIAEYARNK 134

DB 38 SGLTRFLLEAAVPEAGPALGLP---DIWGLGVDDQSLFRLQIEQLIRQIEITELERNR 93

QY 135 ALSELEGNNYQLYLTALAEWEENPGSRALDRVNRREIFLDSLTQYMPSPRVNFEV 194

DB 94 ATAILTGLSSSNLYVEALREWENPNPNPASQERVTRFRLTDDAIVTGLPLAIRNLEV 153

QY 195 PLYTVYMAANLHLLKDAIFEGEWSGHTTTINNYDROMKLTAEYSDHCKVKTETGL 254

DB 154 VNLVSYYQAANLHLSRLDVAIFYGRWGLTQANIEDLYTRLTSTNIQEYSDHCAWYNOGL 213

QY 255 AKLKGTSAKQWYDYNQFREMTLAVLDVVALLPNDYTRYVPMETKALREVYTDPLGAV 314



Db 214 NEIGGSR---YLDFODLTISVLDIVLFPNPDYDRTPIPTQSLTRITYTSPVAV 269  
QY 315 NVSSIGSWYDKAPSGVLESSVIRPPHVDYITGLTVTQSRSSIRYIRHWAGHQS 374  
Db 270 NI-----NFGSLANVLRAPHLMDRIDRIVIT-----NSVSTPYWAGHEIS 313  
QY 375 HRVSRGSLQ---QMYGTNQLHSTSTPFTNYD-----IYKTLSDKAVLL 417  
Db 314 RRTGOGGNEIRPPLYGAANAEPVPIRPTGFTDQQRWYRARSRVVSRSSGQDFSLV 373  
QY 418 DIVVPGYIIFGHEPEVFFWQVNLNTRKLYKYNPVSQDIASRDSELELPPETSQP 477  
Db 374 DAV--GLTIP-----SAVSIYRNGFGFTDID-----EPIEGTDP- 409  
QY 478 NYESVHRLCHITSIPATG--NTTGLVPVSWTHESADLNNTIYSDKITQIPAVKCDNL 535  
Db 410 -FTGSHRLCHVGLASSPFIQYARAPISWTHRSATLNTIAPDVITQIPLVKAFNLH 468  
QY 536 PFPVVKPGHGTGDLLOYNRSTGSGVTLFLARYGLALEKAKYRVRLYA--TDADI 593  
Db 469 SGATVKGPGTGGDILR-RINVSFGDM--RVNITAPLSQRYRVRIRYASTDLOPYT 524  
QY 594 EVNDAQOM-----PKTMNGBDLTSTKTFKVAADAITLNLATSSALKKNLGEDPNSTLSG 650  
Db 525 XINGTTINIGFSSSTMSGDDLOVGRFVAGFTPTPTSDANSTFTICAGFGSPNNE--- 581  
QY 651 IVVYDRLEFIPVDEYAEQLEBAKAVNALFTNTKD--GLRPGVTDYEVNQAANLVECL 709  
Db 582 -VYIDRLEFPAEVTTFEAYDLEKAKAVNALFTSSNOIGLKTVDTHIDKVNLSVCL 640  
QY 710 SDDLVPNEKRLFLDAVRAKLSARNLLQDPDOFIN--GENGWASTGTGIEVIGDALF 767  
Db 641 SDFCLDEKRESEKVKHAKLSDEENLLQDPNFGINRQPDGRGSGTDITIQGDDVP 700  
QY 768 KGRVLRIPGAREIDTETPTLYXQKVEGVLKPYTRYLRGLRFGVSSQGLEIFTIRHOTNR 827  
Db 701 KENYVTLPGTDP--GCYPTLYXQKIDSKLVKRYTRYQLRGVIEDSQLEIYLIRYNAKH 757  
QY 828 IVKNVDD---LLPDVSPVNSDGSINRSEKQYVNSLEVENRSGE-----AHEFSPTI 878  
Db 758 ETNVNPGTSLWPLSAQSPIGKCGEFPNRCAPHELNWPNPLDCSRNGEKAHHSHFLDI 817  
QY 879 DTGSDIDYENAGIWWGFKITPEGVATIGNLELVEEGLSDALERLQREKQOWKIOMTR 938  
Db 818 DVGCTDLNEDLVWVIFKIKTQDGHARGNLGFLTEKPLGLENLARVKAEEKWDEK 877  
QY 939 RRETDRRYMAKQAVRLYADYQDQQLNPVIEITDLTAADLIQSIPIVYNEMPEPIPG 998  
Db 878 LELETNIIVYKEAKESVDALFVNSQYDQLQADTNIAHAAADKRVHSIREAYLPELSVPF 937  
QY 999 MNYTKFTLTDLQOAWSLYDORNALPNGDFENGLSNNAATPGVEV-QQINHTSVLVI 1057  
Db 938 YNAAFEELEGRIFTAFSLDARNYKNGDFNGLSCWNVGHVDVBEQNHRSLVAVPE 997  
QY 1058 WDEQVSOQFTQPNORYLVRATKRGVNGVYSIRDCGNOTETLTF----- 1105  
Db 998 WEAEVSQEVCPGEGYILRTAYKEGGEGCVTHIBENNTDELKFNCEVEEYVY 1057  
QY 1106 --ASDYDTN-----GMNTQVSNYNTGYNNTNAYNTQASSTNGYNNANNYN---TOASNT 1154  
Db 1058 VTCNDYNTANQEEYKAY---TSHNGY--DEAYGNPNVPADYTP--VYEKAYTDGRRE 1110  
QY 1155 NGYNTNSVYNDQT---GYIKTVTFPIPTDQMWIEMSETETGTFYIESVELIV 1203  
Db 1111 NPCESNRGYDGYTLPAGYVTKLEYFPETDKVWIEIGETGTFIVESVELIL 1163

## RESULT 14

S32647

parasporal crystal protein cry1db1 - Bacillus thuringiensis

C;Species: Bacillus thuringiensis

C;Date: 20-Feb-1995 #sequence #revision 20-Feb-1995 #text\_change 01-Dec-2000

C;Accession: S32647  
R;Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A;Reference number: S32645  
A;Accession: S32647  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1160 <LAMB>  
A;Cross-references: EMBL:Z22511; NID:g295863; PIDN:CAA80234.1; PID:g295864  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 32.6%; Score 2065; DB 2; Length 1160;  
Best Local Similarity 39.3%; Pred. No. 4.2e-111;  
Matches 480; Conservative 190; Mismatches 426; Indels 126; Gaps 28;

QY 33 PTNALQNDYKDYKMSAGNASEYPGSEVLVSGQDAKAAIDIVGKLLGLVFPVGP 92  
Db 11 PYNCLSN---PDAILLDA-----ERLETGNTVADISLGLINFLYSNP-VPGGG 56  
QY 93 VSLYTQIDILWPSEKESQWEIEMQVEELINOKIAEYARNKALSELEGIGNNYOLY 152  
Db 57 VG-----LLELWGVGFSQWEIFLAQLEQLISQRIEFARNQALSRLEGLSN 112  
QY 153 LEEWEPNPGSRALDRVNRFEILDSLFTQYMPSFRTVNFVEPFLTVYMAANLHLL 212  
Db 113 FRAMEKOPSNPALREEMRTQFVNNSALIAAIPLLRVNVEVALLSVVQAANLH 172  
QY 213 DASIFGEWGSTTTINNYDROMKLTABYSDHCVKMYETGLAKLKTSAKOWDYNO 272  
Db 173 DVSVYQGWGDPATVNSRYSDLTRELHVYTDHCVDTYNDGLKNLEGRSLSDWV 232  
QY 273 REMTLAVLDVVALPNDYTRTPMETKAQLTREVYTD--PLGAVNVSSIGSWYDKAP 331  
Db 233 RRLTISVLIDITAFPNVDIEAYPIQTASQLTREVYLDLPFVNETLSPSPSY 288  
QY 332 IESSVIRPPHVDYITGLTVTQSRSSIRYIRHWAGHQSIRHVRSGSL--QOMY 389  
Db 289 AESAIIRSPHLVDLNSFTIYTD--SLASYAY---WGHVLVNSFTGTITNLRSP 343  
QY 390 NQNLHSTSTPFT--NYDIYKTLSDKAVLLDIVPGYTVIFF-----GMPEVE 438  
Db 344 EGENTERPVTISASPSVPIFRTLS-----YFTGLNNPNVAGIEGVF-- 385  
QY 439 VNQLNTRKTLKYNPVSQDIASR--DSELELPETSQDNVSSYSHRLCHITSIPAT 496  
Db 386 -----QNTISRSIYRKSGPIDSPSELPDPQSVSPALGYSHRLCHATP 433  
QY 497 NTTGLVPVSWTHRSADLNNTIYSDKITQIPAVKCDNLFPVVPVVKFGHTGGD 556  
Db 434 GPRTAGTVFVSWTHRSASPINEVSPSRITQIPWKAHTLASGASVIKGFGTG 492  
QY 557 STGSGVTLFLARYGLALEKAKYRVRLYATDADIVLHVNDAQ-----IQMP 611  
Db 493 SMGDLGALRVFTTGRLPQ---SYIRFRYASVANRSGTFRYSQPPSYGISFP 549  
QY 612 LTKTEKVAADITLNLATSSALKKNLGEDPNSTLSGIYVVDRIEPIPVDETVE 671  
Db 550 LITSRF-----AHTLFTPTFSRA-----QEEFDLYIQSGVYIDRIEPI 600  
QY 672 LEAKAKVNALFTNTKD--GLRPGVTDYEVNQAANLVECLSDLPNEKRLFLDA 730  
Db 601 LERAKAVNALFTSTNQLGKLTVDTHIDQVSNLVECLSDPECLDEKRESEK 660  
QY 731 LSEARNLQDPPDOFIN--GENGWASTGTGIEVIGDALFKGRIYLRPLPGARID 788  
Db 661 LSDERNLLQDPNFRGINRQPDGRWKGSTDTIQGDDVFKENYVTLTGTDF-- 717  
QY 789 LYQKVEGVLKPYTRYLRGLRFGVSSQGLEIFTIRHOTNRIVKNVDD---LL 844  
Db 718 LYQIDESKLYKAYTRYQLRGVIEDSQLEIYLIRYNAKHIEIVNVPNGTSL 777  
QY 845 SDGSINRSEKQYVNSRLEVENRSGE-----AHEFSIPTDGTGIDYENAGI 899

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Db 778 KCPEPNRCAPHLEWNPDLDCSCREKCAHSHHFLSDIDVGCTDLNEDLGWVFIKKT 837
Qy 900 PEGYATIGNLELVEEGLSGDALERLQREEQOWKIQMTRREEDTDYRMASKQAVDRILYA 959
Db 838 QDGHARLGNLEFLBEKLVGEALARVRAEKKWRDKREKLELENTIYVYKEAKESVDALFV 897
Qy 960 DYDQOOLNPVEITDLTAAQDLIQSIYVYNEMFPEIPGMNNTKFTLTDRLOQAWSLYD 1019
Db 898 NSQYDQLOADNTNMIHAAKRVHSIREAYLPESLVIPGNVAGIFELEGREIFTAYSLYD 957
Qy 1020 ORNAIPNGDFRNGLSNNWATPGVEV-QQINHTSVLVLPNWDQVSQFTVQPNQRYVLV 1078
Db 958 ARNVKNGDFNGLSCWNVKGVHVDVEQNNHRSVLVPEWEAEVSQEVVCPGGRGYILRV 1017
Qy 1079 TARKEGVGVVSRDGGNGTETLTFSASDYDTNGMYNTQVSTNGYNTNNAYNQASST 1138
Db 1018 TAYKEGEGECVTIHEVDNNTDELKF--SNCEKEQVYVPGNTVACNDKXKHGANACSSRN 1075
Qy 1139 NGYNANNMYNT-----QASNTNGYNTNSVYNDQ-----TGVIKTVTFIFPTD 1181
Db 1076 RGYDESYESNSSIPADYAPVVEEAYTDGQGNCFEFGHTPLPAGVTALELYFPETD 1135
Qy 1182 QMNIEMSETEGTFVIBSVELIV 1203
Db 1136 TVWVEIGETEGTFIVDSVELLL 1157

RESULT 15
S02215
parasporal crystal protein cryA - Bacillus thuringiensis (strain entomocidus)
C:Species: Bacillus thuringiensis
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 01-Dec-2000
C:Accession: S02215
R:Masson, L.; Marcotte, P.; Prefontaine, G.; Brousseau, R.
Nucleic Acids Res. 17, 446, 1989
A:Title: Nucleotide sequence of a gene cloned from Bacillus thuringiensis subsp. ent
A:Reference number: S02215; MUID:89098405; PMID:2911478
A:Accession: S02215
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1176 <MAS>
A:Cross-references: EMBL:X13535; NID:g40266; PIDN:CAA31886.1; PID:g40267
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 32.6%; Score 2063.5; DB 2; Length 1176;
Best Local Similarity 39.5%; Pred. No. 5.3e-111;
Matches 492; Conservative 175; Mismatches 441; Indels 137; Gaps 33;

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Qy 78 KLLSLGLGVFPVGVIVSLYTLQDILIMPSEKESQWEIFMEQVEELINQKIAEYARNKALS 137
Db 40 LSLTQFLLSFV-PGAGFVLGLVDIIWGIFGPSQWADAPPVQIEQLINQRIEFPARNQAS 98
Qy 138 ELSEGLNNYQLYLTALBEWENPNSRALRDVRNRPFLDSLTQYQWPSFRVTFVFPFL 197
Db 99 RLEGLSLYQIYAESFREFWEADPTNPALEEMRIQFNDMSALTTAIPLLAVQNYQVPL 158
Qy 198 TVYAMAANLHLLKADASIFGEEWGSWTTTNNYVDQMKLTAEYSDBHCKWYETGLAKL 257
Db 159 SVVQAAANLHLSVLRDVSFGQRFQGFDAATINSYNDLTRLIGNYTDYAVRWYNTGLERV 218
Qy 258 KGTSAKOWDYNQFRREMTLAVLDVALFPNYDTRTPMETKAQLTREVYTDPLGAVNVS 317
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Qy 318 SIGSWYDKAPSGFVIESVIRPPHFVYITGLTVYTSQSSISSARYIRHWAGHAGISYHRV 377
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Qy 378 --SRGSNLQOMYGTNQLHSTSTFTDFTNYDIYKTLGSKDAVLDDIVYPGYTYIFFG----- 430
Db 327 GFSGPFAPPLFGNAGNAAPPVLVSLTGLGIFRLSS-----PLYRRIILGSGPNN 377
Qy 431 -----MPEVEFFMVNOLNNRTRKLYKNPVSKOIIASTRDESELEPPETSDQPNYBSYSHR 465
Db 378 QBLFVLDTGTEFSPASLTNLPSTI-YRQ-----RGTVDSLDVIPPQDNSVPPRAGFSHR 430
Qy 486 LCHITSIPATGNT--TGLVPVFSWTHRSADLNTIYSDKITQIPAVKCDWNLFPVPVVK 543
Db 431 LSHVTWMLSOAGAAYVYTLRAPTFWQHSRSEAFNNIIPSSQITQIPLTKSTNLSGSGTSVVK 450
Qy 544 PGHTGDLQYNRSTGSGVTLFLARYGLALEKAGKRVRLRYATDADIHLVHN-DA----- 558
Db 491 PGFTGGDLR-RTSPQIGISTL---RVNITAPLSQRVVRIRVASTTNLQPHSTIDGRPIN 546
Qy 599 QIQMPTKMPGDELTSKTFKVAADAITLNLATDSSL-----ALKHNLGDEPNSTLSGIVYV 654
Db 547 QGNFATMSGSGNLQSGSFRTVGTFTFPNFSNGSVPTLSAHVFNSGNE-----VYI 598
Qy 655 DRIEFTPVDETYEABODLEAAKAVNALPTNTKD-GLRPGVTDYEVNQANLVECLSDDL 713
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Job time : 51 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2003, 05:16:28 ; Search time 43 Seconds  
(without alignments)  
531.524 Million cell updates/sec

Title: US-10-032-717-2  
Perfect score: 6332  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 19951520 residues  
Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2          | 5673   | 89.6        | 1210   | 12    | US-10-032-717-4  |
| 3          | 3511   | 55.4        | 669    | 12    | US-10-032-717-10 |
| 4          | 3511   | 55.4        | 669    | 12    | US-10-032-717-16 |
| 5          | 3502   | 55.3        | 667    | 12    | US-10-032-717-6  |
| 6          | 3499   | 55.3        | 673    | 12    | US-10-032-717-12 |
| 7          | 3499   | 55.3        | 673    | 12    | US-10-032-717-22 |
| 8          | 3499   | 55.3        | 673    | 12    | US-10-032-717-40 |
| 9          | 3485.5 | 55.0        | 670    | 12    | US-10-032-717-24 |
| 10         | 3485.5 | 55.0        | 670    | 12    | US-10-032-717-44 |
| 11         | 3229   | 51.0        | 616    | 12    | US-10-032-717-20 |
| 12         | 3217   | 50.8        | 620    | 12    | US-10-032-717-30 |
| 13         | 3217   | 50.8        | 620    | 12    | US-10-032-717-32 |
| 14         | 3217   | 50.8        | 620    | 12    | US-10-032-717-42 |
| 15         | 3203.5 | 50.6        | 617    | 12    | US-10-032-717-34 |
| 16         | 3203.5 | 50.6        | 617    | 12    | US-10-032-717-46 |
| 17         | 2852   | 45.0        | 673    | 12    | US-10-032-717-18 |
| 18         | 2821   | 44.6        | 667    | 12    | US-10-032-717-8  |
| 19         | 2335   | 36.9        | 1186   | 10    | US-09-826-660-23 |

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| 20 | 2208   | 34.9 | 1163 | 10 | US-09-756-526A-2  | Sequence 2, Appli |
| 21 | 2181.5 | 34.5 | 1316 | 9  | US-10-120-544A-4  | Sequence 4, Appli |
| 22 | 2151.5 | 34.0 | 1163 | 10 | US-09-826-660-21  | Sequence 21, Appl |
| 23 | 2116.5 | 33.4 | 1386 | 9  | US-10-120-544A-6  | Sequence 6, Appli |
| 24 | 2061   | 32.5 | 1177 | 10 | US-09-873-873-26  | Sequence 26, Appl |
| 25 | 2061   | 32.5 | 1177 | 10 | US-09-873-873-28  | Sequence 28, Appl |
| 26 | 2053   | 32.4 | 1155 | 10 | US-09-756-643-2   | Sequence 2, Appli |
| 27 | 2053   | 32.4 | 1177 | 10 | US-09-873-873-10  | Sequence 10, Appl |
| 28 | 2053   | 32.4 | 1177 | 10 | US-09-873-873-12  | Sequence 12, Appl |
| 29 | 2053   | 32.4 | 1177 | 10 | US-09-873-873-14  | Sequence 14, Appl |
| 30 | 2050   | 32.4 | 1193 | 10 | US-09-873-873-30  | Sequence 30, Appl |
| 31 | 2042   | 32.2 | 1177 | 10 | US-09-873-873-34  | Sequence 34, Appl |
| 32 | 2028.5 | 32.0 | 1332 | 9  | US-10-120-544A-18 | Sequence 2, Appli |
| 33 | 2023.5 | 32.0 | 1178 | 10 | US-09-851-194-2   | Sequence 6, Appli |
| 34 | 2020   | 31.9 | 1174 | 10 | US-09-826-660-6   | Sequence 15, Appl |
| 35 | 2007.5 | 31.7 | 1156 | 10 | US-09-826-660-15  | Sequence 20, Appl |
| 36 | 2006.5 | 31.7 | 1344 | 9  | US-10-120-544A-20 | Sequence 2, Appli |
| 37 | 1992   | 31.5 | 1148 | 10 | US-09-826-660-2   | Sequence 4, Appli |
| 38 | 1827.5 | 28.9 | 1109 | 10 | US-09-756-526A-4  | Sequence 25, Appl |
| 39 | 1274   | 20.1 | 643  | 10 | US-09-826-660-25  | Sequence 2, Appli |
| 40 | 1194.5 | 18.9 | 644  | 10 | US-09-943-692-2   | Sequence 27, Appl |
| 41 | 1079   | 17.0 | 655  | 10 | US-09-826-660-27  | Sequence 11, Appl |
| 42 | 1070   | 16.9 | 547  | 10 | US-09-826-660-11  | Sequence 4, Appli |
| 43 | 931    | 14.7 | 605  | 10 | US-09-826-660-4   | Sequence 6, Appli |
| 44 | 687    | 10.8 | 1257 | 10 | US-09-738-363-6   | Sequence 4, Appli |
| 45 | 672    | 10.6 | 333  | 10 | US-09-851-194-4   |                   |

ALIGNMENTS

RESULT 1  
US-10-032-717-2  
; Sequence 2, Application US/10032717  
; Patent No. US0020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; PESTICIDAL ACTIVITY AGAINST COLEOPTERANS  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1206  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-032-717-2

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|-----------------------|-----------------|--|-----------|--------------|
| Query Match           | 100.0%;         | Score 6332;  | DB 12;    | Length 1206; |
| Best Local Similarity | 100.0%;         | Pred. No. 0;   |           |              |
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241 QY EYSDHCWKYETGLAKGTSKQWVDYNOFREMVLAVLDVVALPNNYDTRTPMETKA 300  
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301 QY QLTREVYTDPLGAVNVSSIGSWDKAPSGFVIESSVIRPPHVDYITGLTVYTSRSISS 360  
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421 QY YPGYTYIFPGMPEVEPFVWNLNTRTKLYNPVSKDIIASTRDSLELPPETSDQPNYE 480  
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RESULT 2  
US-10-032-717-4  
; Sequence 4, Application US/10032717  
; Patent No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With  
; Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1210  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
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594 QY HVNDAQIOM-----PKTMNPGEDLTSTKPKVADATITLMLATDSSLALKHNLGSDPNSTLS 649  
596 DB YINPSEENVKSHAQKTNRGEALTYNKFNYA-TLPPIKFTT-----TEPPTILG 643

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DB 764 VIEGDALFKRYLRLPGAREIDTETPTLYLQKVEEGLVLPYTYRURLPFGVSSQGLEIF 823
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DB 824 TIRHQTNRIVKNVPDDLDPVSPVNSDGSINRCSEQKYVNSRLEVENRSGEAHFSIPID 883
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QY 1180 TDQWMIEMSETEGFFYIESVELIYDVE 1206
DB 1184 TDQWMIEMSETEGFFYIESVELIYDVE 1210

RESULT 3
US-10-032-717-10
; Sequence 10, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT FILING DATE: 2001-10-23
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Maize optimized Cry1218-1
US-10-032-717-10

Query Match 55.4%; Score 3511; DB 12; Length 669;
Best Local Similarity 100.0%; Pred. No. 5.6e-239;
Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MSPNNONEYEI IDATPSTSVSNDNRYRPFANEPTNALQNMDYKDYLKMSAGNASSEYPGSP 60
DB 1 MSPNNONEYEI IDATPSTSVSNDNRYRPFANEPTNALQNMDYKDYLKMSAGNASSEYPGSP 60
QY 61 EVLVSGQDAKAAIDIVGKLLSGLVFPFVGVPIVSLYTLQILIDILWPSGEKQOWEIFMEQVE 120
DB 61 EVLVSGQDAKAAIDIVGKLLSGLVFPFVGVPIVSLYTLQILIDILWPSGEKQOWEIFMEQVE 120
QY 121 ELINQKIAEYARNKALSELEGLGNNTQLYLTALBEEENPNSGRALRDVNRREIFDLSLF 180
DB 121 ELINQKIAEYARNKALSELEGLGNNTQLYLTALBEEENPNSGRALRDVNRREIFDLSLF 180
QY 181 TQMPSPFRVTNPFVPLTVYMAAANLHLLLLKDSIFGEGWGSTTTINNYDROMKLTATA 240
DB 181 TQMPSPFRVTNPFVPLTVYMAAANLHLLLLKDSIFGEGWGSTTTINNYDROMKLTATA 240
QY 241 EYSDHCVKMYETGLAKTSGTSAQWVDYVYQFREMFLAVLDVVVALFPNYDTRTYPMETKA 300
DB 241 EYSDHCVKMYETGLAKTSGTSAQWVDYVYQFREMFLAVLDVVVALFPNYDTRTYPMETKA 300
QY 301 QLTREYVTDPLGAVNYSSTGSWYDKAPSGVIBESSVIRPHVFDYITGLTVYTSRSISS 360
DB 301 QLTREYVTDPLGAVNYSSTGSWYDKAPSGVIBESSVIRPHVFDYITGLTVYTSRSISS 360
QY 361 ARYIRHWAGHOISYHRVSRGSLNQMYGTNQLHSTSTFTDFTNYDIYKTLSDKAVLLDIV 420
DB 361 ARYIRHWAGHOISYHRVSRGSLNQMYGTNQLHSTSTFTDFTNYDIYKTLSDKAVLLDIV 420
QY 421 YPGYTYIFFGMPVEPFVFNQNLNTRKTLKYNPVSVDIIASTRDSSELELPETSDQPNYE 480
DB 421 YPGYTYIFFGMPVEPFVFNQNLNTRKTLKYNPVSVDIIASTRDSSELELPETSDQPNYE 480
QY 481 SYSHRLCHITSPATGNTTGLVFPVSWTHRSADLNNTIYSDKITQIPAVKCNWNLFPVPV 540
DB 481 SYSHRLCHITSPATGNTTGLVFPVSWTHRSADLNNTIYSDKITQIPAVKCNWNLFPVPV 540
QY 541 VKGPGHTGDLQYNRSTGSGVTLFLARYGLALEKAGKYRVRLYRATDADIVLHVNDQAI 600
DB 541 VKGPGHTGDLQYNRSTGSGVTLFLARYGLALEKAGKYRVRLYRATDADIVLHVNDQAI 600
QY 601 QMPKTNVPGEDLTSTKTFKVADAITTLNLTATDSSSLAKHNLGDPNSTLSGIVVVDRIEFI 660
DB 601 QMPKTNVPGEDLTSTKTFKVADAITTLNLTATDSSSLAKHNLGDPNSTLSGIVVVDRIEFI 660
QY 661 PVDETYEAE 669
DB 661 PVDETYEAE 669

RESULT 4
US-10-032-717-16
; Sequence 16, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT FILING DATE: 2001-10-23
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 669
; TYPE: PRT
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ORGANISM: Bacillus thuringiensis (truncated)  
US-10-032-717-16

Query Match 55.4%; Score 3511; DB 12; Length 669;  
Best Local Similarity 100.0%; Pred. No. 5.6e-239;  
Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPNNQNEYEIIIDATPSTSVNSDSNRYPFANEPTNALQNDYKDYKMSAGNASEYFGSP 60  
DB 1 MSPNNQNEYEIIIDATPSTSVNSDSNRYPFANEPTNALQNDYKDYKMSAGNASEYFGSP 60  
QY 61 EVLVSGQDAAKAAIDIVGKLLSGLGVFPVGVIVSLYQTLIDILWPSEKSWEIFMEQVE 120  
DB 61 EVLVSGQDAAKAAIDIVGKLLSGLGVFPVGVIVSLYQTLIDILWPSEKSWEIFMEQVE 120  
QY 121 ELINQKIAEYARNKALSELGLGNNYQLYLTALBEEWENPNSGRALDRVRNRFILDSLF 180  
DB 121 ELINQKIAEYARNKALSELGLGNNYQLYLTALBEEWENPNSGRALDRVRNRFILDSLF 180  
QY 181 TOYMPSPRVTFNFEVFPFLTVYMAAANLHLLLLKDAISIFGEWGWSTTTINNYDQMKLTA 240  
DB 181 TOYMPSPRVTFNFEVFPFLTVYMAAANLHLLLLKDAISIFGEWGWSTTTINNYDQMKLTA 240  
QY 241 EYSDHCVKYETGLAKLGTSAKQWVDYQFRREMTLAVLDVVALFPNYDTRTYPMETKA 300  
DB 241 EYSDHCVKYETGLAKLGTSAKQWVDYQFRREMTLAVLDVVALFPNYDTRTYPMETKA 300  
QY 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTSRIS 360  
DB 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTSRIS 360  
QY 361 ARYIRHWAGHQISYHRVSRGSLNQMGYNQNLHSTSTFDTNNDIYKTLSDAVLLDIV 420  
DB 361 ARYIRHWAGHQISYHRVSRGSLNQMGYNQNLHSTSTFDTNNDIYKTLSDAVLLDIV 420  
QY 421 YPGYTIFFGMEPEVEFFMVNQLNTRKTLKYNPVSQDIIASTRDSELELPETSDQNYE 480  
DB 421 YPGYTIFFGMEPEVEFFMVNQLNTRKTLKYNPVSQDIIASTRDSELELPETSDQNYE 480  
QY 481 SYSHRLCHITSIIPATGNTTGLVPFVSWTHRSADLNNTIYSDKITQIPAVKCDNLPPVPV 540  
DB 481 SYSHRLCHITSIIPATGNTTGLVPFVSWTHRSADLNNTIYSDKITQIPAVKCDNLPPVPV 540  
QY 541 VKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKRVRLRYATDADIVLVNDAQI 600  
DB 541 VKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKRVRLRYATDADIVLVNDAQI 600  
QY 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSSLAKHNLGEPNSTLSGIVYVDRIEPI 660  
DB 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSSLAKHNLGEPNSTLSGIVYVDRIEPI 660  
QY 661 PVDETYEAE 669  
DB 661 PVDETYEAE 669

RESULT 5  
US-10-032-717-6  
; Sequence 6, Application US/10032717  
; Patent No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Peng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032.717  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838

PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 667  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis (truncated)  
US-10-032-717-6

Query Match 55.3%; Score 3502; DB 12; Length 667;  
Best Local Similarity 100.0%; Pred. No. 2.4e-238;  
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPNNQNEYEIIIDATPSTSVNSDSNRYPFANEPTNALQNDYKDYKMSAGNASEYFGSP 60  
DB 1 MSPNNQNEYEIIIDATPSTSVNSDSNRYPFANEPTNALQNDYKDYKMSAGNASEYFGSP 60  
QY 61 EVLVSGQDAAKAAIDIVGKLLSGLGVFPVGVIVSLYQTLIDILWPSEKSWEIFMEQVE 120  
DB 61 EVLVSGQDAAKAAIDIVGKLLSGLGVFPVGVIVSLYQTLIDILWPSEKSWEIFMEQVE 120  
QY 121 ELINQKIAEYARNKALSELGLGNNYQLYLTALBEEWENPNSGRALDRVRNRFILDSLF 180  
DB 121 ELINQKIAEYARNKALSELGLGNNYQLYLTALBEEWENPNSGRALDRVRNRFILDSLF 180  
QY 181 TOYMPSPRVTFNFEVFPFLTVYMAAANLHLLLLKDAISIFGEWGWSTTTINNYDQMKLTA 240  
DB 181 TOYMPSPRVTFNFEVFPFLTVYMAAANLHLLLLKDAISIFGEWGWSTTTINNYDQMKLTA 240  
QY 241 EYSDHCVKYETGLAKLGTSAKQWVDYQFRREMTLAVLDVVALFPNYDTRTYPMETKA 300  
DB 241 EYSDHCVKYETGLAKLGTSAKQWVDYQFRREMTLAVLDVVALFPNYDTRTYPMETKA 300  
QY 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTSRIS 360  
DB 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTSRIS 360  
QY 361 ARYIRHWAGHQISYHRVSRGSLNQMGYNQNLHSTSTFDTNNDIYKTLSDAVLLDIV 420  
DB 361 ARYIRHWAGHQISYHRVSRGSLNQMGYNQNLHSTSTFDTNNDIYKTLSDAVLLDIV 420  
QY 421 YPGYTIFFGMEPEVEFFMVNQLNTRKTLKYNPVSQDIIASTRDSELELPETSDQNYE 480  
DB 421 YPGYTIFFGMEPEVEFFMVNQLNTRKTLKYNPVSQDIIASTRDSELELPETSDQNYE 480  
QY 481 SYSHRLCHITSIIPATGNTTGLVPFVSWTHRSADLNNTIYSDKITQIPAVKCDNLPPVPV 540  
DB 481 SYSHRLCHITSIIPATGNTTGLVPFVSWTHRSADLNNTIYSDKITQIPAVKCDNLPPVPV 540  
QY 541 VKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKRVRLRYATDADIVLVNDAQI 600  
DB 541 VKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKRVRLRYATDADIVLVNDAQI 600  
QY 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSSLAKHNLGEPNSTLSGIVYVDRIEPI 660  
DB 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSSLAKHNLGEPNSTLSGIVYVDRIEPI 660  
QY 661 PVDETYE 667  
DB 661 PVDETYE 667

RESULT 6  
US-10-032-717-12  
; Sequence 12, Application US/10032717  
; Patent No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Peng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims

; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; FILE REFERENCE: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 673  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis (mutated)  
US-10-032-717-12

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Query Match          55.3%; Score 3499; DB 12; Length 673;
Best Local Similarity 99.4%; Pred. No. 3.9e-238;
Matches 669; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 MSPNNQNEYEIIIDATPSTSVSNDNRYPPFANEPTNALQNMDYKDYLKMSAGNASEYFGSP 60
   |||||
Db 1 MSPNNQNEYEIIIDATPSTSVSNDNRYPPFANEPTNALQNMDYKDYLKMSAGNASEYFGSP 60

QY 61 EVLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYQLIDILWPSEKSKQWEIFMEQVE 120
   |||||
Db 61 EVLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYQLIDILWPSEKSKQWEIFMEQVE 120

QY 121 ELINOKIAEYARNKALSEGLEGNVQYLTALREWEENP-----NGSRALRDVNRFEIL 176
   |||||
Db 121 ELINOKIAEYARNKALSEGLEGNVQYLTALREWEENP-----NGSRALRDVNRFEIL 180

QY 177 DLSFTQMPSPRVNPEVPLTVYMAANLHLLLLKDAISIFGEWGWSTTTINNYDROM 236
   |||||
Db 181 DLSFTQMPSPRVNPEVPLTVYMAANLHLLLLKDAISIFGEWGWSTTTINNYDROM 240

QY 237 KLTAEYSDHCVKVYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVVALPNDYTRTPM 296
   |||||
Db 241 KLTAEYSDHCVKVYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVVALPNDYTRTPM 300

QY 297 ETQAQLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSR 356
   |||||
Db 301 ETQAQLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSR 360

QY 357 SSSARVIRHWAGHQISYHRVSRGSLNQMYGTNQLHSTSTFTFTNYDIYKTLSDAVL 416
   |||||
Db 361 SSSARVIRHWAGHQISYHRVSRGSLNQMYGTNQLHSTSTFTFTNYDIYKTLSDAVL 420

QY 417 LDIVYPGYTIFFGMPVEPFPMVNLNNTKTLKYNPVSXKDIIASTRDSELELPPTSQ 476
   |||||
Db 421 LDIVYPGYTIFFGMPVEPFPMVNLNNTKTLKYNPVSXKDIIASTRDSELELPPTSQ 480

QY 477 PNYESYSHRLCHITSIPTAGNTTGLVPVSWTHRSADLANNTIYSDKITQIPAVKCDNLP 536
   |||||
Db 481 PNYESYSHRLCHITSIPTAGNTTGLVPVSWTHRSADLANNTIYSDKITQIPAVKCDNLP 540

QY 537 FVPVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHV 596
   |||||
Db 541 FVPVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHV 600

QY 597 DAOIQMPKTNPGEDLTSTKTFKVADAITTLNLTATDSSSLAKHNLGDPNSTLSGIVYVDR 656
   |||||
Db 601 DAOIQMPKTNPGEDLTSTKTFKVADAITTLNLTATDSSSLAKHNLGDPNSTLSGIVYVDR 660

QY 657 IEFIPVDETYEAE 669
   |||||
Db 661 IEFIPVDETYEAE 673
```

## RESULT 7

US-10-032-717-22  
; Sequence 22, Application US/10032717  
; Patent No. US20020151709A1  
; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; FILE REFERENCE: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/242,838  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 673  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis (mutated)  
US-10-032-717-22

```
Query Match          55.3%; Score 3499; DB 12; Length 673;
Best Local Similarity 99.4%; Pred. No. 3.9e-238;
Matches 669; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 MSPNNQNEYEIIIDATPSTSVSNDNRYPPFANEPTNALQNMDYKDYLKMSAGNASEYFGSP 60
   |||||
Db 1 MSPNNQNEYEIIIDATPSTSVSNDNRYPPFANEPTNALQNMDYKDYLKMSAGNASEYFGSP 60

QY 61 EVLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYQLIDILWPSEKSKQWEIFMEQVE 120
   |||||
Db 61 EVLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYQLIDILWPSEKSKQWEIFMEQVE 120

QY 121 ELINOKIAEYARNKALSEGLEGNVQYLTALREWEENP-----NGSRALRDVNRFEIL 176
   |||||
Db 121 ELINOKIAEYARNKALSEGLEGNVQYLTALREWEENP-----NGSRALRDVNRFEIL 180

QY 177 DLSFTQMPSPRVNPEVPLTVYMAANLHLLLLKDAISIFGEWGWSTTTINNYDROM 236
   |||||
Db 181 DLSFTQMPSPRVNPEVPLTVYMAANLHLLLLKDAISIFGEWGWSTTTINNYDROM 240

QY 237 KLTAEYSDHCVKVYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVVALPNDYTRTPM 296
   |||||
Db 241 KLTAEYSDHCVKVYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVVALPNDYTRTPM 300

QY 297 ETQAQLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSR 356
   |||||
Db 301 ETQAQLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSR 360

QY 357 SSSARVIRHWAGHQISYHRVSRGSLNQMYGTNQLHSTSTFTFTNYDIYKTLSDAVL 416
   |||||
Db 361 SSSARVIRHWAGHQISYHRVSRGSLNQMYGTNQLHSTSTFTFTNYDIYKTLSDAVL 420

QY 417 LDIVYPGYTIFFGMPVEPFPMVNLNNTKTLKYNPVSXKDIIASTRDSELELPPTSQ 476
   |||||
Db 421 LDIVYPGYTIFFGMPVEPFPMVNLNNTKTLKYNPVSXKDIIASTRDSELELPPTSQ 480

QY 477 PNYESYSHRLCHITSIPTAGNTTGLVPVSWTHRSADLANNTIYSDKITQIPAVKCDNLP 536
   |||||
Db 481 PNYESYSHRLCHITSIPTAGNTTGLVPVSWTHRSADLANNTIYSDKITQIPAVKCDNLP 540

QY 537 FVPVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHV 596
   |||||
Db 541 FVPVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHV 600

QY 597 DAOIQMPKTNPGEDLTSTKTFKVADAITTLNLTATDSSSLAKHNLGDPNSTLSGIVYVDR 656
   |||||
Db 601 DAOIQMPKTNPGEDLTSTKTFKVADAITTLNLTATDSSSLAKHNLGDPNSTLSGIVYVDR 660

QY 657 IEFIPVDETYEAE 669
   |||||
Db 661 IEFIPVDETYEAE 673
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RESULT 8  
US-10-032-717-40  
; Sequence 40, Application US/10032717  
; Patent No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR FILING DATE: 60/242,838  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 40  
; LENGTH: 673  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis (mutated)  
US-10-032-717-40  
  
Query Match 55.3%; Score 3499; DB 12; Length 673;  
Best Local Similarity 99.4%; Pred. No. 3.9e-238;  
Matches 669; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
  
QY 1 MSPNNQVEIIDATPSTSVNSDNRYPFANEPTNALQNDMDYKDYKXMSAGNASEYPGSP 60  
DB 1 MSPNNQVEIIDATPSTSVNSDNRYPFANEPTNALQNDMDYKDYKXMSAGNASEYPGSP 60  
QY 61 EVLVSGDAAKAIDIVGKLLSGLVFVPGPIVSLYTLQIDILWPSGEKSQWEIFMEQVE 120  
DB 61 EVLVSGDAAKAIDIVGKLLSGLVFVPGPIVSLYTLQIDILWPSGEKSQWEIFMEQVE 120  
QY 121 ELINOKIAEYARNKALSELGLGNNYQLYLTALKEEENP-----NGSRALRDVNRREIL 176  
DB 121 ELINOKIAEYARNKALSELGLGNNYQLYLTALKEEENP-----NGSRALRDVNRREIL 180  
QY 177 DSLFTQMPSPRVNTFVPEPLTVYMAANLHLLKXDAISIFGEWGWSTTTINNYDROM 236  
DB 181 DSLFTQMPSPRVNTFVPEPLTVYMAANLHLLKXDAISIFGEWGWSTTTINNYDROM 240  
QY 237 KLTAEYSDHCWKVETGLAKLKGTSAKQWVDYNOFRREMTLAVLDVVVALPNDYDTRTPM 296  
DB 241 KLTAEYSDHCWKVETGLAKLKGTSAKQWVDYNOFRREMTLAVLDVVVALPNDYDTRTPM 300  
QY 297 ETKAQLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSR 356  
DB 301 ETKAQLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSR 360  
QY 357 SSSARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFDFTNYDIYKTLSDKDAVL 416  
DB 361 SSSARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFDFTNYDIYKTLSDKDAVL 420  
QY 417 LDIVYGYTYIFFGMPVEVFMVNLNTRKTLKYNPVSKDIIASTRDSSELELPETSQ 476  
DB 421 LDIVYGYTYIFFGMPVEVFMVNLNTRKTLKYNPVSKDIIASTRDSSELELPETSQ 480  
QY 477 PNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKTIQIPAVKCDNLP 536  
DB 481 PNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKTIQIPAVKCDNLP 540  
QY 537 FVPVKGPGHGTGDLQYNRSTSGVTLFLARYGLALEKAGKVRVLRATDADIVLHVN 596  
DB 541 FVPVKGPGHGTGDLQYNRSTSGVTLFLARYGLALEKAGKVRVLRATDADIVLHVN 600  
QY 597 DAQIQMPKTMNPGEDLTSKTFKVADAITTLNLATDSSLALKHNLGDPNSTLSGIVVYDR 656

DB 601 DAQIQMPKTMNPGEDLTSKTFKVADAITTLNLATDSSLALKHNLGDPNSTLSGIVVYDR 660  
QY 657 IEFIPVDETYEAR 669  
DB 661 IEFIPVDETYEAR 673  
  
RESULT 9  
US-10-032-717-24  
; Sequence 24, Application US/10032717  
; Patent No. US20020151709A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Nicholas B. Duck  
; APPLICANT: Xiang Feng  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Lynn E. Sims  
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With  
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans  
; FILE REFERENCE: 35718/237005  
; CURRENT APPLICATION NUMBER: US/10/032,717  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR FILING DATE: 60/242,838  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 670  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis (mutated)  
US-10-032-717-24  
  
Query Match 55.0%; Score 3485.5; DB 12; Length 670;  
Best Local Similarity 99.6%; Pred. No. 3.5e-237;  
Matches 667; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
  
QY 1 MSPNNQVEIIDATPSTSVNSDNRYPFANEPTNALQNDMDYKDYKXMSAGNASEYPGSP 6C  
DB 1 MSPNNQVEIIDATPSTSVNSDNRYPFANEPTNALQNDMDYKDYKXMSAGNASEYPGSP 60  
QY 61 EVLVSGDAAKAIDIVGKLLSGLVFVPGPIVSLYTLQIDILWPSGEKSQWEIFMEQVE 120  
DB 61 EVLVSGDAAKAIDIVGKLLSGLVFVPGPIVSLYTLQIDILWPSGEKSQWEIFMEQVE 120  
QY 121 ELINOKIAEYARNKALSELGLGNNYQLYLTALKEEENP-----NGSRALRDVNRREIL 179  
DB 121 ELINOKIAEYARNKALSELGLGNNYQLYLTALKEEENP-----NGSRALRDVNRREIL 180  
QY 180 FTQYMPSPRVNTFVPEPLTVYMAANLHLLKXDAISIFGEWGWSTTTINNYDROMKLT 239  
DB 181 FTQYMPSPRVNTFVPEPLTVYMAANLHLLKXDAISIFGEWGWSTTTINNYDROMKLT 240  
QY 240 AEYSDHCWKVETGLAKLKGTSAKQWVDYNOFRREMTLAVLDVVVALPNDYDTRTPMETK 299  
DB 241 AEYSDHCWKVETGLAKLKGTSAKQWVDYNOFRREMTLAVLDVVVALPNDYDTRTPMETK 300  
QY 300 AQLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSRIS 359  
DB 301 AQLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESVIRPHVFDYITGLTVYTQSRIS 360  
QY 360 SARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFDFTNYDIYKTLSDKDAVL 419  
DB 361 SARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFDFTNYDIYKTLSDKDAVL 420  
QY 420 VYPGYTYIFFGMPVEVFMVNLNTRKTLKYNPVSKDIIASTRDSSELELPETSQPNY 479  
DB 421 VYPGYTYIFFGMPVEVFMVNLNTRKTLKYNPVSKDIIASTRDSSELELPETSQPNY 480  
QY 480 ESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKTIQIPAVKCDNLP 539  
DB 481 ESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKTIQIPAVKCDNLP 540

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Qy 540 VVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVNDQAQ 599
Db 541 VVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVNDQAQ 600
Qy 600 IOMPKTNWPGEDLTSKTKFKVADATTTLNLTATDSSSLAKHNLGDEPNSTLSGIVVVDRIEF 659
Db 601 IOMPKTNWPGEDLTSKTKFKVADATTTLNLTATDSSSLAKHNLGDEPNSTLSGIVVVDRIEF 660
Qy 660 IPVDETYEAE 669
Db 661 IPVDETYEAE 670

RESULT 10
US-10-032-717-44
; Sequence 44, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-10-032-717-44

Query Match 55.0%; Score 3485.5; DB 12; Length 670;
Best Local Similarity 99.6%; Pred. No. 3.5e-237;
Matches 667; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTNALQWMDYKYLKMSAGNASYPGSP 60
Db 1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTNALQWMDYKYLKMSAGNASYPGSP 60
Qy 61 EVLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYTQIDILWPSGKSWEIFMEQVE 120
Db 61 EVLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYTQIDILWPSGKSWEIFMEQVE 120
Qy 121 ELINQKIAEYARNKALSLEGLGNNYQLYLTALAEWEENP-NGSALRDVRNRPILDSL 179
Db 121 ELINQKIAEYARNKALSLEGLGNNYQLYLTALAEWEENP-NGSALRDVRNRPILDSL 180
Qy 180 FTQYMPFRVTFNFEVFLTVYAMAANLHLLKLDASIFGEEWGWSTTTNNYDQMKLT 239
Db 181 FTQYMPFRVTFNFEVFLTVYAMAANLHLLKLDASIFGEEWGWSTTTNNYDQMKLT 240
Qy 240 AEYSDHCVKWYETGLAKLGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTPMETK 299
Db 241 AEYSDHCVKWYETGLAKLGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTPMETK 300
Qy 300 AOLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVDYITGLTVYTSRSIS 359
Db 301 AOLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVDYITGLTVYTSRSIS 360
Qy 360 SARYIRHWAGHOISYHRVSRGSLNQMYGTQNHLSTSTFDFTNYDIYKLSKDAVLDDI 419
Db 361 SARYIRHWAGHOISYHRVSRGSLNQMYGTQNHLSTSTFDFTNYDIYKLSKDAVLDDI 420
Qy 420 VYPGYTYIFFGMEPEVEFFMVNQLNTRKTLKYNPVSCKDIIASTRDSLELPPETSDQPNY 479
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Db 421 VYPGYTYIFFGMEPEVEFFMVNQLNTRKTLKYNPVSCKDIIASTRDSLELPPETSDQPNY 480
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Db 481 ESYSHRLCHITTSIPATGNTTGLVPVFSWTHRSADLNTTIYSDKITQIIPAVKCMWNLFPVP 540
Qy 540 VVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVNDQAQ 599
Db 541 VVKGPGHTGGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVNDQAQ 600
Qy 600 IOMPKTNWPGEDLTSKTKFKVADATTTLNLTATDSSSLAKHNLGDEPNSTLSGIVVVDRIEF 659
Db 601 IOMPKTNWPGEDLTSKTKFKVADATTTLNLTATDSSSLAKHNLGDEPNSTLSGIVVVDRIEF 660
Qy 660 IPVDETYEAE 669
Db 661 IPVDETYEAE 670

RESULT 11
US-10-032-717-20
; Sequence 20, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (truncated)
US-10-032-717-20

Query Match 51.0%; Score 3229; DB 12; Length 616;
Best Local Similarity 100.0%; Pred. No. 3.3e-219;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 MSAGNASYPGSPSEVLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYTQIDILWPSG 107
Db 1 MSAGNASYPGSPSEVLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYTQIDILWPSG 60
Qy 108 EKSQWEIFMEQVEELINQKIAEYARNKALSLEGLGNNYQLYLTALAEWEENPNSRALR 167
Db 61 EKSQWEIFMEQVEELINQKIAEYARNKALSLEGLGNNYQLYLTALAEWEENPNSRALR 120
Qy 168 DVNRNPEILDSLFTQYMPFRVTFNFEVFLTVYAMAANLHLLKLDASIFGEEWGWSTTT 227
Db 121 DVNRNPEILDSLFTQYMPFRVTFNFEVFLTVYAMAANLHLLKLDASIFGEEWGWSTTT 180
Qy 228 INNYDQMKLTABYSYSDHCVKWYETGLAKLGTSAKQWVDYNQFRREMTLAVLDVVALFP 287
Db 181 INNYDQMKLTABYSYSDHCVKWYETGLAKLGTSAKQWVDYNQFRREMTLAVLDVVALFP 240
Qy 288 NYDTRTPMETKAOQLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVDYIT 347
Db 241 NYDTRTPMETKAOQLTRVYTDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVDYIT 300
Qy 348 GLTVYTSRSISARYIRHWAGHOISYHRVSRGSLNQMYGTQNHLSTSTFDFTNYDIY 407
Db 301 GLTVYTSRSISARYIRHWAGHOISYHRVSRGSLNQMYGTQNHLSTSTFDFTNYDIY 360
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|    |     |  |     |
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| QY | 287 | PNYDTRTPMETRAQLTREYVTDPLGAVNVSSIGSWYDKAPSGFVIESSVIRPPHVPDYI    | 346 |
| Db | 241 | PNYDTRTPMETRAQLTREYVTDPLGAVNVSSIGSWYDKAPSGFVIESSVIRPPHVPDYI    | 300 |
| QY | 347 | TGLTVYTQSRSSISSARYIRHWAGHQISYHRVSRGSNLQOMYGTNQNHLHSTSTFDFTNYDI | 406 |
| Db | 301 | TGLTVYTQSRSSISSARYIRHWAGHQISYHRVSRGSNLQOMYGTNQNHLHSTSTFDFTNYDI | 360 |
| QY | 407 | YKTLSDAVLLDVIYPGYTYIFFGMPVEVEPFMVNQLNTRKTLKYNPVSXDIITASTRDSE   | 466 |
| Db | 361 | YKTLSDAVLLDVIYPGYTYIFFGMPVEVEPFMVNQLNTRKTLKYNPVSXDIITASTRDSE   | 420 |
| QY | 467 | LELPPESTDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQI   | 526 |
| Db | 421 | LELPPESTDQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQI   | 480 |
| QY | 527 | PAVKCNDNLPFPVVKPGHGTGGDLLQYNRSTGSGVTLFLARYGLALEKAGKYRVLRYA     | 586 |
| Db | 481 | PAVKCNDNLPFPVVKPGHGTGGDLLQYNRSTGSGVTLFLARYGLALEKAGKYRVLRYA     | 540 |
| QY | 587 | TDADIVLHVNDAOIQMPKTNPGEDLTSTKFKVADAITTLNLATDSSLALKHNLGEDPNS    | 646 |
| Db | 541 | TDADIVLHVNDAOIQMPKTNPGEDLTSTKFKVADAITTLNLATDSSLALKHNLGEDPNS    | 600 |
| QY | 647 | TLSGIVYVDRIEIPVD   | 663 |
| Db | 601 | TLSGIVYVDRIEIPVD   | 617 |

Search completed: January 7, 2003, 05:26:10  
Job time : 45 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2003, 00:49:27 ; Search time 89 seconds  
(without alignments)  
12477.265 Million cell updates/sec

Title: US-10-032-717-1  
Perfect score: 3621  
Sequence: 1 atgagtcacaaataatcaaaa.....tgattagacgtagagtaa 3621

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCRU COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1          | 2565.2 | 70.8        | 3507   | 1  | US-08-315-468-3  |
| 2          | 1812.2 | 50.0        | 3471   | 1  | US-07-876-280-29 |
| 3          | 1812.2 | 50.0        | 3471   | 1  | US-07-812-180A-1 |
| 4          | 1812.2 | 50.0        | 3471   | 1  | US-08-315-468-1  |
| 5          | 1812.2 | 50.0        | 3471   | 4  | US-07-941-650A-1 |
| 6          | 1180   | 32.6        | 3797   | 1  | US-07-915-203-1  |
| 7          | 1180   | 32.6        | 3797   | 1  | US-08-272-887-1  |
| 8          | 1180   | 32.6        | 3797   | 1  | US-08-789-449-1  |
| 9          | 883.4  | 24.4        | 4344   | 2  | US-08-532-547-4  |
| 10         | 883.4  | 24.4        | 4344   | 2  | US-08-379-656B-4 |
| 11         | 883.4  | 24.4        | 4344   | 3  | US-08-455-838-4  |
| 12         | 883.4  | 24.4        | 4344   | 3  | US-09-019-809-4  |
| 13         | 883.4  | 24.4        | 4344   | 4  | US-09-471-177-4  |
| 14         | 882.8  | 23.4        | 3471   | 4  | US-09-002-285-73 |
| 15         | 848.6  | 23.4        | 3759   | 1  | US-08-542-921-1  |
| 16         | 848.6  | 23.4        | 3759   | 2  | US-08-880-685-1  |
| 17         | 848.6  | 23.4        | 3759   | 2  | US-08-880-684-1  |
| 18         | 822.2  | 22.7        | 3453   | 4  | US-09-002-285-75 |
| 19         | 734.2  | 20.3        | 3411   | 4  | US-09-002-285-77 |
| 20         | 733.6  | 20.3        | 3414   | 1  | US-07-973-320-3  |
| 21         | 731.4  | 20.2        | 3414   | 1  | US-07-973-320-1  |
| 22         | 678    | 18.7        | 3934   | 1  | US-08-100-709-3  |
| 23         | 678    | 18.7        | 3934   | 1  | US-08-176-865-3  |
| 24         | 678    | 18.7        | 3934   | 1  | US-08-474-038-3  |
| 25         | 678    | 18.7        | 3934   | 2  | US-08-779-046-3  |
| 26         | 678    | 18.7        | 3934   | 2  | US-08-881-340-3  |
| 27         | 673.6  | 18.6        | 4074   | 1  | US-08-377-690-1  |

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|----|-------|------|------|---|------------------|
| 28 | 659.2 | 18.2 | 3684 | 1 | US-08-448-170-7  |
| 29 | 659.2 | 18.2 | 3684 | 3 | US-08-961-803-5  |
| 30 | 618.6 | 17.1 | 3567 | 6 | 5188960-5        |
| 31 | 615.4 | 17.0 | 3567 | 2 | US-08-980-071-5  |
| 32 | 615.4 | 17.0 | 3567 | 2 | US-08-980-071-58 |
| 33 | 615.4 | 17.0 | 3567 | 2 | US-08-757-536-5  |
| 34 | 615.4 | 17.0 | 3567 | 3 | US-09-314-093-5  |
| 35 | 615.4 | 17.0 | 3567 | 3 | US-09-314-093-58 |
| 36 | 615.4 | 17.0 | 3567 | 3 | US-09-250-848-5  |
| 37 | 615.4 | 17.0 | 3567 | 4 | US-09-251-885-5  |
| 38 | 615.4 | 17.0 | 3567 | 4 | US-09-337-635-5  |
| 39 | 615.4 | 17.0 | 3567 | 4 | US-09-337-635-58 |
| 40 | 615.4 | 17.0 | 3567 | 4 | US-09-337-280-5  |
| 41 | 615.4 | 17.0 | 3567 | 4 | US-09-337-280-58 |
| 42 | 613.8 | 17.0 | 3567 | 1 | US-08-602-737-1  |
| 43 | 613.8 | 17.0 | 3567 | 2 | US-08-980-071-1  |
| 44 | 613.8 | 17.0 | 3567 | 2 | US-08-980-071-9  |
| 45 | 613.8 | 17.0 | 3567 | 2 | US-08-980-071-11 |

ALIGNMENTS

RESULT 1  
US-08-315-468-3  
; Sequence 3, Application US/08315468  
; Patent No. 5554534  
; GENERAL INFORMATION:  
; APPLICANT: Michaels, Tracy Ellis  
; APPLICANT: Fonceerrada, Luis  
; APPLICANT: Narva, Kenneth E.  
; TITLE OF INVENTION: Process for Controlling Scarab Pests  
; TITLE OF INVENTION: with Bacillus thuringiensis Isolates  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/315,468  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/014,941  
; FILING DATE: 01 FEB 1993  
; APPLICATION NUMBER: 07/828,430  
; FILING DATE: 30-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/808,316  
; FILING DATE: 16-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: MAY3.C2  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3507 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO

ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Bacillus thuringiensis  
 STRAIN: kumamotoensis  
 INDIVIDUAL ISOLATE: 50C  
 IMMEDIATE SOURCE:  
 LIBRARY: LambdaGEN-11(tm) library of L. Poncerrada  
 CLONE: 50C(b)  
 US-08-315-468-3

Query Match 70.8%; Score 2565.2; DB 1; Length 3507;  
 Best Local Similarity 85.1%; Pred. No. 0;  
 Matches 2906; Conservative 0; Mismatches 493; Indels 15; Gaps 3;

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 DB 61 TCCAAATGATTTCTAAACAGATACCTTTTGGCAATGAGCCCAAAATGCGCTACAAAATATG 120  
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 DB 121 GATTATAAAGATTTATTTAAATATGCTGCGGGAATGCTAGTGAATACCCCTGTTCACT 180  
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 DB 181 GAGGTATTTCTAAGCGGACAGATGAGCTAAGCGCGCAATTTGATATAGTAGTAATTA 240  
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 QY 301 GATATTTCTGGCTTTGAGGGAAGAGTCAATGGGAATTTTATGGAACTAGTAA 360  
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 QY 361 GAATCTATTAATCAAAAATAGCAGATATGCAAGGAATTAAGCGCTTTGCGAATTAGAA 420  
 DB 361 GAATCTATTAATCAAAAATAGCAGATATGCAAGGAATTAAGCGCTTTGCGAATTAGAA 420  
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 DB 601 ACAAUGGAGCAACCTTCAATTTACTTGTATTTATTAAGAGCGCATCAATTTTGGAGAGAA 660  
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 QY 781 ACGGCTAAACAAATGGGTTGACTATAACCAATTCGTTAGAGAAATGACACTGGCGGTTTA 840  
 DB 781 ACGGCTAAACAAATGGGTTGACTATAACCAATTCGTTAGAGAAATGACACTGGCGGTTTA 840  
 QY 841 GATGTTGTTGCTATTTTCCAAATATATGACACGACGCTACCAATGGGAAACGAAAGCA 900  
 DB 841 GACGTTGTTGCTATTTTCCAAATATATGACACGCTACCAATGGGAAACGAAAGCA 900

QY 901 CAACCTAACAGGGAGTATATACAGATCCACTCGGCGGTAAACGTGTCTTCAATTGGT 960  
 DB 901 CAGCTTACAGGGAGTATATACAGATCCACTCGGCGGTAAACGTGTCTTCAATTGGC 960  
 QY 961 TCCTGGTATGACAAAGCACCTTTCTTGGAGTATAGAAATCATCGTTTATTCGACACCC 1020  
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 QY 1021 CATGTTTGTATATATAACGGGACTCACAGTGTATACAAATCAAGAAGCAATTTCTTCC 1080  
 DB 1021 CATGTTTGTATATATAACGGGACTCACAGTGTATACAAATCAAGAAGCAATTTCTTCT 1080  
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 DB 1081 GATCGTTATATAGATATTTGGGCTGGTCAATATAGCTATATAAGCATATCGGTACGAGT 1140  
 QY 1141 AGTAATCTTCAACAAATGTATGGAACTTAATCAAAATCTACACAGCATAGTACCTTTGAT 1200  
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 DB 1201 TTTACGAATATATATTTTACAAGACTCTATCAAAAGATGCGTACTCTTGTATATAGTT 1260  
 QY 1261 TACCTGGTATATAGTATATTTTGGATGCGAGAGTCCAGTCTTTCATGTTAAAC 1320  
 DB 1261 TACCTGGTATATAGTATATTTTGGATGCGAGAGTCCAGTCTTTCATGTTAAAT 1320  
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 DB 1321 CAATGTAATATACAGAAAGCGTTAAAGTATATTAATCCAGTTTCCAAAGATATATAGAT 1380  
 QY 1381 AGTACAAGAGATTCGGAATTAAGATTAATCTCCAGAACTTCAGATCAACCAATATATGAG 1440  
 DB 1381 CGGACAGAGATTCGGAATTAAGATTAATCTCCAGAACTTCAGGTCAACCAATATATGAG 1440  
 QY 1441 TCATATAGCAGATATATGTCATATCAAGTATTTCCGCGGCGAGGTTAACTACCGGA 1500  
 DB 1441 TCATATAGCAGATATATGTCATATCAAGTATTTCCGCGGCGAGGTTAACTACCGAG 1497  
 QY 1501 TTAGTACCTGTATTTCTTGGACATATCGAAGTGCAGATTTAAACATATACATATATTTCA 1560  
 DB 1498 TATGTACCTGTATTTCTTGGACATATCGAAGTGCAGATTTAAACATATACAGTTAAAGT 1557  
 QY 1561 GATATAATCATCAAAATTCGCGCGCTTAAATGTTGGGATTAATTTACCGTTTGTTCAGTG 1620  
 DB 1558 GCGGAAATCAACCAATACAGGGGCGAAGTCTAGCACCATAGGCGAGAAATATATATA 1617  
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 DB 1618 ATAAAGGGCGTGTATATACAGGGGAGACTTAGTGGCTTTAAGCGGCGCATCGGAAGT 1677  
 QY 1681 GTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAGAGGAGGAAATATCGT 1740  
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 QY 1741 GTAAGCTGAGATATGCTACTGATGCGATATTTGTTGATGTAAACGATGCTCAGATT 1800  
 DB 1738 TCTAATGAACCTAGTTATATTTAGTTATACGGACTAAACCAAGCGGAACCTTTAAATTC 1797  
 QY 1801 CAGATGCCAAACCAATCAACCCAGGTGAGGATCTGACATCTTAAACCTTTTAAAGTTCA 1860  
 DB 1798 AACGAGATATTTTAAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1857  
 QY 1861 GATGCTATCAACAACTTAAATTTAGCAACAGATAGTTTCGCTAGCATTTGAAACATATTTA 1920  
 DB 1858 GAATATC---CAAGAGTCAATTTGATTAATGCTTCTTCAACATACAGAGGTTATCTATA 1914  
 QY 1921 GGTGAAGACCTTAATTCACATTTATCTGTTATAGTTTACGTTGACCGGAATCGAATTCATC 1980  
 DB 1915 GGTATACAAACGAATACAAATTTATTTATTTA-----GACCGAATCGAATTCATC 1965



QY 1981 CCAAGTAGATGAGCATATGAAGCGGAAACAAGATTAGAGCAGCGAAGAAAGCAGTGAAT 2040  
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QY 2041 GCCTTGTTCAGGAATACAAAGAGTGGCTTAGACACAGCGGTACGGATTAAGAGTGAAT 2100  
DB 2026 GCCTTGTTCAGGAATACAAAGAGTGGATTAACGACAGGTGTAACGGATTAAGAGTGAAT 2085  
QY 2101 CAAAGCGGCAAACTTAGTGGAAATGCTTACGATGATTTGATCCAAATGAAGAAACGATTCG 2160  
DB 2086 CAAAGCGGCAAACTTAGTGGAAATGCTTACGATGATTTGATCCAAATGAAGAAACGATTCG 2145  
QY 2161 TTATTTGATGACAGTAGAGAGGCAAAACGCTCAGTGAAGCAAGTAAATTTGCTTCAAGAT 2220  
DB 2146 TTATTTGATGACAGTAGAGAGGCAAAACGCTTAGCGAGGACCGGACTTACTACAAGAT 2205  
QY 2221 CCAGATTTCCAGAGATAAATGAGAAATGCTGCGAGCGAGTAGCGGAATTTGAGGTT 2280  
DB 2206 CCAGATTTCCAGAGATAAATGAGAAATGCTGCGAGCGAGTAGCGGAATTTGAGGTT 2265  
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DB 2266 ATAGAAGGGGATGCTTATTTCAAGGGCGTTATCTAGCGCTTACCGAGTGGAGAAATA 2325  
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QY 2401 TACACAGATATAGATTGAGAGGTTTGTGCGAAGCAGTCAAGATTTGAAATTTTACCA 2460  
DB 2386 TACACAGGATATAGATTGAGAGGTTTGTGCGAAGTGTGCGAAGTGTGCGAAGTGTGCGA 2445  
QY 2461 ATTCTGTATCAACAGCAAGCAATTTGTAAGAAATGTAACCGATGTTGTCGCGAGTGA 2520  
DB 2446 ATTCTGTATCAACAGCAAGCAATTTGTAAGAAATGTAACCGATGTTTACTGCGAGTGA 2505  
QY 2521 TCTCTGTATTAACGATGATGATCAATCGATGCGAGCGAACAAGATGTGGAATAGC 2580  
DB 2506 CTTCTGTATTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2565  
QY 2581 CTTTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640  
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QY 2641 GGTGAATCGATTACAAATGAAGATGAGGATGATGATGATGATGATGATGATGATGATGAT 2700  
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DB 2686 GAGGGATATGCAACACTCGGAAACCTAGATTTGTTGGAAGGAGCCTTTATCAGGAGAC 2745  
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QY 3001 TATACCAAGTTTACAGATTAACAGATGATGATGATGATGATGATGATGATGATGATGAT 3060  
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QY 3361 AATACAAATGATATACAAACAATTAATGCGTATATGATATGATATGATATGATATGATATGATATGAT 3414  
DB 3346 AATACAAATGATATACAAACAATTAATGCGTATATGATATGATATGATATGATATGATATGATATGAT 3399

## RESULT 2

US-07-876-280-29

Sequence 29, Application US/07876280

Patent No. 5262158

GENERAL INFORMATION:

APPLICANT: Payne, Jewel M.

APPLICANT: Cannon, Raymond J.C.

APPLICANT: Bagley, Angela L.

TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for

TITLE OF INVENTION: Controlling Acarides

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: David R. Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/876,280

FILING DATE: 19920430

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: W/S 104

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 3471 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Bacillus thuringiensis

STRAIN: kumamotoensis

INDIVIDUAL ISOLATE: PS50C

IMMEDIATE SOURCE:

CLONE: E. coli NM522(pMYC2320) NRRL B-18769

```

Db   4271 GATCAAAATGTGGATTGAGATGATGGACAGAGAAGCTACAATTCCTATATATAGAAAAGTGTAGAA 4330
Qy   3601 TTGATTGTAGACGCTAGAGTAA 3621
      |||||
Db   4331 TTGATTGTAGACGCTAGAGTAA 4351

RESULT 3
US-10-032-717-3
; Sequence 3, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins With
; FILE OF INVENTION: Periodic Activity Against Coleopterans
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3633
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3633)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry12I8-2
US-10-032-717-3

Query Match          87.0%; Score 3151.8; DB 12; Length 3633;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 3353; Conservative 0; Mismatches 262; Indels 24; Gaps

Qy   1 ATGAGTCCAAATAATCAAATAATGAATATGAATATATAGATGCGACACCTTTCTACTCTGTGA 60
Db   1 ATGAGTCCAAATAATCAAATAATGAATATGAATATATAGATGCGACACCTTTCTACTCTGTGA 60
Qy   61 TCCAATGATCTTAACAGATACCCTTTTGGAATGAGCACAATAATGCCTACAAATATG 120
Db   61 TCCAATGATCTTAACAGATACCCTTTTGGAATGAGCACAATAATGCCTACAAATATG 120
Qy   121 GATTATATAAGATTATTAAAAATGTCGCGGGAATGCTAGTGAATACCTGGTTTCACCT 180
Db   121 GATTATATAAGATTATTAAAAATGTCGCGGGAATGCTAGTGAATACCTGGTTTCACCT 180
Qy   181 GAAGTACTTGTTAGCGGACAAGATGCAGCTAAGGCCGCAATTGATATAGTAGGTAATAATTA 240
Db   181 GAAGTACTTGTTAGCGGACAAGATGCAGCTAAGGCCGCAATTGATATAGTAGGTAATAATTA 240
Qy   241 CTATCATGTTTtaggggtcccaatttggttgggcccagatagtgaagtcttttatctcaacttaatt 300
Db   241 CTATCATGTTTtaggggtcccaatttggttgggcccagatagtgaagtcttttatctcaacttaatt 300
Qy   301 GATATCTGTGGCCTTCAGGGGAAAAGAGTCAATCGGHAATTTTTTATCGAACCAAGTAGAA 360
Db   301 GATATCTGTGGCCTTCAGGGGAAAAGAGTCAATCGGHAATTTTTTATCGAACCAAGTAGAA 360
Qy   361 GAACCTCAATTAATCAAAAAATAGCAGAAATATGCAAGGAATAAGCGCTTTTCGGAATTAGAA 420
Db   361 GAACCTCAATTAATCAAAAAATAGCAGAAATATGCAAGGAATAAGCGCTTTTCGGAATTAGAA 420
Qy   421 GGATTAGGTAATAATTACCAATTATATCTAACTCGCCTTGGAAGTAATGGGAAGNAATAATCCA 480

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|    |      |  |      |
|----|------|--|------|
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| DB | 2635 | TCTATTCTCTATTGATATACAGTGGAAATCGATTCAATGAAATGACGAAATATCGGTTTGG    | 2694 |
| QY | 2683 | TTTAAAGATTACGGACCCAGAGGGATATGCAACTCTCGGAAACCTTAGAAATTTGGTTCGAGAG | 2742 |
| DB | 2695 | TTTAAAGATTACGGACCCAGAGGGATATGCAACTCTCGGAAACCTTAGAAATTTGGTTCGAGAG | 2754 |
| QY | 2743 | GGACCTTTATCAGGAGACGCATTAGAACGCTTTCGAAAGAGAAGAAACAACAGTGGGAAGATT  | 2802 |
| DB | 2755 | GGACCTTTATCAGGAGACGCATTAGAACGCTTTCGAAAGAGAAGAAACAACAGTGGGAAGATT  | 2814 |
| QY | 2803 | CAAAATGACAAGAGACGCTGAGAGAAACAGATAGAGAGGTATATGCGATCGAAACCAAGCGGTA | 2862 |
| DB | 2815 | CAAAATGACAAGAGACGCTGAGAGAAACAGATAGAGAGGTATATGCGATCGAAACCAAGCGGTA | 2874 |
| QY | 2863 | GATCGTTTATATGCCGATTATCAGGATCAGCAACTGAACTCCTGATGTAGAGATTACAGAT    | 2922 |
| DB | 2875 | GATCGTTTATATGCCGATTATCAGGATCAGCAACTGAACTCCTGATGTAGAGATTACAGAT    | 2934 |
| QY | 2923 | CTTACTGCGGCCCAAGATCTGATPACAGTCCATTCTTACGTATATACGAAATGTTTCCCA     | 2982 |
| DB | 2935 | CTTACTGCGGCCCAAGATCTGATPACAGTCCATTCTTACGTATATACGAAATGTTTCCCA     | 2994 |
| QY | 2983 | GAATATCACAGGGATGAATCTATACGAAAGTTTACAGATTATACAGATCGATCCCAACAGCG   | 3042 |
| DB | 2995 | GAATATCACAGGGATGAATCTATACGAAAGTTTACAGATTATACAGATCGATCCCAACAGCG   | 3054 |
| QY | 3043 | TGGAGTTTGTATGATCAGCGAAATGCCATACCAATGCTGATTTTCGAAATGCTGTTAAGT     | 3102 |
| DB | 3055 | TGGAGTTTGTATGATCAGCGAAATGCCATACCAATGCTGATTTTCGAAATGCTGTTAAGT     | 3114 |
| QY | 3103 | AAITGGAAITGCAACGGCTGGCGTAGAAGTACACAAATCAATCATCATCTGCTCTTGTG      | 3162 |
| DB | 3115 | AAITGGAAITGCAACGGCTGGCGTAGAAGTACACAAATCAATCATCATCTGCTCTTGTG      | 3174 |
| QY | 3163 | ATTTCGAAATCGGGATCAGCAAGTTTCGCAACAGTTTACAGTTCACACCGATCAAGATAT     | 3222 |
| DB | 3175 | ATTTCGAAATCGGGATCAGCAAGTTTCGCAACAGTTTACAGTTCACACCGATCAAGATAT     | 3234 |
| QY | 3223 | GTGTTACGAGTTACTGCGAGAAAGAGGGGTAGGAAATGGAATGTAAAGTATCCGTGAT       | 3282 |
| DB | 3235 | GTGTTACGAGTTACTGCGAGAAAGAGGGGTAGGAAATGGAATGTAAAGTATCCGTGAT       | 3294 |
| QY | 3283 | GGTGGAAATCAACAGAAACGCTTACTTTTAGTGCAGCGATTATGATACAAATGGAATG       | 3342 |
| DB | 3295 | GGTGGAAATCAACAGAAACGCTTACTTTTAGTGCAGCGATTATGATACAAATGGAATG       | 3354 |
| QY | 3343 | TATTAATACGCAAGTGTCCAAATACAAATGATATACACAAATAATGCGGTATATATACAA     | 3402 |
| DB | 3355 | TATTAATACGCAAGTGTCCAAATACAAATGATATACACAAATAATGCGGTATATATACAA     | 3414 |
| QY | 3403 | GCATCGAGTACAAACGGATATACGCAAAATAATGTATTAATACGCAAGCATCGAATACA      | 3462 |
| DB | 3415 | GCATCGAGTACAAACGGATATACGCAAAATAATGTATTAATACGCAAGCATCGAATACA      | 3474 |
| QY | 3463 | AACGGATATACAAATAGTGTGTACATGATCAAAACGGCTATATACAAATAACAGTG         | 3522 |
| DB | 3475 | AACGGATATACAAATAGTGTGTACATGATCAAAACGGCTATATACAAATAACAGTG         | 3534 |
| QY | 3523 | ACATTCAATCCCGTATACAGATCAAATGTGGAATGAGATGAGACAGAGGTACATTTC        | 3582 |
| DB | 3535 | ACATTCAATCCCGTATACAGATCAAATGTGGAATGAGATGAGACAGAGGTACATTTC        | 3594 |
| QY | 3583 | TATATAGAAAGTGTAGATTGATTGTAGACGTAGAGTAA                           | 3621 |
| DB | 3595 | TATATAGAAAGTGTAGATTGATTGTAGACGTAGAGTAA                           | 3633 |

## RESULT 4

US-10-032-717-28  
; Sequence 28, Application US/10032717  
; Patent No. US20020151709A1

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2003, 00:42:52 ; Search time 3176 Seconds  
(without alignments)  
18464.691 Million cell updates/sec

Title: US-10-032-717-1  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estro.\*  
7: em\_estro.\*  
8: em\_hc.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estcom.\*  
17: gb\_gss.\*  
18: em\_gss\_hum.\*  
19: em\_gss\_inv.\*  
20: em\_gss\_pln.\*  
21: em\_gss\_vrt.\*  
22: em\_gss\_fun.\*  
23: em\_gss\_mam.\*  
24: em\_gss\_mus.\*  
25: em\_gss\_other.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| c 1        | 61    | 1.7         | 1101   | 17    | CNS0039G    |
| 2          | 55.6  | 1.5         | 832    | 17    | CNS0081L    |
| 3          | 53.6  | 1.5         | 407    | 13    | BJ389814    |
| c 4        | 53.6  | 1.5         | 531    | 13    | BJ438828    |
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| 7    | 53.6 | 1.5 | 638  | 13 | BJ389815 |
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| c 13 | 52.6 | 1.5 | 773  | 17 | BM651171 |
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| 24   | 50.6 | 1.4 | 943  | 17 | AZ690351 |
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| c 27 | 50.2 | 1.4 | 1160 | 14 | BQ673427 |
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| c 29 | 49.8 | 1.4 | 811  | 17 | CNS03YQO |
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| 31   | 49.8 | 1.4 | 982  | 17 | CNS004WF |
| 32   | 49.8 | 1.4 | 1101 | 17 | CNS0182P |
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| c 45 | 48.8 | 1.3 | 1101 | 17 | CNS0083U |

#### ALIGNMENTS

#### RESULT 1

#### LOCUS

#### DEFINITION

#### ACCESSION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

CNS0039G 1101 bp DNA linear GSS 03-JUN-1999  
Drosophila melanogaster genome survey sequence TET3 end of BAC #  
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
AL063921  
AL063921.1 GI:4941778  
GSS.  
Drosophila melanogaster.  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1101)  
Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ohsogawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial



```

REFERENCE 1 (bases 1 to 407)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the slug stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source
1. .407
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/clone="dds20m03"
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/sex="mat A"
/dev_stage="slug stage"
BASE COUNT 219 a 20 c 49 g 119 t
ORIGIN
Query Match 1.5%; Score 53.6; DB 13; Length 407;
Best Local Similarity 53.1%; Pred. No. 0.014;
Matches 138; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 3258 AATGGATATGTAAGTATCCGTGATCGTGGAAATCAACAGAAACGCTTACTTTTAGTGC 3317
|||
Db 73 AATATTAATGAAGATTTGAATATATGAATGAATGAATGAATGAATGAATGAATGAATGA 132
|||

QY 3318 AACGGATATGATCAAAATGGAATGTATATACGCAAGTGTCCATACAAATGGATATAA 3377
|||
Db 133 AA---ATGAAGATTAAATATATATATATATATATATATATATATATATATATATATAT 189
|||

QY 3378 CACAATATCGGTATATATACACAGCATCGAGTACAAACGGATATACGCAATATATAT 3437
|||
Db 190 TAATGATATATGATATATATATATATATATATATATATATATATATATATATATAT 249
|||

QY 3438 GTATATATACGCAAGTATACAAACGGATATATACAAATATAGTGTGTCACATGATCA 3497
|||
Db 250 AATATATGGAATATATACCAATATATATATATATATATATATATATATATATATATGA 309
|||

QY 3498 AACCGGCTATATACAAAAA 3517
|||
Db 310 AATAATGAATTTGAAGAA 329
|||

RESULT 4
BJ438828/c
LOCUS BJ438828 Dictyostelium discoideum cDNA library, VF Dictyostelium
DEFINITION dictoideum cDNA clone ddv38115 3', mRNA sequence.
ACCESSION BJ438828
VERSION BJ438828.1 GI:19413550
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 531)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the vegetative
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
source
1. .531
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddv38115"
/clone_lib="Dictyostelium discoideum cDNA library, VF"
/sex="mat A"
/dev_stage="Growth phase"
BASE COUNT 278 a 37 c 99 g 202 t
ORIGIN
Query Match 1.5%; Score 53.6; DB 13; Length 617;
Best Local Similarity 53.1%; Pred. No. 0.016;
Matches 138; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

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/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
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/clone_lib="Dictyostelium discoideum cDNA library, VF"
/sex="mat A"
/dev_stage="Growth phase"
BASE COUNT 161 a 70 c 56 g 236 t
ORIGIN
Query Match 1.5%; Score 53.6; DB 13; Length 531;
Best Local Similarity 49.3%; Pred. No. 0.015;
Matches 134; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 3226 TTACGAGTTACTCGGAAAGAGGGTAGGAAATGGATATGTAAGTATCCGTGATGGT 3285
|||
Db 462 TTGCCATCATTCAGATGATGAAATTTTGATGATGATGATGATGATGATGATGATGAT 403
|||

QY 3286 GGAATCAACAGAAACGCTTACTTTTAGTGAAGGATATGATCAAAATGGAATGAT 3345
|||
Db 402 GATGATGAAATATATAGCAGTACAGTGGTGAATATGATATTAATTAATTAATTAAT 343
|||

QY 3346 AATACGCAAGTGTCCATACAAATGGATATACCAATTAATCGGTATATACACAGCA 3405
|||
Db 342 AATAATTAATATGTCATAGCAATATGATACCAATTAATTAATTAATTAATTAAT 283
|||

QY 3406 TCGAGTACAAACGGATATACGCAATATATGTAATTAATACGCAAGCATCGAATACAAAC 3465
|||
Db 282 ACACTACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 223
|||

QY 3466 GGATATAACCAAAATAGTGTGTCACATGATCA 3497
|||
Db 222 AATAATTAATTAATTAATTAATTAATTAATGA 191
|||

RESULT 5
BJ410977
LOCUS BJ410977 Dictyostelium discoideum cDNA library, VF Dictyostelium
DEFINITION dictoideum cDNA clone ddv2f16 3', mRNA sequence.
ACCESSION BJ410977
VERSION BJ410977.1 GI:19323672
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 617)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the vegetative
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
source
1. .617
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddv2f16"
/clone_lib="Dictyostelium discoideum cDNA library, VF"
/sex="mat A"
/dev_stage="Growth phase"
BASE COUNT 278 a 37 c 99 g 202 t
ORIGIN
Query Match 1.5%; Score 53.6; DB 13; Length 617;
Best Local Similarity 53.1%; Pred. No. 0.016;
Matches 138; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

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QY 3258 AATGGATATGTAAGTATCCGTGATGGGAAATCAACAGAAAGCGTTACTTTTAGTGC 3317
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Db 89 AATATTAAATGAAGTATTGAATAATGAATAATGAATAATGAATAATGAATAATGA 148
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QY 3318 AAGCGATTATGATCAAAATGAATGTATAATACGCAAGTGTCCTCAATCAAAATGGATATA 3377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 149 AA---ATGAAGATTAAATAATAATAATAATAATAATGATGAAATAATAATAAGATGA 205
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QY 3378 CACAATAATCGGTATATATACACAGCATCGAGTACAAACGATATACGCAATAATAT 3437
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Db 206 TAATGATAATGATAATGATAATAATAATGATAATAATGATGATGATAATAATAAT 265
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QY 3438 GTATAATACGCAAGCATCGATACAAACGATATAACCAAAATAGTGTGTCATGATCA 3497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 266 AATAATGGAATATAACATATAATAATAATAATAATAATAATAATAATAATAATA 325
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3498 AACCGGTATATCAAAAA 3517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 326 AATAATGAAATTCGAAGAA 345
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RESULT 6
BJ389714 619 bp mRNA linear EST 08-MAR-2002
LOCUS BJ389714 Dictyostelium discoideum cDNA library, SF Dictyostelium
DEFINITION dictyostelium cDNA clone dds19f23 5', mRNA sequence.
ACCESSION BJ389714
VERSION BJ389714.1 GI:19300800
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.
REFERENCE 1 (bases 1 to 619)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the slug stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
FEATURES
    source
        1..619
            /organism="Dictyostelium discoideum"
            /strain="AX4"
            /db_xref="taxon:44689"
            /clone="dds19f23"
            /clone_lib="Dictyostelium discoideum cDNA library, SF"
            /sex="mat A"
            /dev_stage="slug stage"
            /dev_stage="99 g 203 t 1 others"

BASE COUNT 278 a 38 c 99 g 203 t 1 others
ORIGIN
Query Match 1.5%; Score 53.6; DB 13; Length 619;
Best Local Similarity 53.1%; Pred. No. 0.016;
Matches 138; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 3258 AATGGATATGTAAGTATCCGTGATGGGAAATCAACAGAAAGCGTTACTTTTAGTGC 3317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89 AATATTAAATGAAGTATTGAATAATGAATAATGAATAATGAATAATGAATAATGA 148
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3318 AAGCGATTATGATCAAAATGAATGTATAATACGCAAGTGTCCTCAATCAAAATGGATATA 3377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 149 AA---ATGAAGATTAAATAATAATAATAATAATAATGATGAAATAATAATAAGATGA 205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3378 CACAATAATCGGTATATATACACAGCATCGAGTACAAACGATATACGCAATAATAT 3437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 206 TAATGATAATGATAATGATAATAATAATGATAATAATGATGATGATAATAATAAT 265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3438 GTATAATACGCAAGCATCGATACAAACGATATAACCAAAATAGTGTGTCATGATCA 3497
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Db 266 AATAATGGAATATAACCAATATAATAATAATAATAATAATAATAATAATAATA 325
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QY 3498 AACCGGTATATCAAAAA 3517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 326 AATAATGAAATTCGAAGAA 345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
BJ389815 638 bp mRNA linear EST 08-MAR-2002
LOCUS BJ389815 Dictyostelium discoideum cDNA library, SF Dictyostelium
DEFINITION dictyostelium cDNA clone dds20m04 5', mRNA sequence.
ACCESSION BJ389815
VERSION BJ389815.1 GI:19300901
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.
REFERENCE 1 (bases 1 to 638)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the slug stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
FEATURES
    source
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            /organism="Dictyostelium discoideum"
            /strain="AX4"
            /db_xref="taxon:44689"
            /clone="dds20m04"
            /clone_lib="Dictyostelium discoideum cDNA library, SF"
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            /dev_stage="slug stage"
            /dev_stage="289 a 38 c 110 g 201 t"

BASE COUNT 289 a 38 c 110 g 201 t
ORIGIN
Query Match 1.5%; Score 53.6; DB 13; Length 638;
Best Local Similarity 53.1%; Pred. No. 0.017;
Matches 138; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 3258 AATGGATATGTAAGTATCCGTGATGGGAAATCAACAGAAAGCGTTACTTTTAGTGC 3317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 AATATTAAATGAAGTATTGAATAATGAATAATGAATAATGAATAATGAATAATGA 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3318 AAGCGATTATGATCAAAATGAATGTATAATACGCAAGTGTCCTCAATCAAAATGGATATA 3377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 AA---ATGAAGATTAAATAATAATAATAATAATAATAATAATAATAATAATA 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3378 CACAATAATCGGTATATATACACAGCATCGAGTACAAACGATATACGCAATAATAT 3437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 TAATGATAATGATAATGATAATAATAATGATAATAATGATAATGATAATGATA 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3438 GTATAATACGCAAGCATCGAATCAAAACGATATACCAAAATAGTGTGTCATGATCA 3497
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Db 250 AATAATGGAATATAATAACCAATATAATAATAATAATAATAATAATAATAATA 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3498 AACCGGTATATCAAAAA 3517
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Db 310 AATAATGAAATTCGAAGAA 329
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RESULT 8
CNS0106X 1101 bp DNA linear GSS 26-JUL-1999
LOCUS CNS0106X Drosophila melanogaster genome survey sequence T7 end of BAC
DEFINITION BACN03K20 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

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QY 3481 AGTGTACATGATCAAAACCGCTATATACAAAA 3517
Db 321 AAAAAAGAAATGATACAGCGGTATAGCCCAATA 357

RESULT 10
CNS060QXV
LOCUS
DEFINITION
T7 end of clone AW0AA009H09 of library AW0AA from strain CLIB 89 of
Yarrowia lipolytica, genomic survey sequence.
ACCESSION
AL411257
VERSION
AL411257.1 GI:12180512
KEYWORDS
GSS.
SOURCE
Yarrowia lipolytica.
ORGANISM
Yarrowia lipolytica
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
1 (bases 1 to 759)
Bouciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
lipolytica
FEBS Lett. 487 (1), 95-100 (2000)
20584711
11152876
2 (bases 1 to 759)
Casaregola,S., Neuveglise,C., Lepingle,A., Bon,E., Feynerol,C.,
Artiguenave,F., Wincker,P. and Gaillardin,C.
Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
lipolytica
FEBS Lett. 487 (1), 95-100 (2000)
20584727
11152892
3 (bases 1 to 759)
Direct Submission
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segrif@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
FEATURES
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Location/Qualifiers
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/organism="Yarrowia lipolytica"
/strain="CLIB 89"
/db_xref="taxon:4952"
/clone="AW0AA009H09"
/clone_lib="AW0AA"
/notes="end : T7"
BASE COUNT 356 a 53 c 51 g 206 t 93 others
ORIGIN
Query Match 1.5%; Score 53; DB 17; Length 759;
Best Local Similarity 37.3%; Pred. No. 0.025;
Matches 152; Conservative 45; Mismatches 210; Indels 0; Gaps 0;

QY 3201 AGTTCAACCGAATCAAGATATGTTACGAGTACTCGGAGAAAGAGGGGTAGGAAA 3260
Db 151 ATWWATWTATATWTATATATATATATATATATATATATATATATATATATATAT 210
QY 3261 TGGATATGTAAGTATCCGTGATGGTGGAAATCAAAACAGAAACGGCTTACTTTTAGTGCAAG 3320

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Db 211 ATAAATWTATATWWAAWAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 270
QY 3321 CGATTATGATACAAATGGAATGTATATATATATATATATATATATATATATATAT 3380
Db 271 AAAAAAACAACAAAAAATTTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 330
QY 3381 AAATAATGCGTATATATACACACAGCATCGAGTACAAACGGGATATATATATATAT 3440
Db 331 AAATAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 390
QY 3441 TAATACGCAAGCATCGAATACAAACGGATATATATATATATATATATATATATAT 3500
Db 391 TAATAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 450
QY 3501 CGGTATATACAAAAACAGTGACATTCATCCGATATATATATATATATATATATAT 3560
Db 451 MCAWAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 510
QY 3561 GAGTGAACAGAGGATACATTCATATATATATATATATATATATATATATATAT 3607
Db 511 GAGCTTTTGTGGACATGTATTTCCAGGATTAACCTTGGATTATTTTG 557

RESULT 11
BJ405337/c
LOCUS
DEFINITION
BJ405337 Dictyostelium discoideum cDNA library, SP Dictyostelium
discoideum cDNA clone dds31j07 3', mRNA sequence.
ACCESSION
BJ405337
VERSION
BJ405337.1 GI:19318254
KEYWORDS
EST.
SOURCE
Dictyostelium discoideum.
ORGANISM
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE
1 (bases 1 to 483)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the slug stage
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
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/sex="mat A"
/dev_stage="Slug stage"
BASE COUNT 149 a 67 c 49 g 217 t 1 others
ORIGIN
Query Match 1.5%; Score 52.8; DB 13; Length 483;
Best Local Similarity 49.6%; Pred. No. 0.024;
Matches 135; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

QY 3226 TTACGAGTTCCTCGAGAAAGAGGGGTAGGAAATGGATATATATATATATATATATAT 3285
Db 409 TTACCAATCATTCACATGATGATAAAATTCCTGATGATGATGATGATGATGATGAT 350
QY 3286 GGAATCAACAGACAGCGCTTACTTTTAGTGCAAGCGATTTATGATCAATGGAATGAT 3345
Db 349 GATGATGAAATAATATAGCAGTACAGTGGTGAATAATATATATATATATATATAT 290
QY 3346 AATACGCAAGTGTCCCAATACAAATGGATATATACAAATATCGGTATATATACAGCA 3405
Db 289 AATAATAATATGTCATAGCAATATATGATACCAATATATATATATATATATATAT 230

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Qy 3378 CACAAATAATCGTATTAATACACAGCATCGAGTACAAACGGATATACACGCAATAATAT 3437
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
632 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 573
Qy 3438 GTATTAATACGCAAGCATCGAATACAAACGGATATACACAAATAGTGTGTAATGATCA 3497
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
572 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 513
Qy 3498 AACCGCTTATTCACAAACAGTGCATCTTCATCCGATATACAGATCAATTCGATGCA 3557
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
512 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 453
Qy 3558 GATGAGTCAGACAGAGGTACATCTTCATATAGAAAGTGTAGATGCA 3604
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
452 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 406

RESULT 14
BM468018          1300 bp  mRNA  linear  EST 05-FEB-2002
LOCUS             AGENCOURT 6437618 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5532913
DEFINITION        5', mRNA sequence.
ACCESSION         BM468018
VERSION           BM468018.1 GI:18517060
KEYWORDS          EST.
SOURCE            human.
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE         1 (bases 1 to 1300)
                  NIH-MGC http://mgi.nci.nih.gov/.
                  National Institutes of Health, Mammalian Gene Collection (MGC)
                  Unpublished (1999)
JOURNAL           Contact: Robert Strausberg, Ph.D.
                  Email: cgapbs-remail.nih.gov
COMMENT           Tissue Procurement: ATCC
                  cDNA Library Preparation: Life Technologies, Inc.
                  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                  DNA Sequencing by: Agencourt Bioscience Corporation
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LLNL at:
                  http://image.llnl.gov
                  Plate: LLAM12216 row: p column: 02
                  High quality sequence stop: 434.

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                     /tissue_type="leiomyosarcoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.1 kb."
BASE COUNT         586 a 102 g 112 t 388 others
ORIGIN
Query Match          1.5%; Score 52.6; DB 13; Length 1300;
Best Local Similarity 25.9%; Pred. No. 0.039;
Matches 196; Conservative 0; Mismatches 560; Indels 0; Gaps 0;

Qy 2792 AGTGGGAAGATTCAAATGACAAGACGCTGAAGAAACAGATAGAGGTATATGGCATCA 2851
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
507 ANNNNNNANNNNANNNNANNNNANNNNANNNNANNNNANNNNANNNNANNNNANNA 566
Qy 2852 AACAAACGGGTAGATCGTTTATATGCGGATATACAGGATCAGCAACTGAATCTCGATG 2911
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
567 AAANNANANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 626
Qy 2912 AGATTACAGATCTTACTGCGGGCCAGATCTGTATACAGTCCTTCCTTAGGTATATAACG 2971
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
747 NNNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNNNNNNN 806
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807 AAAANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 866
Qy 3152 CTGCTCTTGTGATTCCAAATCGGATGAGCAAGTTTCGCAACAGTTTACAGTTTCAACCGA 3211
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
867 AANANNNNANNNNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 926
Qy 3212 ATCAAAGATATGTGTCGAGTTTACTGCGAGAAAAGAGGGGTAGGAAATGGATGTAA 3271
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
927 AANANNNANNNNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 986
Qy 3272 GTATCCGTGATGGTGGAAATCAACACAGAACGCTTACTTTTAGTGCAGCGATTATGATA 3331
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
987 AANNNNNANNNNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 1046
Qy 3332 CAAATGGAATGTATAATACGCAAGTGTCCAATACAAATGGATATAACACAAATATGCGT 3391
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1047 AANANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 1106
Qy 3392 ATAATACACAGCATCGAGTACAAACGGATATACGCGAAATAATATGTATATACGCAAG 3451
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1107 AAAAAAAAAAAAAAAAAANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 1166
Qy 3452 CATCGAATACAAACGGATATACACAAATAGTGTGTAATGATCAATCAACCGGCTATATCA 3511
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1167 ANAANNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNNANNA 1226
Qy 3512 CAAAAACAGTGACATTCATCCGCTGATACAGATCAAA 3547
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1227 NAAAAAAAAANNNANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1262

RESULT 15
BM355703/c
LOCUS             BM355703
DEFINITION        BM355703 Dictyostelium discoideum cDNA library, AF Dictyostelium
                  discoideum cDNA clone dda57o22 3', mRNA sequence.
ACCESSION         BM355703
VERSION           BM355703.1 GI:19255297
KEYWORDS          EST.
SOURCE            Dictyostelium discoideum.
                  Dictyostelium discoideum.
ORGANISM          Dictyostelium discoideum
                  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE         1 (bases 1 to 415)
AUTHORS           Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE             Full length cDNA of Dictyostelium discoideum at the aggregation
                  stage
JOURNAL           Unpublished (2002)
COMMENT           Contact: Tadasu Shin-i
                  Center For Genetic Resource Information
                  National Institute of Genetics
                  1111 Yata, Mishima, Shizuoka 411-8540, Japan
                  Tel: 81-559-81-6856
                  Fax: 81-559-81-6855
                  Email: tshini@gene.nig.ac.jp.
                  Location/Qualifiers
                     1..415
                     /organism="Dictyostelium discoideum"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="dda57o22"
                     /clone_lib="Dictyostelium discoideum cDNA library, AF"
                     /sex="mat A"

FEATURES             source

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2003, 03:37:58 ; Search time 26 Seconds  
(without alignments)  
1923.864 Million cell updates/sec

Title: US-10-032-717-2  
Perfect score: 6332  
Sequence: 1 MSPNNQNEYIIDATSTSV.....MSETEGTFYIESVELIVDS 1206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------|
| 1          | 4959.5 | 78.3        | 1169   | 1  | C8BA_BACUK  |
| 2          | 3950.5 | 62.4        | 1157   | 1  | C8AA_BACUK  |
| 3          | 3066   | 48.4        | 1160   | 1  | C8CA_BACTP  |
| 4          | 2595.5 | 41.0        | 1157   | 1  | C9CA_BACTO  |
| 5          | 2558.5 | 40.4        | 1169   | 1  | C9DA_BACTP  |
| 6          | 2449   | 38.7        | 1150   | 1  | C9EA_BACTA  |
| 7          | 2415.5 | 38.1        | 1215   | 1  | C1KA_BACTM  |
| 8          | 2397   | 37.9        | 1138   | 1  | C7AB_BACTA  |
| 9          | 2394.5 | 37.8        | 1229   | 1  | C1BB_BACTU  |
| 10         | 2388   | 37.7        | 1138   | 1  | C7AB_BACTU  |
| 11         | 2359.5 | 37.3        | 1231   | 1  | C1BD_BACTZ  |
| 12         | 2356.5 | 37.2        | 1227   | 1  | C1BE_BACTU  |
| 13         | 2348   | 37.1        | 1138   | 1  | C7AA_BACTU  |
| 14         | 2340   | 37.0        | 1228   | 1  | C1BA_BACTK  |
| 15         | 2321.5 | 36.7        | 1233   | 1  | C1BC_BACTM  |
| 16         | 2208   | 34.9        | 1163   | 1  | CQAA_BACTF  |
| 17         | 2185.5 | 34.5        | 1189   | 1  | C1CA_BACTE  |
| 18         | 2150.5 | 34.0        | 1156   | 1  | C9AA_BACTG  |
| 19         | 2145   | 33.9        | 1176   | 1  | C1CB_BACTG  |
| 20         | 2125   | 33.6        | 1170   | 1  | C1JB_BACTU  |
| 21         | 2115.5 | 33.4        | 1172   | 1  | C1HA_BACTU  |
| 22         | 2078.5 | 32.8        | 1165   | 1  | C1DA_BACTA  |
| 23         | 2069   | 32.7        | 1166   | 1  | C1GA_BACTU  |
| 24         | 2068.5 | 32.7        | 1167   | 1  | C1JA_BACTU  |
| 25         | 2065   | 32.6        | 1160   | 1  | C1DB_BACTU  |
| 26         | 2063.5 | 32.6        | 1176   | 1  | C1AA_BACTK  |
| 27         | 2063   | 32.6        | 1179   | 1  | C1AD_BACTA  |
| 28         | 2058   | 32.5        | 1181   | 1  | C1AE_BACTL  |
| 29         | 2053   | 32.4        | 1155   | 1  | C1AB_BACTK  |
| 30         | 2053   | 32.4        | 1174   | 1  | C1EB_BACTA  |
| 31         | 2048.5 | 32.4        | 1171   | 1  | C1EA_BACTX  |
| 32         | 2035.5 | 32.1        | 1169   | 1  | C1GB_BACTZ  |
| 33         | 2029.5 | 32.1        | 1169   | 1  | C1FB_BACTM  |

ALIGNMENTS

RESULT 1

C8BA\_BACUK  
ID C8BA\_BACUK STANDARD; PRT; 1169 AA.  
AC Q45705;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pesticidal crystal protein cry8Ba (Insecticidal delta-endotoxin  
DE CryVIII(a)) (Crystalline entomocidal protoxin) (134 kDa crystal  
DE protein).  
GN CRY8BA OR CRYVIII(A) OR 50C(B).  
OS Bacillus thuringiensis (subsp. kumamotoensis).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
RX NCBI\_TaxID=132267;  
ON [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NRRL B-18746 / PS50C;  
RA Michaels T.E., Fonceirada L., Narva K.E.;  
RT "Process for controlling scarab pests with Bacillus thuringiensis  
RT isolates.";  
RL Patent number WO9315206, 05-AUG-1993.  
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
CC EPITHELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABAEID BEETLES.  
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
CC OF THE SPORE COAT.  
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE  
CC N-TERMINUS.  
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.  
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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL: U04365; AAA21118.1; -  
CC HSP: P07130; 1DLC.  
CC InterPro: IPR001178; Endotoxin.  
CC Pfam: PF00555; endotoxin; 1.  
CC KW Toxin; Sporulation.  
SQ SEQUENCE 1169 AA; 133543 MW; 22EEFCFSD699909 CRC64;  
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Query Match 78.3%; Score 4959.5; DB 1; Length 1169;

Best Local Similarity 79.8%; Pred. No. 4.5e-269; Indels 49; Gaps 8;

Matches 967; Conservative 68; Mismatches 128;

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DB 1 MSPNNQNEYIIDATSTSVSNDNRYPPFANETNALQNNDYKDKMSAGNASEYFGSP 60

QY 61 EVLVSQDAAKAADIVGKLLSLGLGVFPFVGPIVSLYTLQIDILWPSEKQSWEIFMEQVE 120

DB 61 EVFLSEQDAVKAADIVGKLLTGLGVFPFVGPIVSLYTLQIDILWPSEKQSWEIFMEQVE 120



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DB 121 ELINOKIAEYARNKALSELEGLNNGYQLYLTALFEWEENPNGRALRDVRRNREILDSLF 180
QY 181 TQMPSEFRVTFNFEVPELTVYVYMAANLHLLLLKQASIFGEBWGHSTTTINNYDROMKLT 240
DB 181 TQMPSEFRVTFNFEVPELTVYVYMAANLHLLLLKQASIFGEBWGHSTTTINNYDROMKLT 240
QY 241 EYSDHCWKVETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALFPNYDTRTYPMETKA 300
DB 241 EYSDHCWKVETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALFPNYDTRTYPMETKA 300
QY 301 QLTREYVTDPLGAVNVSSIGSWDKAPSGFVIESSVIRPPHVDYITGLTVYTTQSRSS 360
DB 301 QLTREYVTDPLGAVNVSSIGSWDKAPSGFVIESSVIRPPHVDYITGLTVYTTQSRSS 360
QY 361 ARVIRWAGHQISYHRVRSRNSNQMGYGTQNLHSTSTFTFTNYDYIKTISKQAVLLDIV 420
DB 361 DRYMYWAGHQISYKHIGTSTFTQMYGTQNLQSTSNFDTFTNYDYIKTISNGAVLLDIV 420
QY 421 YPGYTYIFFGMPVEFPPMVLNNTKTLKYNPVSKDIIASTRDSLELEPPETSDQNYE 480
DB 421 YPGYTYIFFGMPVEFPPMVLNNTKTLKYNPVSKDIIASTRDSLELEPPETSDQNYE 480
QY 481 SYSHRLCHITSPATGNTTGLVPVFSWTHRSADLNNTYISDKTIQIPAVKWCNDLNPFPV 540
DB 481 SYSHRLCHITSPATGNTTGLVPVFSWTHRSADLNNTYISDKTIQIPAVKWCNDLNPFPV 540
QY 541 VKPGHGTGDLQVNRSTSGVGLTFLARYGLALEKAKYRVLRYADAVILHV-----N 596
DB 541 VKPGHGTGDLQVNRSTSGVGLTFLARYGLALEKAKYRVLRYADAVILHV-----N 596
QY 597 DAOIOMPKT-MNPGC-DLTSKTFKVAIAITLNLATDSSLKALHNLGCDNPSLTSIGVYV 654
DB 597 DAOIOMPKT-MNPGC-DLTSKTFKVAIAITLNLATDSSLKALHNLGCDNPSLTSIGVYV 654
QY 655 DRIEFTPVDETYEABQDLAKKAVNALFTNTKDGRLPGVTDYEVNQANLVECLSDDL 714
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QY 775 PGAREIDTETPTLYOKVEGVLKPYTRVRLRGFVSSQGLREFTIRHOTNRIVKQVND 834
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QY 895 FKTDPEGYATLGNLELVGEGPLSGDALERLOREQQWKIOMTRREEDRBYWASQAV 954
DB 895 FKTDPEGYATLGNLELVGEGPLSGDALERLOREQQWKIOMTRREEDRBYWASQAV 954
QY 955 DRLYADYQDQALNPVBITLTAADLIQSIPIYVYNMFPEIPGMNTYKTFELTDRLQQA 1014
DB 955 DRLYADYQDQALNPVBITLTAADLIQSIPIYVYNMFPEIPGMNTYKTFELTDRLQQA 1014
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DB 1075 VLVARTARKEGVGNGYVIRDCGNGQTEILTFPSASDYDNGMNTQVSNYNGYNTNNAINTQ 1134
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DB 1135 ASSSTNGYNNMNTQASNTNGYNTNSVYNDQTYITKTFIPYTDQMTIEMSETGTF 1194
QY 1109 -----MYDQASNTNGYNTNSVYMIKPAISRTVDISSVYQNMQMIETSETGTF 1157
DB 1109 -----MYDQASNTNGYNTNSVYMIKPAISRTVDISSVYQNMQMIETSETGTF 1157
```

```
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DB 1158 YIESVELIVDVE 1169

RESULT 2
C8AA_BACUK STANDARD; PRT; 1157 AA.
AC Q45704;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Pesticidal crystal protein cry8Aa (insecticidal delta-endotoxin
DE CryIIIA(a)) (Crystalline entomocidal protoxin) (131 kDa crystal
DE protein).
GN CRY8AA OR CRYVIIIA(A).
OS Bacillus thuringiensis (subsp. kumamotoensis). Bacillus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132267;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL B-18746 / PS50C;
RA Payne J.M., Sick A.J., Poncerrada L.;
RT "Novel coleopteran-active Bacillus thuringiensis isolate and a novel
RT gene encoding a coleopteran-active toxin."
RL Patent number EP0498537, 12-AUG-1992.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF COLEOPTERA.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE germination AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U04364; AAA21117.1; -
DR HSSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1157 AA; 131009 MW; 687B5C49DE93683B CRC64;

Query Match 62.4%; Score 3950.5; DB 1; Length 1157;
Best Local Similarity 65.5%; Pred. No. 9.1e-213;
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

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QY 61 EVLVSQDAKAADIVGKLSGLGVPFVGVPTVSLYTLQIDILWPSGEKSQWEIEMBOVE 120
DB 61 ETPIIS-SSTIQTGIGVIRILGALGVFFASQASVFISFVIGQLWPSKSDVIMGEIMERVE 119
QY 121 ELINOKIAEYARNKALSELEGLNNGYQLYLTALFEWEENPNGRALRDVRRNREILDSLF 180
DB 121 ELINOKIAEYARNKALSELEGLNNGYQLYLTALFEWEENPNGRALRDVRRNREILDSLF 180
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DB 181 TQMPSEFRVTFNFEVPELTVYVYMAANLHLLLLKQASIFGEBWGHSTTTINNYDROMKLT 240
QY 180 VSSIPSFAVSGHEVLLAVYAQAVNLHLLLRDASIFGEBWGPTEGEISFRFYNRQVQLTA 239
DB 180 VSSIPSFAVSGHEVLLAVYAQAVNLHLLLRDASIFGEBWGPTEGEISFRFYNRQVQLTA 239
QY 241 EYSDHCWKVETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALFPNYDTRTYPMETKA 300
DB 241 EYSDHCWKVETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALFPNYDTRTYPMETKA 300
QY 240 EYSDYCVKWKYKIGLDKLGTTSKWLNTHQFREMTLLVLDLVALFPNYDTHMYPIETTA 299
DB 240 EYSDYCVKWKYKIGLDKLGTTSKWLNTHQFREMTLLVLDLVALFPNYDTHMYPIETTA 299
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[illegible]

### RESULT 3

| ACROSS 3 | ACROSS 4 | ACROSS 5 | ACROSS 6 | ACROSS 7 | ACROSS 8 | ACROSS 9 | ACROSS 10 | ACROSS 11 | ACROSS 12 | ACROSS 13 | ACROSS 14 | ACROSS 15 | ACROSS 16 | ACROSS 17 | ACROSS 18 | ACROSS 19 | ACROSS 20 | ACROSS 21 | ACROSS 22 | ACROSS 23 | ACROSS 24 | ACROSS 25 | ACROSS 26 | ACROSS 27 | ACROSS 28 | ACROSS 29 | ACROSS 30 | ACROSS 31 | ACROSS 32 | ACROSS 33 | ACROSS 34 | ACROSS 35 | ACROSS 36 | ACROSS 37 | ACROSS 38 | ACROSS 39 | ACROSS 40 | ACROSS 41 | ACROSS 42 | ACROSS 43 | ACROSS 44 | ACROSS 45 | ACROSS 46 | ACROSS 47 | ACROSS 48 | ACROSS 49 | ACROSS 50 | ACROSS 51 | ACROSS 52 | ACROSS 53 | ACROSS 54 | ACROSS 55 | ACROSS 56 | ACROSS 57 | ACROSS 58 | ACROSS 59 | ACROSS 60 | ACROSS 61 | ACROSS 62 | ACROSS 63 | ACROSS 64 | ACROSS 65 | ACROSS 66 | ACROSS 67 | ACROSS 68 | ACROSS 69 | ACROSS 70 | ACROSS 71 | ACROSS 72 | ACROSS 73 | ACROSS 74 | ACROSS 75 | ACROSS 76 | ACROSS 77 | ACROSS 78 | ACROSS 79 | ACROSS 80 | ACROSS 81 | ACROSS 82 | ACROSS 83 | ACROSS 84 | ACROSS 85 | ACROSS 86 | ACROSS 87 | ACROSS 88 | ACROSS 89 | ACROSS 90 | ACROSS 91 | ACROSS 92 | ACROSS 93 | ACROSS 94 | ACROSS 95 | ACROSS 96 | ACROSS 97 | ACROSS 98 | ACROSS 99 | ACROSS 100 |
|----------|----------|----------|----------|----------|----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|
| ACROSS 3 | ACROSS 4 | ACROSS 5 | ACROSS 6 | ACROSS 7 | ACROSS 8 | ACROSS 9 | ACROSS 10 | ACROSS 11 | ACROSS 12 | ACROSS 13 | ACROSS 14 | ACROSS 15 | ACROSS 16 | ACROSS 17 | ACROSS 18 | ACROSS 19 | ACROSS 20 | ACROSS 21 | ACROSS 22 | ACROSS 23 | ACROSS 24 | ACROSS 25 | ACROSS 26 | ACROSS 27 | ACROSS 28 | ACROSS 29 | ACROSS 30 | ACROSS 31 | ACROSS 32 | ACROSS 33 | ACROSS 34 | ACROSS 35 | ACROSS 36 | ACROSS 37 | ACROSS 38 | ACROSS 39 | ACROSS 40 | ACROSS 41 | ACROSS 42 | ACROSS 43 | ACROSS 44 | ACROSS 45 | ACROSS 46 | ACROSS 47 | ACROSS 48 | ACROSS 49 | ACROSS 50 | ACROSS 51 | ACROSS 52 | ACROSS 53 | ACROSS 54 | ACROSS 55 | ACROSS 56 | ACROSS 57 | ACROSS 58 | ACROSS 59 | ACROSS 60 | ACROSS 61 | ACROSS 62 | ACROSS 63 | ACROSS 64 | ACROSS 65 | ACROSS 66 | ACROSS 67 | ACROSS 68 | ACROSS 69 | ACROSS 70 | ACROSS 71 | ACROSS 72 | ACROSS 73 | ACROSS 74 | ACROSS 75 | ACROSS 76 | ACROSS 77 | ACROSS 78 | ACROSS 79 | ACROSS 80 | ACROSS 81 | ACROSS 82 | ACROSS 83 | ACROSS 84 | ACROSS 85 | ACROSS 86 | ACROSS 87 | ACROSS 88 | ACROSS 89 | ACROSS 90 | ACROSS 91 | ACROSS 92 | ACROSS 93 | ACROSS 94 | ACROSS 95 | ACROSS 96 | ACROSS 97 | ACROSS 98 | ACROSS 99 | ACROSS 100 |

Pesticidal crystal protein cry8Ca (Insecticidal delta-endotoxin protein) (Crystalline entomocidal protoxin) (130 kDa crystal protein).

CRY8CA OR CRYVIII(CA) OR CRYIII.

Bacillus thuringiensis (subsp. japonensis).

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

NCBI\_TaxID=128936;

[1]

SEQUENCE FROM N.A.

STRAIN=Buibui;

MEDLINE=94259786; PubMed=7764305;

Sato R., Takeuchi K., Ogiwara K., Minami M., Kaji Y., Suzuki N., Hori H., Asano S., Ohba M., Iwahana H.;

"Cloning, heterologous expression, and localization of a novel crystal protein gene from Bacillus thuringiensis serovar japonensis strain buibui toxic to scarabaeid insects.";

Curr. Microbiol. 28:15-19(1994).

[2]

SEQUENCE OF 1-14 AND 56-64, AND CHARACTERIZATION.

MEDLINE=94259659; PubMed=8200856;

Hori H., Suzuki N., Ogiwara K., Himejima M., Indrasith L.S., Minami M., Asano S., Sato R., Ohba M., Iwahana H.;

"Characterization of larvicidal toxin protein from Bacillus thuringiensis serovar japonensis strain Buibui specific for scarabaeid beetles.";

J. Appl. Bacteriol. 76:307-313(1994).

-1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABAEID BEETLES SUCH AS ANOMALA CUPREA, A. RUFOCUPREA AND POPILLIA JAPONICA.

-1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF THE SPORE COAT.

-1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.

-1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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EMBL; U04366; AAA21119.1; --

DR HSPP; P07130; IDLC.

DR InterPro; IPR001178; Endotoxin.

DR Pfam; PF00555; endotoxin; 1.

KW Toxin; Sporulation.

SQ SEQUENCE 1160 AA; 130425 MW; C16C3D912EEB8751 CRC64;

Query Match 48.4%; Score 3066; DB 1; Length 1160;

Best Local Similarity 50.3%; Pred. No. 2.1e-163;

Matches 632; Conservative 180; Mismatches 298; Indels 146; Gaps 23;

Qy 1 MSPNNQNEYIIDA TPSTSVSDNSRYPFANEPTNALQNNMDYDKYLGKSGAGNASEYEGSP 60

Db 1 MSPNNQNEYIIDA LPTSVDNSIRYPLANDQNTLNQNNYDKYLGKSTNAELSRNP 60

Qy 61 EVLVSGQDAKAAIDIVGKLLGLGVFPVFGIVSLYLTQLIDILWPSGEKSWEIFMQEVE 120

Db 61 GTFTISQDAVGTGIDIVSTTIISGLIGIPVLGEVFSILGSLIGLLWPSNNENWQIFMNRVE 120

Qy 121 ELINOKIAEYARNKALSELGSLGNVQLYLTAAEEENPNSGRLADVNRREILDSLF 180

Db 121 ELIDDKILDSVRSATIDLANSRVAYEYQNALEDWRKNPSTSAALVXERPGNAEAIL 180

Qy 181 TQYMPSPRVNFEVPFETVYAMAANLHLLLKDAISFGEWGWSTTTINNYYDQMKLTA 240

Db 181 RTNMGSPQTYETPLPTTAQAASLHLVWRDVQIVGKEWGPQNDIDILFYKEQVSYTA 240

Qy 241 EYSDHCVKWYETGLAKLKGTSKQWVDYDQFREMTLAVLDVVALLPNTYDTRTPYMETKA 300

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Db 241 RYSDHCQVWYNAGLNKLGRTGAKQWVDYNNRFRNMVMDLVALFPNYDARIYPLETNA 300
Qy 301 QLTREVYTDPLGAV--NVSSIGSWYD---KAPSGVIESSVIRPPHPVDYITGLTYVT 353
Db 301 ELTREIFTPDVGSVYTGSSSLISWYDMIPALPSFSTLE-NLLRKPDPFFLLQOEIRMYT 359
Qy 354 QSRISARIYIRHWAGHOISYHRSVRSNLOQMTGNTGNLHS-----TSTFDEFTNYDIY 407
Db 360 SFRQNGTIEYNYNGQRLT-----LSYIGSSFNKYSGVLGAEEDIIIPVQNDIY 410
Qy 408 KTLISKDAVLIDIVPG-YTYIFFGMPEVEFPFWMVQNLNTRTKLYKNPVSKDIIASTRDS 466
Db 411 RVV-----WTYIGRTNLLGVNPVTFYF--SNNTKTYS-KPKQFAGGKITDSDG 458
Qy 467 LELPETSQDNYESYSHRLCHITS--IPATGNTT-GLVPFVSWTHRSADLNNTIYSDKI 523
Db 459 BELTYE-----NYOSYSHRVYIISFEKSTGGTVLGVPIPGWTHSSASRNNIYATKI 513
Qy 524 TQIPAVKC-----WDNLFPV---PVRKPGHGTGDLLOYNRSTGSGVTLFLARYGL 571
Db 514 SQIPINKASRTSGGAVNMFQGLYNGPVMKLSG-SGSOVINLRVATDAKGA----- 564
Qy 572 ALEKAGKVRULRVATDADIVLHN-----DAQIOMPKTNPGEDLTSKTFKVAD 621
Db 565 ----SQRIRIRIRYASDRAGKFTISSRSPENPATYSASIAYTNTMTNASTYSTFAYAE 620
Qy 622 AITTLNLTADSS-----LALKHNLGEDPNSTLSGIVYVDRIEFTPVDSYEAODLEAK 676
Db 621 S-GPINIGISGSRFTDISITKEAG-----ANLYIDRIEFTPVNLFEBEEDLVAK 672
Qy 677 KAVNALFTNTDGLRPGVTDYEVNQANLVECLSDLYPNEKRLFLDVAEAKRLSEARN 736
Db 673 KAVNGLFTNEKDALQTSYTDYQVNOAANLIECLSDLYPNEKRLMDVAEAKRLVQARN 732
Qy 737 LQDPDFQIEINGENGWTAETGIEVEGALPKGRVLRPLGAREIDTETPTLYLKQVEEG 796
Db 733 LQDGTGNRINGENGWGTSTGIEVEGDLFKDRSLRLTSAREIDTETPTLYLQOIDES 792
Qy 797 VLKPYTRYLRGFGVSSOGLIEFTIRHOTNIRVKNVPDILLPVSPVNSDGSINRCSBK 856
Db 793 LLKPYTRYLRGFGVSSOGLIEFTIRHOTNIRVKNVPDILLPVSPVNSDGSINRCSBK 852
Qy 857 YVNSRLEVENR-----SGRAHEFSIPDTGIEIDYNAGIWWGPKITDPGEYATLGNLE 910
Db 853 YVDANLALENGNGENGMSSDSHAFSHDITGIEIDLNENTGIWIVFKIPTTNGNATLGNLE 912
Qy 911 LVESGPLSGDALERLQREEQWQKQMTRRRETDRLRYMASKQAVDRLVADYQDQQLNPDV 970
Db 913 FVEEGPLSGETLEWAQQOQOQWQDKRAKRAASEKTYTAAKQAIQDLFPADYQDQKLNSGV 972
Qy 971 BITDLTAQDILQISIPYVYNEMFPEIPGMNTYTKFTELDRLOQAWSLYDORNAIPNGDPR 1030
Db 973 EMSDLLAAQNLVQSIPIVYNALPEIPGMNTYTKFTELDRLOQAWSLYDORNAIPNGDPR 1032
Qy 1031 NGLSNWNPATPGVEYQQINHITSVLVIPPNDVQSVQSQFTVPQPNQRYVLRVATKRGVNGYV 1090
Db 1033 NGLSNWNPATPGVEYQQINHITSVLVIPPNDVQSVQSQFTVPQPNQRYVLRVATKRGVNGYV 1092
Qy 1091 SIRGGNQTETLTSASDYDTNGMYNTQVNTNGYNTNAYNTQASSTNGYNNMNTQ 1150
Db 1093 IIRGANGQTETLTENICDDDT-GVLST----- 1118
Qy 1151 ASNTNGYNTNAYNTQVNTNGYNTNAYNTQASSTNGYNTNAYNTQASSTNGYNTNAYNTQ 1206
Db 1119 -----DQTSYIYTKVETFTSTEQVWIDMSETEGVFNIESVELVLEEE 1160
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RESULT 4

C9CA\_BACTO

ID\_C9CA\_BACTO STANDARD; PRT; 1157 AA.

AC Q45733;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry9Ca (Insecticidal delta-endotoxin
DE CryIXC(a)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN CRY9CA OR CRYIXC(A).
OS Bacillus thuringiensis (subsp. tolworthi).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1442;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=BTS02618A;
RX MEDLINE=96141404; PubMed=8572715;
RA Lambert B., Buysse L., Decock C., Janssens S., Piens C., Saey B.,
RA Seurinck J., Van Audenhove K., Van Rie J., Van Vliet A., Peferoen M.;
RT "A Bacillus thuringiensis insecticidal crystal protein with a high
RT activity against members of the family Noctuidae.";
RL Appl. Environ. Microbiol. 62:80-86(1996).
CC -|- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF LEPIDOPTERA LARVAE. HAS A FAIRLY BROAD
CC SPECTRUM OF ACTIVITY AGAINST MEMBERS OF THE FAMILIES PYRALIDAE,
CC PLUTELLIDAE, SPHINGIDAE, AND NOCTUIDAE. IT IS THE FIRST
CC INSECTICIDAL CRYSTAL PROTEIN WITH ACTIVITY AGAINST CUTWORMS. NO
CC ACTIVITY IS OBSERVED AGAINST SOME BEETLES, SUCH AS COLORADO POTATO
CC BEETLE.
CC -|- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOROGATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -|- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
CC -|- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; Z37527; CAA85764.1; -.
DR HSP; P07130; IDLC.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1157 AA; 129775 MW; C3643918F7DFDB8A CRC64;
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Query Match 41.0%; Score 2595.5; DB 1; Length 1157;
Best Local Similarity 44.1%; Pred. No. 3.8e-137;
Matches 554; Conservative 197; Mismatches 348; Indels 157; Gaps 22;

Qy 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNDYKDYKMSAGNASEYPCSP 60
Db 1 MNRNNQNEYIIDAPHCPCSDDDVRYPLASDPNALQNNYKDYLTQMTDEYDTSYNP 60

Qy 61 EVLVSGQDAKAAIDYVGLSLGVPFVGPVLSLYTQILIDILWPSGKSEWEIPEQVE 120
Db 61 SLSISGRDAVQTALTVVGRILGALGVFPFSQIVSYFYQLNTLWPNVDTAIWEAFMQVE 120

Qy 121 ELINOKIAEYARNKALSELGLGNNYQIYLTAEWEENPNSPALRDVNRPIILSLP 180
Db 121 ELVNNQQTTEFARNOALRQGLGDSFNVYQSRQLNWLADRNDTRNLSSVRAQFTALDLDF 180

Qy 181 TOVNPSPFRVTFVPPFTVYVMAANLHLLKQASIFGEEGWSVTNNYNYDRQMKLTA 240
Db 181 VNAIPLFAVNGQQVPLLSVTAQAVNLHLLKQASLFGEGWGFTQGEISTYIDQLEITA 240

Qy 241 EYSDHCVKVYETGLAKGTSAKQWVDYNNRFRNMVMDLVALFPNYDARIYPLETNA 300
Db 241 KYTNVCEWTYNTGLDRLGRTNTEBSLRYHQFRREMTVLVDVVALFPYDVLRYPTGSP 300

Qy 301 QLTREVYTDPL-----GAVNVSISGSW-----YDKAPSGFVIESSVIRPPHPVDYITGLTYVT 353
Db 301 QLTREVYTDPLVFNFPNPPANVGLCRRWGNTPNY---TFSELENAFIRPPHPLFRNLATIS 356
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QY 354 QRSISSARYIRHWAGHOISYHRVSRGSLNQOMYG-----TNQNLHSTSTDFNTYD 405
DB 357 SNRPVSNFMDYSGHTLRSYLANDSAVQSDSLTITATINPGVDGTRISTAVD 416
QY 406 IYKTLSDAVLLDIVPGYTYIFPGMEVEPFVFMVQNLNTRKTLKYNPVSKDIIASTRDS 465
DB 417 FRSALIG-----IYGVNRASFPVGLFNGT--TSPANGGCRDLY---DT 455
QY 466 ELELPPTSDOPNYESYSHRLCHITSIPATCN-----TTGLVPFVSWTHRSADLNNTIY 519
DB 456 NDELPPDEST-----GSSTHRLSHVTPFSQTNQAGSTANAGSVTYVWTRDRVDLNNIT 511
QY 520 SDKITQIPAVKCMNDLPVVPVKGFGHTGGDLLOVNRSTGSGVTLFLARYGLALEKAGKY 579
DB 512 PNRITQIPLVKASAPVSGTIVLKGFGTGGILR--RTINGTFTGL---RVTVNSPLTQOY 567
QY 580 RVLRYATADIVLH-----VNDAGIQMPKTMNFGEDLTSK-----TF 617
DB 568 RLRVFPASTGNFIRVLRGVSGVIGDVRGLGSTWNRGQELTYESFPTRFTTGPFPNPTF 627
QY 618 KVADAITLNLATSSALKNLGSDPNSTLSGIVYVDRIEPIFVDETYEAEODLEAKK 677
DB 628 TQAEIILTVAEGVST-----GGEYIIDRIEIVPNPAREAEEDLEAKK 672
QY 678 AVNALFTNTKDLRPGVTDYEVNOAANLVECLSDLYPNEKRLLFDAVREAKRLSEARNL 737
DB 673 AVASLFTTRDGLQVNTDYQDQANLVCLSDBOYGHDKMLLEAVRAAKRLSERNL 732
QY 738 LQDPDPQOING--ENGWTPASTGIEVIGDALFKGRYLPLGAREIDTETPTIYLYQKVE 795
DB 733 LQDPDFNTINTEENGWAKASGVITSEGGPFKGRALQASAR-----ENYPTIYQKVA 788
QY 796 GVLKDYTRYLRGFGVSSQGLEIFTRQTNRIKVNVDLDPVSPVNSDGS-----INRC 852
DB 789 SVLKPYTRYLRDGFYKSSQDLIEDLIHKKVHLVKNVPDNL---VSDTYSQSGCSGINRC 845
QY 853 SEQKYVNSRLVEN-----RSGEAHFSIPIDTGEIDYENAGIIVGFKITDPEGYATL 906
DB 846 DEQHQVDQLDAEHHPMDCCBAQAQTHEFSSYNTGDNASVDQGLVWVLKVRTDGYATL 905
QY 907 GNLEVEBGLSDALERLQREBQOWKIOMTRRREEDRRYVMAKQAVDRLYADYQDOOL 966
DB 906 GNLEIVEVGLSGSELEQRDNKNAELGKRAEIDRVYLAQAQAINHLFVDYQDOOL 965
QY 967 NPDVEITDLTAAQDLIOSIPVYNEMFPEIPGMNTTKTELTDRLQQAWSLYDQNAIPN 1026
DB 966 NPEIGLABINEASNLVESISGVSDTLQIPGINYEIVTELSDRLQQAASLYTSERNAVON 1025
QY 1027 GDFRGLSNWATPGVEVQOINHTSVIIPNWDEOVSOQFTVQNRVYLVARTARKEGVG 1086
DB 1026 GDFNSGLDSWNTWDASVQDDGNHFLVLSHWDQVSOOLRVNPKYVLRVARTARKEGVG 1085
QY 1087 NGYVSIROGNGOTETLTFSSADYDNGMYNTQVNTNGYNTNNAVNTQASSTNGYNANM 1146
DB 1086 DGYVTRDGAHQEELITNACDYVNGY-----1114
QY 1147 YNTQASNTNGYNTSVYNDQGTIYTKTVPITPPTQMIEMSETGTFYIESVELI 1202
DB 1115 -----VNDNS-----YITEEVVFPYETKHMVVESESGSFYIDSIEFI 1153
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RESULT 5  
C9DA BACTP STANDARD; PRT; 1169 AA.  
ID C9DA BACTP  
AC O06014;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Pesticidal crystal protein cry9Da (insecticidal delta-endotoxin  
DE CryIXD(a)) (Crystalline entomocidal protoxin) (132 kDa crystal  
DE protein).  
GN CRY9DA OR CRYIXD(A).

OS Bacillus thuringiensis (subsp. japonensis).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
NCBI\_TaxID=128936;  
[1]\_TaxID=128936;  
RN SEQUENCE FROM N.A.  
RC STRAIN=N141;  
RA Asano S.;  
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
-!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
EPITHELIAL CELLS OF INSECTS.  
-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART  
OF THE SPORE COAT.  
-!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE  
N-TERMINUS.  
-!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
CC EMBL; D85560; BAA19948.1; --  
DR HSP; P07130; 1DLIC.  
DR InterPro; IPR001178; Endotoxin.  
DR Pfam; PF00555; endotoxin; 1.  
KW Toxin; Sporulation.  
SQ SEQUENCE 1169 AA; 132228 MW; 659AB25729DE5E9 CRC64;  
Query Match 40.4%; Score 2558.5; DB 1; Length 1169;  
Best Local Similarity 43.8%; Pred. No. 4 4e-135;  
Matches 555; Conservative 188; Mismatches 356; Indels 169; Gaps 25;  
QY 1 MSPNNQNEYIIDIATPSTSVSNDNRYPFANEPTNALQNMNDYKDYLMKMSAGNASEYEGSP 60  
DB 1 MNRNNQNEYVIDAPHGCPADVVKYPLTDDPNAGLQNMNYKEYLQTYGDDYTDPLNP 60  
QY 61 EVLVSGDAAKAIDIVKLLSGLVGPPFVPIVSLYTLQIDILWPSCGKQWELFMEQVE 120  
DB 61 NLSVSGKDVIVQGINIVGRLLSFFGFPSSQWTVTYLLNSLWLPDDENSVDAMERVE 120  
QY 121 ELINOKTAERYARKALSELGKNNVQLYLTAALEENENPGSRALDRVNRPIILSLF 180  
DB 121 ELIDQKISEAVKGRALDDLTGLQVNYLYEALDEWLNRPNGAKSL--VSORFNILSLF 179  
QY 181 TQVMPST---RVTNFVPEPLTVYMAAANLHLLKLDASIFGEEGWSTTTNNIYDROM 236  
DB 180 TQFMPFSGSGGSONYATILLPVYQAANLHLLKLDADIVGARWGLNQIQIDQFHSRQ 239  
QY 237 KLTAEYSDHCVKYETGLAKLGTSAKQWVDYQFRREMTLAVLDVVALPNNYTRYPM 296  
DB 240 SLTQTYTHNCVTAYNDGLAELRGTTAESWFKYQYREMTLTAMDVALFPYNYLRQYD 299  
QY 297 ETKAQLTREVYT---DPLGANNVSSIGSWYDKAP-----SFGVISSVIRPPHVPDYI 346  
DB 300 GTNPQLTREVYTDPIAFDPLEQPTQICRSYINPAPFNHLNFSVLENSLRPPHLPRL 359  
QY 347 TGLVYVYQSRSSISSARYIRHWAGHOISYHRVSRGSLNQOMY-----GTNQLHSTSTF 399  
DB 360 SNLQILVNYQTNGSA-----WRGSRVRYHYLHSSIIQEKSYGLLSDPVGANINQ----- 409  
QY 400 DFTNYDIYKTLSDAVLLDIVPGYT-----YIFPGMEVEFFWVNO 441  
DB 410 ---NNDIYQIISQVSNFASPVGSSYSVMDTNFYLSSGQVSGISGYTQGIQIPAV---CLQQ 463  
QY 442 LNNTRKTLKYNPVSKDIIASTRDSLELPETSDQPNVESYSHRLCHITSI----- 492  
DB 464 RNSTDLEPLSNP-EGDII-----RNYSHRLSHITQYRFOATQSGS 502  
QY 493 PATGNTTGLVFPVFSWTHRSADLNNTIYSDKITQIPAVKCMNDLPVVPVKGFGHTGGDL 552

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Db 503 PST--VSANLPTCVTHRDVLDNTITANQITOLPLVKAVELSSCATVVKGGTGGDVI 560
QY 553 QYNSTSGVGLFLARVGLALEKAGKRVRLRYATDADIVLHVND-----QIOMPTKMN 607
Db 561 R-RTNTGCGFAIRVSATGPTQ---RYRIRPRYASTIDFDFVTRGGTTINNFRFTTMN 616
QY 608 PGEDLTSTKPKVADAITLNLATDSSIALKHNLEDNPNSTLSGIVYVDRIEPIVDIYE 667
Db 617 RGQSRVSTVETFTPTNFNTQSDIIRTSIQGLSGN-----GEVLDRIEIIIPNPAE 672
QY 668 AEQDLEAAKAVNA-LFTNTKXGRLPGVTDYEVNQAANLVECLSDDLYPNEKRLFLDAVR 726
Db 673 AEEDLEAAKAAARQNLFTRTRDGLQVNVTDYQVQAANLVECLSDDEQVGHDKMLLEAVR 732
QY 727 EAKLSARNLLQDPDFQIEING--ENGWASTGIEVTEGDALFKGRVYRLPGAREIDTET 784
Db 733 AAKLSERNLLQDPDFNTINSTENGWASKASGVITISEGGFFFKGRALQLASAR-----EN 788
QY 785 YPTLYQKVEEGLKPYTRYRLRGVSSQGLEIFTRHQTNRIVKXNVPDLDLDPVSPVN 844
Db 789 YPTIYQKVASULKPYTRYRLDGFVKSSQDLEIDLHYHKVHLVKXNVPDNL---VSDTY 845
QY 845 SDGS---INRCSEQKYNRSLEVEN-----RSGEAHEFSIPIDTGBIDYNNAGIWWG 894
Db 846 SDGSCGMRCEEQMNAQLTEHHHPMDCCAAQTHFESSYINTGDLNASVDQGIWV 905
QY 895 FKTDPSGYATLGNLVEGPLSGDALERLQREBQKQIOMTTRRRETDTRYWASKOAV 954
Db 906 LKVRTTDCYATLGNLVEGPLSGESLERQDRONAKWNAELGRKRAEIDRVYLAQAI 965
QY 955 DRLYADYQDQQLNPDVEITDLTAQDILQSTPYVYNMFEPIPGWNYTKFTELDRLOQA 1014
Db 966 NHLFVDYQDQQLNPEIGLAEINEASNLVESISGVISDTLLQIPGINVEIYELSDRLQQA 1025
QY 1015 WSLYDQRNAIPNGDFRNGLSNWNATPGVEVQOINHTSVIPIPNDEQVSOQFTVPQNRQ 1074
Db 1026 SYLYTSRNAVQNGDFNSGLDSWNTTASVQDGNMHPFLVSHWDAQVSOQLRVNPKY 1085
QY 1075 VLRVTKARKEGVNGVYIRDDGNGOTELTFPSASDYDNGMYNTQVNTNGYNTNNAVNTQ 1134
Db 1086 VLRVTKARVGGGQGVYIRDGAHHEOETLTFNACDYVNGTY----- 1126
QY 1135 ASSTNGYNANNMYNTQASNTNGYNTNSVYNDQTVTKTFTFIPYTDQMWLEMSSTGTP 1194
Db 1127 -----VNDNS-----YITEEVVYFETKHMWVEVSESGSF 1157
QY 1195 YIESVELI 1202
Db 1158 YIDSIEPI 1165

```

## RESULT 6

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C9EA_BACTA STANDARD; PRT; 1150 AA.
ID C9EA_BACTA
AC Q9ZNL9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry9Aa (insecticidal delta-endotoxin
DE CryIXE(a)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN CRY9EA OR CRYIXE(A).
OS Bacillus thuringiensis (subsp. aizawai).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1433;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SSK-10;
RA Midon N., Oyama K.;
RT "Bacillus thuringiensis cry gene for insecticidal crystal protein."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

```

```

CC -!- EPIITHELIAL CELLS OF INSECTS.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB011496; BAA34908.1; -.
DR HSSP; P07130; IDLC.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1150 AA; 129895 MW; 7D6AB93D6EDC97EB CRC64;

Query Match 38.7%; Score 2449; DB 1; Length 1150;
Best Local Similarity 43.4%; Pred. No. 5.6e-129;
Matches 541; Conservative 198; Mismatches 362; Indels 146; Gaps 30;

QY 1 MSPNNQNEVEIIDATSTSVSNDNSRYPFANEPTNALQNNQNDYKDKMSAGNASIEYRGS- 59
Db 1 MNRNNPNEVEIIDAPYCGCPDSDVRYPLASDPNAFQNNNYKEYLQYDG---DYTGSL 57
QY 60 --PEVLVSGQDAKAIDIVKLLSGLPVPGVIVSLVLTQILDLWPSGEKQWEIEME 117
Db 58 INPNLSINPRDVLQGTGINVIGRILGFLGVFAGQVTFYTFLLNQLNPTNDNAVWEAFMA 117
QY 118 QVEELINQIKAEYARNKALSELGLGNVLYLTALKEEENENGSRALDRVNRPIILD 177
Db 118 QIEELIDOKISAQVNRNALDDLGLHDHYEYLALEWLERENGARA-NLVQRFENLH 176
QY 178 SLFTQWMPSPRV---TNFVPPPLTVYMAANLHLLKDDASIPGSEWGSTTTNNYD 233
Db 177 TAPVTRMPSPSGTQSDAVALTVYQAANLHLLKDDAEIYGARWGLQGOQNLNYPN 236
QY 234 ROMKLAIEYSDHCXKVEYGLAKLKTSAQWVDYQNFREMTLAVLDVVALPENYDTRT 293
Db 237 AQQRTRYIYNHCVETYNRGLGLEDVGRNTESWLNHRFREMTLMAVMDLVALPFFVNVQ 296
QY 294 YPMETKAQLTREYVTDPL---GAVNVSSIGSWYDKA-PGFGVIESVIRPPHVPDYITGL 349
Db 297 YPGANPQLTREIYTDPIVYVNPANOGICRWGNPNYTFSELENAFIRPHLPERLNL 356
QY 350 TV-----YTSRSISARYIRHWAGHOISYHRVSRGSLNQOMYGTQNLHSTSTDFDPTNYD 405
Db 357 TISRNYTAPTNS---FLDYMSGHTLQSOHANNPTTYETSYG-QITSNTRLEFNTN-- 409
QY 406 IYKLSKDAVLVDIVPGYIYF---FGPVEVEFF---MVNQLNTRKILKYNPVSQDII 459
Db 410 -----GARIDSARNFGNLYANLYGVSSLNIFPTGVMSSEITNAANTCRODLTTE-- 460
QY 460 ASTRDSELEPPPTSPQPNVSYSHRLCHITSIPATGNTT-----GLVPVFSWTHRS 511
Db 461 -----ELPLENN-----FNLLSHVTFI--RPNTTQGGPLATLGFVPVYVWTRD 503
QY 512 ADLNTIYSDKITQIPAVKCDNLFPVVPVKGPGHTGGDLLOVNRSTSGVGTFLARYGL 571
Db 504 VDFNTITADRIATQLPWRKASEIGGGTVVKGPGTGGDILR-RTDGAAGVTI---RANV 559
QY 572 ALEKAGYRVRLRYATDADIV--LHVND--AQIQMPTKXNPGEDLTSTKPKVADAITTLN 627
Db 560 NAFPLTQOYIRLRYASTYFVNLNFVNSAAGTFLPSTMAQNSGLSTYESFNTLEVTHTIR 619
QY 628 LATDSSLAKHNLGDPNSTLSG-IYVVDRIEPIVDIYEASQDLEAKKAVNALPFTNT 686

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Db 620 F-SQSDTTLRLNI-----FPSISGQEVYVDKLEIVIPINPTREABEDLEDAKAVASLEFRT 674
Qy 687 KGLRPGVTDYEVNQAAANVLECLDLYPNEKRLLEFLDAVREAKRLSEARNLLQDPDQEI 746
Db 675 RDGLQVNTDYQVDDQAAANVLECLDQEGHDKMLLEAVRAAKRLSERNNLLQDPDNEI 734
Qy 747 NG--ENGWTAAGTAGEVIEGDALFKGRYLRLPGAREIDTETPTLYLYQKVEGVLPKPTRY 804
Db 735 NSTEENGKASNGVTISEGGPFPGKRALQLASAR---ENYPTIYQKVDASTLKPTRY 790
Qy 805 RLKGFVSSQGLEFTTRHQTNRIRVKNVDPDLLPDPVSPVNSDGS---INRCSEOKYNSR 861
Db 791 KLKDFVQSSQDLEIDLHHRKHLVKNVNDL---VSDTYSGSCSGINRCSEHQVDVQ 847
Qy 862 LEVEN-----RSGEAHEFSPIDTGRIDVNNENAGIWDGFKITDPEGVATIGNLELVEG 915
Db 848 LDAEDHPKDCCEAAQTTFEFSYIHTGDLNASVDQGIWVLQVTRTDTGATIGNLELVEG 907
Qy 916 PLGSDALERLQREBQWKIOMTRREBETDRRYMASQAVDRLYADYQDQQLNPQVEITDL 975
Db 908 PLGSESLEREQDNKAWNEEVGRKRAETDRIYQDAKQAINHLFVDYQDQQLSPVGMADI 967
Qy 976 TAAQDLIQSPYVNEPPEIPGANYKFTPTLDRLOQAWSLYDQRNAIPNGDPRNGLSN 1035
Db 968 IDAQNLIASISDVYSDAVLQIPGINEMYETLSNRLQOASLYTSRVNVQVQDGFNSGLDS 1027
Qy 1036 WNATPGVEVQOINHTSVLIPNWDQVSOQFTVQPNORYLVRTARKEGVNGVYSIRDG 1095
Db 1028 WNATTDVAVODGNHFLVSHWDQVSOQFRVQPNCKYLVURVAKKVGNGDGVITIQDG 1087
Qy 1096 GNQETITLFSASDYDTNGMYNTQVSNNGYNTNAYNTQASSTNGYNANNMYNTQASNTN 1155
Db 1088 AHRETLTFAACDYDVNGTH-----1107
Qy 1156 GYNTNSVNDQGTGHTKVTPIPTDQWMIEMSETEGTFYIESVELI 1202
Db 1108 -VNDNS-----YITKELVFPKTEHMMVSETEGTFYIDSIEFI 1146

RESULT 7
CIXA_BACTM STANDARD; PRT; 1215 AA.
ID CIXA_BACTM AC Q45715;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cryIka (insecticidal delta-endotoxin
GN CRYIKA OR CRYIK(A) OR CRYIK.
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1441,
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=F190;
RX MEDLINE=96102856; PubMed=8586263;
RA Koo B. T., Park S. -H., Choi S. -K., Shin B. S., Kim J. I., Yu J. H.;
RT "Cloning of a novel crystal protein gene cryIka from Bacillus
RT thuringiensis subsp. morrisoni.";
RL FEMS Microbiol. Lett. 134:159-164 (1995).
CC -I- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF INSECTS. SELECTIVELY TOXIC TO ARTOGEDIA RAPAE
CC AND NOT ACTIVE ON PLUTELLA XYLOSTELLA.
CC -I- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOREULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -I- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -I- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
DR EMBL; U28801; AAB00376.1; -
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
DR Toxin; Sporulation.
SQ SEQUENCE 1215 AA; 137378 MW; 7CA7A7A3311893D9B CRC64;

Query Match 38.1%; Score 2415.5; DB 1; Length 1215;
Best Local Similarity 42.9%; Pred. No. 4.5e-127;
Matches 538; Conservative 201; Mismatches 421; Indels 95; Gaps 28;

Qy 1 MSPNQNEYEIIIDATSTSVNSDNRYPFANETNALQNMDYKDYLMKMSAGNASEYEGSP 60
Db 1 MNSNRKNEEIIINALGIPAVSNHSAQMDLSPDAR-----IEDSLCAEGNNID----P 49
Qy 61 EVLVSGQDAAKAIDIVGKLLGLGVPPFVGVPIVSLYLTQLIDILWPSCGEKOWEIFMEQVE 120
Db 50 FVSAS---TVQTGISAGRIELGVLPFFAGQLASFYSFLVGLWPSC-RDPWEILFMEHVE 105
Qy 121 ELI-NQKIAEYARNKALSELEGLGNYYQLYLTALAEENPNPNSRRLRDVNRPEILDLS 179
Db 106 QIVRQQITDSVDRTAARLEGLGRGYRSYQQALETWLDNRNDARSRIIRERVIALELD 165
Qy 180 FTQMPFSRVTVNEVEPFLTVYMAANLHLLLLKDAISFGSEGWSTTTINNYDRQMKLT 239
Db 166 ITTAIPLFSIRNEVEPLLMYQAANLHLLLRDASLFGSEGMWSSADVNAQYQEQIRYT 225
Qy 240 AEYSDHCWKVEYGLAKLKGTSAKQWVDYQNPQREMTLAVLDVVVALFPNPDTRYPMETK 299
Db 226 EYSNHCVMQNTGLNRKLRGTTAETWVRYNQFRDLFLGLVDLVALPSPDTRYPIPTT 285
Qy 300 AQLTREYVTDPLGAVNVSSISGWDYKAPSGVIESVIREPPHVDYITGLTVYTSRSIS 359
Db 286 AQLTREYVTDPLGVV-AGPNNSMFRNGASFAIENAIIRQPHLYDFTLNTIYTR-RSQV 343
Qy 360 SARYIRHWAGHQSIRHVRSGSNLQMGYNQNLHSTSTFDFTNYDIYKTLSDKDALDI 419
Db 344 GTTIMNLWAGHRTFNRIOGGSSEMYGAIITNPVSVSDIPFVNRDRVYRTVSLAGGSL 403
Qy 420 VYFGYTVIFPGMEVEPFMYNQLNTRKT-LKYNPVSKDIIASTRDSLELPPTSDPN 478
Db 404 -----SGIRYGLTRVDMDIFRNHPDIVTGLFVHPGAGIATQVKDSDELPPPTSDPN 458
Qy 479 YESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNTIYSDKITQIPAVKWDNLFFV 538
Db 459 YRAFSLLSHISMGPTTQD---VPPVYVSWTHQSADRNTINSRITQIPLVKAHTLQSGT 515
Qy 539 PVKPGHGTGDDLQVNRSTGVTGLPLARYGLALEKAGKYRVLRYATDADIVLHND 598
Db 516 TVKPGPGTGGDILR-RTSG--GPFASFNVNLDNFNLRSQYRARIYASTNLRILYVTA 571
Qy 599 -----QIQMPKTNPGEDLTSKTKVADAITTLNLA-----TDSSLAKHNLGSDPNSTL 648
Db 572 GERIPAGQDKTMDAGAPLTFQSFVA-----TINTAFTFPERSSSL-----TIGADTFSS- 622
Qy 649 SGIVYVDRIEFIPVDETYEAEQLEAAKAVNALFTNTKD-GLRPGVTDYEVNQAAANLVE 707
Db 623 GNEVYVDRFELIQVATFAESDLERAKAVNALFTSTNPRGLKTDVTDYHIDQVSNLVE 682
Qy 708 CLSDLYPNRKLLFDVAAREAKRLSEARNLLQDPDPOEING--ENGWTAAGTAGEVIEGDA 765
Db 683 CLSDEFCLDKKRELLERVEVKARLSDERNLQDPTFTSISQTDGRGWIGSTGISIQGDD 742
Qy 766 LFKGRYLRLPGAREIDPETYLYLYQKVEGVLPKPTRYELRVGVSGSQGLEFTIRHOT 825
Db 743 IFKENYVRLPGT--VD-ECYPTLYLKIDBSQLKSYTRYQLRGYIEDSQDLLEYLYRNA 799
Qy 826 NRIVKNVDDLLP----DVSPVNSDGSINRCSEOKYNSRLEVENRSGE-----AHEFSI 876
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Db 800 KHTLSVPGTESPWPSSGVPYSGRCPNRCAPRIEMNPDLDSCRYGKCVHSHHFSL 859  
Qy 877 PIDGEIDYENAGIWGFKITDEGVATLGNLELVEBGLSGDALERLOROEQWQIOM 936  
Db 860 DIDVGCITLDELGLWVFIKTDQGHAKGNLFIEBIEPLGLKALSKVKAERKWDKY 919  
Qy 937 TRREEDRRYMASQVADRLYADYQDQOLNPDVEITDLTAAQDLIOISIPVYVNMPEI 996  
Db 920 EKLOLETKRVYTEAKESVDALFVDSQYDKLQANTNIGIHHGADQVHRIEPIYSELPI 979  
Qy 997 PGMYTFTLTDRLQAWSLYDORNAIPNGDFRNGLSNNWATPGVEVQOQNHVSILVIP 1056  
Db 980 PSINAAIPEELEHIFKAYSILYDARNVKNKNGDFNGLSCMNKGVHDVQOQHRSVLVLS 1039  
Qy 1057 NWDSQVQOFTVQPNQVRLVATKGGVNGVYIRDDGNGQTLTFSASDYDTNGMYN 1116  
Db 1040 EWEAEVSQKVRVCPDRGYILRVATKGGVNGVYIRDDGNGQTLTFSASDYDTNGMYN 1097  
Qy 1117 TOVSNTNGYNTNAYNTQASSTNGYNA-----NMVNTQAS-----NTN 1155  
Db 1098 NNTVTCNDYTNQSAEGSTDACSNGYEDGYENRYEPNPSAPVNYTPTYEEGMYTDQ 1157  
Qy 1156 GYN---TNSVNDOT---GYITKTVTFIPYTDQWIMSEMSETEGTFYIESVELIV 1203  
Db 1158 GYNHCVSDRGYRNHTPLPAGVYVLELFPETEQWIEGTEGTFYIVGSVELLL 1212

RESULT 8  
C7AB\_BACUA STANDARD; PRT; 1138 AA.  
ID C7AB\_BACUA  
AC Q45707;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pesticidal crystal protein cry7AB (insecticidal delta-endotoxin  
DE CryIIA(b) (Crystaline entomocidal protoxin) (130 kDa crystal  
DE protein).  
GN CRY7AB OR CRYIIA(B).  
OS Bacillus thuringiensis (subsp. dakota).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=132268;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HD511.  
RA Payne J.M., Fu J.M.; Bacillus thuringiensis isolates and genes encoding  
RT coleopteran-active toxins.";  
RL Patent number US5286486, 15-FEB-1994.  
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
CC EPITHELIAL CELLS OF COLEOPTERA.  
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF  
CC THE SPORE COAT.  
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-  
CC TERMINUS.  
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U04367; AAA21120.1; -  
DR HSSP; P07130; 1DLCL.  
DR InterPro; IPR001178; Endotoxin.  
DR Pfam; PF00555; endotoxin; 1.  
KW Toxin; Sporulation.  
SQ SEQUENCE 1138 AA; 129778 MW; 01DF702C074CE88 CRC64;

Query Match 37.9%; Score 2397; DB 1; Length 1138;  
Best Local Similarity 42.4%; Pred. No. 4.4e-126;  
Matches 524; Conservative 208; Mismatches 367; Indels 138; Gaps 30;  
Qy 1 MSPNNQNEYEIIIDATFSTSVNSDNRYPFANFPTNALQNDYKDYLRMSAGNASEYVGPSP 60  
Db 1 MNLNNGGYE-----DSNRTLNNSLYPTOKALSPSLKNNYQDFLSITERE-----QP 49  
Qy 61 EVLVSGDAAKAALDIVKGLSGVFPVGVPIVSLYLTQLDILWPSGEKSWELFMEQVE 120  
Db 50 EALASGNTAINTVSVGATLSALGVPGASFITNFKITGLLWPH-NKNWIDFEMTEVE 108  
Qy 121 ELINOKIAYARNKALSEGLGNNYQLYLTALEEENPENGSRALRDVNRREILSLF 180  
Db 109 TLIEQKIEQVARNKALAEGLGNNLTIIYQALDMLNPPDPATITRVIDRFRILDALP 168  
Qy 181 TQMPSPRVNFEVPLFVYVYMAANLHLLKQASIFGEWGWSTTTNNYIDROMKLT 240  
Db 169 ESMPSFVAGYBIPLLTVYAQAANLHLLRDSTLYGDKWGTQNNIEENYNRQKHIS 228  
Qy 241 EYSDHCVKVETGLAKLKGTSAKOWVDYNOFREMTLAVLDVVALPNYDTRTYPMETKA 300  
Db 229 EYSHCVKWTNGLSLNGSTYEQWINYRFRREMILWLDIAAVFPIDYPRMYMETST 288  
Qy 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGFVIESSVIRPPHVFEDYITGLTVYTQSRSS 360  
Db 289 QLTREVYTDPI-SLSISN-----PDIGPSFSQMENTAPRTHLVLDYLDLYIYSKYKAPS 343  
Qy 361 ARY---IRHWAGHOISYHRVSRGSLNQ--MYGTNQLHSTSTFDFTNYDIYKTLSDAV 415  
Db 344 HEIQPDLFYWCVHKVSPKK-SEQSNLYTTGIYKTSYSSGAYSPRGNDIYRTLAAPSV 402  
Qy 416 LLDIVVPGYTYIFPGWPEVEFFVWNLNTRKTLKYNVPSKDIILASTRDSLELPPETSD 475  
Db 403 ---VVP-ITQ-NYGEQVEFYGVKGHVHVRGNKYD-----LYDSIDQLPPD--G 447  
Qy 476 QPNYESYSHRLCHITSI---PATGNTTGLVPVFSWTHRSADLNNTIYSKTIQIPAVKC 531  
Db 448 EPIHEKYTHLCHATAISKSTPDYDNAT--IPIFSWTHRSAEYNYRYPNKKIPAVKM 505  
Qy 532 WDLNLPFVVPVKGPGHGTGDLLOVNRSTGVSGLTFLARYGLALEKAGKYRVLRYATDADI 591  
Db 506 YKLDLSTVYVKGPGFTGGDLVK-RGSNGYIGDI-KATVNSPLSQ--KYRVRYATSVSG 561  
Qy 592 VLHV--NDAQIOMPK-----TWNPGEGLTSKTKPVADAITLNLATDS---SLALKEN 639  
Db 562 LFNVFIND-BIALQKQFQSTVTEIGEKDUTYGSFGYEVSTTIQPPNEHPKITLHNLH 620  
Qy 640 LGEDPNSTLSGIVVVDRIEPIPVDETYEARQDLEAAKAVNALFTNTKGLRPGVTDYEV 699  
Db 621 SNNSP-----FVDSIEPIPDVNVYDEKEKLEKAKAVNTLFTEGRNALQKYVTDYKV 673  
Qy 700 NQANLVECLSDLLYNEKRLLPDAVREAKRLSEARNLLQDPDFQIBING--ENGWTAFTG 757  
Db 674 DOVSILVDCISGLDYNEKRELQNLVKYKRLSYSRNLLDPTFDSINSSENGWYSGNG 733  
Qy 758 IEVLGDALFKGYRLPGAREIDTETPTLYKYVEEGLKPYTRYLREGLFVGSOGLE 817  
Db 734 IVNGGDFVFGNGLYIFSGTN--DTQ-YPTLYQKIDESKLEYSYKLGKGFTESSODLE 790  
Qy 818 IFTRHQTNRIKVNPPDILLPDVSPVNSDGSINRCSEKQVNSRLEVENRSGE----- 870  
Db 791 AVVIRYDAKHRTLDVSDNLLPDILPENTCGEPNRCAAQVLD-----ENFSRCSNMQDG 845  
Qy 871 ----AHEPSIPIDTGEIDYENAGIWWGFKITDPEGVATIGNLELVEEGLSGDALERLQ 926  
Db 846 ILSDSHSFLNIDTGSINHNENLGIWLFKISTLEGYAKFENLEVEDGDPVIGEARLVK 905  
Qy 927 REEQWKIQWTRREEDRRYMASKQAVDLRYADYQDQOLNPDVEITDLTAAQDLQSIIP 986  
Db 906 RQETKWRNKLAQMTTETQAIYTRAKQALONLFANAQDLSHLKIDVTFATIAAARKVQSI 965  
Qy 987 YVYNEMFPEIPGMNYTKFTLTDLRLQAWSLYDQRNAIPNGDPRNGLSNWNATPGVEVQ 1046



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Db 966 EVTMSWLVVPGVNHPIFTSLGRVORAFQYDVRNVRNGRFLNGLSDWIVTSNVQOE 1025
Qy 1047 INHTSVLVIPNWDQVSOQFTVPQPNQRYLVRTARKEGVGVVSRDGGNQTETLTFSA 1106
Db 1026 ENGNNVLVNNWDAQVRNVKLVQDRGVLRVTRKIGIGEGYITITDEEGHTDQURFTA 1085
Qy 1107 SDYDTGMYNTQVNTNGYNTNAYNTQASSTNGYNANNMYNTQASNTGNTYNTNSVNDQ 1166
Db 1086 CE-----EIDASNAF-----I 1096
Qy 1167 TGVITKTVFIPYTDQWIMSETEGTPIYESVELIV 1203
Db 1097 SGYITKELEFPDTEKVHIEGTGIFLVESIEFL 1133

RESULT 9
C1BB_BACTU
ID C1BB_BACTU STANDARD; PRT; 1229 AA.
AC Q45739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Pesticidal crystal protein cryIIB (insecticidal delta-endotoxin)
DE CryIIB(b) (crystalline entomocidal protoxin) (140 kDa crystal protein).
GN CRYIIB OR CRYIIB(B) OR CRYETS.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=EG5847 / NRRL B-21110;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects.";
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L32020; AAA22344.1; -
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;

Query Match
Best Local Similarity 41.6%; Pred. No. 6.8e-126;
Matches 529; Conservative 194; Mismatches 434; Indels 115; Gaps 26;

Qy 1 MSPNNQNEVEIIDATSTSVNSDNRYPPANBPTNALQNNMDYDKYTKMSAGNASRYPGSP 60
Db 1 MTSNRKNEEIIINALGIPTVSNPSTQ-----MNLSPDARIEDSLCVAENVNID----P 49
Qy 61 EYLVSQDAAKAIDIVGKLISGLGVFPVCPVLSYLTQLIDILWPSGKQWEIPEQVE 120
Db 50 FVSAS---TVQTGINIAGRIAGLVGVPPAGQLASPSFLVGLWPSG-RDPWEIPLHEV 105
Qy 121 ELINQKIAEYARNKALSEGLEGNNTQVLYLTALKEEENPNNGSRALRDVNRREILDSLF 180

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Db 106 QLIRQOVTEINTAIALREGLGRGYSYQQALETWLDNRNDARSRIILERVVALELDI 165
Qy 181 TQYMSFRVTNEVEPLTVYMAANLHLLLLKXASIFGEWGHSTITINNYDRQMKLTA 240
Db 166 TTAIPLFIRNEVEPLVMVYAANLHLLLDASLFGSEWGWASDVNQYQOEIRYTE 225
Qy 241 EYSDHCWKVYETGLAKIGTSAKQVYDVNQFRREMTLAVLDVVVALFPNPDTRYPMETKA 300
Db 226 EYSNHCQWNTYGLNLRGTNAESWLRYNQFRDLTLGVLDLVALFPSYDTRYPINTSA 285
Qy 301 QLTREYVTDPLGAVNVSS---IGSWY-DKAPSGFVIESVIRPPHVFYITGLTVVYQSR 356
Db 286 QLTREIYTDPIKRTNAPSGFASNTMFPNNAPSFAIEAAIFRPPHLLDPPEQLTIYSASS 345
Qy 357 SISSARYIRHWAGHOISYHRVSRGSLQOMYGTQNQLHSTSTFDETNYYDIYKTLSDAVL 416
Db 346 RWSSTOHMYWVGHRLNFRPIGTTLNTSTQGLTNTSINPVLQFTSRDYRTESNAG-- 403
Qy 417 LDIVYPGYTIYFF-----GMPEVEFPVNMQLN-NRKTLLKYNPVSKDIIASTRDSLELP 470
Db 404 -----TNILFTYVNGVPMARFNPNQNIYERGATTYQPYQGVIGIQLFDSETELP 455
Qy 471 PETSQPNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVK 530
Db 456 PETTERPNYESYSHRLSHIGLI--IGNTL-RAPVYSWTHRSADRWTWIGPNRITQIPLVK 512
Qy 531 CWDNLPFPVVKVPGHGTGDDLQYRSTSGVTGLFARYGLALEKAKGRVRLRYA--TD 588
Db 513 ALNLHSGVTVVGPGFTGDDILR-RTNTGTGDI--RLNINVPISQRYRIRYASTTD 568
Qy 589 ADVLHVNDQAQOM---PKTMNPGEDLTSTKTFKVADAITTLATDSSSLAKHNLGEDPN 645
Db 569 LQFFTRINTTWNIGNFSRTMARGNLEFRSPTAGFSTPFPLNAQS---TFTLQAQSF 625
Qy 646 STLGSIVYVDRIEFIPVDETYEAEQDLEAAKAVNALFTNTKD-GLRPGVTYDEVNQAAN 704
Db 626 SNOE--VIIDRVFVPAEVTPEAYEDLERAQKAVNALFTSTNPRRLKTDVTDVHIQVSN 683
Qy 705 LYECISDDLYPNKRLLPDAVREAKELSEARNLQDDPQFEING----- 748
Db 684 MVACISDEFCLDEKRELFEKVYAKRLSDERNLLQDPNFTFISQGLSFASIDQSNFPPI 743
Qy 749 ----ENGWTAETGIEVDGALFKGYRLPGAREIDTETPTLYLQKVVEGVLKPYTRY 804
Db 744 NELSEHGWSGANVTIOGENDVFKENYVTLPGT---FNECYPNLYQKIGESSELKAYTRY 800
Qy 805 RLRFVGSSQGLEIFTRHOTNRIKVNVP--DLLLP--DVSPVNSDGSINRSEEQKYVNS 860
Db 801 QLKGVIEDSQDLEILYIRYNAXHETLDVPGTDSLWPLSVESPIGRCEPNRCAPHFEMNP 860
Qy 861 RLEVENRSGE-----AHEFSIPDITGEIDYNNAGIWWGFKITDPEGYATLGNLELVEEG 915
Db 861 DLDSCRCRDEGCAHSHHFETLIDVGCTDLHENLGVVVVFKITQOEGYARLGNLEFIEK 920
Qy 916 PLSGDALERLQREBOQKIOMTRREETDRRYMAKQAVDRLYADYQDOQLNPDVEITDL 975
Db 921 PLIGEALSRVKAERKAKRDKREKLQLETKRVTEAKEADVALFVDSQYDQLQADTNIGMI 980
Qy 976 TAAQDLIQSIPYVYNEFPPEIFPMNYTKFETLTDRLQQAWSLYDQRNAIPNGDFRNLGN 1035
Db 981 HAADKLHVHRIEAYLSLSELPVIFGVNAEIPFEELEGHITITAMSLYDAENVVKGDFNNGLIC 1040
Qy 1036 WNATPGVEVQOQNHSTSVLVI PNWDQVSOQFTVPQPNQRYLVRTARKEGVGVVSRDGG 1095
Db 1041 MNVKGHVDVQOQSHRSDDLVIPEWEAEVSQAVRCPGRGVIILRVTAKEGVEGCVTIHEI 1100
Qy 1096 GNOTETLTSADYDTNGMYNTQVNTNGYNTNNAVNTQASSTNGYNANNMYNTQASNTN 1155
Db 1101 ENNTDELKE--KNCSEEEVYPTDGTGTCNDYTAHQG-----TAACNSRNAGYEDAYEDTTA 1154
Qy 1156 GYNTNSVYNDQT-----GYITKTVTFFPYTDQWIMSETE 1191

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Db 1155 SVNYKPYEBETDVRDHNCEYDRGVNYPVPAGVVTKELEYFFBETDTVWIEIGETE 1214  
QY 1192 GTFVIESVELIV 1203  
Db 1215 GKFIIVDSVELLL 1226

RESULT 10  
C7AB\_BACUC STANDARD; PRT; 1138 AA.

AC Q45708;  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pesticidal crystal protein cry7ab (Insecticidal delta-endotoxin  
DE CryVIIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal  
DE protein).  
GN CRY7AB OR CRYVIIA(B).  
OS Bacillus thuringiensis (subsp. kumamotoensis).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=132267;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HD867;  
RA Payne J.M., Fu J.M.;  
RT "Coleopteran-active Bacillus thuringiensis isolates and genes encoding  
RT coleopteran-active toxins";  
RL Patent number US5286486, 15-FEB-1994.  
CC -!- FUNCTION: PROMOTES COLEOPTEROTIC LYSIS BY BINDING TO THE MIDGUT  
CC EPITHELIAL CELLS OF COLEOPTERA.  
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART  
CC OF THE SPORE COAT.  
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE  
CC N-TERMINUS.  
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; U04368; AAA21121.1; --  
DR HSP; P07130; IDLC.  
DR InterPro; IPR001178; Endotoxin.  
DR Pfam; PF00555; endotoxin; 1.  
KW Toxin; Sporulation.  
SQ SEQUENCE 1138 AA; 129658 MW; E12DC80C0A56D1DA CRC64;

Query Match 37.78; Score 2388; DB 1; Length 1138;  
Best Local Similarity 42.34; Pred. No. 1.4e-125;  
Matches 521; Conservative 208; Mismatches 374; Indels 130; Gaps 28;

QY 1 MSPNNONEYEIIDAPTSPVSDNSRNPFPANEPTNALQNMDDYKDYKMSAGNASEYPSGP 60  
Db 1 MLNLNLGYE-----DSNRTLNLSNYPYTKALSPSLKNMYPQLSITERE-----QP 49

QY 61 EVLVSGQDAKAAIDIVKLLSGLVGPVPGPIVSLYTLQIDILMPSGEKSQWEIFMEQVE 120  
Db 50 EALASGNNTAINTVSVTGATLSALGVPASFTITFYLKITGLLWPH-DKNIWDFEMTEVE 108

QY 121 ELINQKTAAYARNKALSELEGNGNYQYLTALEWENPNGLRDVNRNFIILSLF 180  
Db 109 TLIBQKTEQVARNKALAELEGNNLTYYQQALEDWLNPPDPATITRVIDRFRILDALF 168

QY 181 TQVMPSTRVTNFEVPELTVYAMAHLHLLKLDASIFCEEWGWSITINNYYDRQMKLTA 240  
Db 169 ESMPSFRVAGYEIPLLTVYQAQANLHLLURDSLTYGDKWEFTQNNEENYRQKKHIS 228

QY 241 EYSDHCVKWVETGLAKLKGTSKQWVDYNQFRREMTLAVLDVWALFPNPDYTRTPMETKA 300

Db 229 EYSHNCVKMNSGLSRLNGSTYEQWYNINFRREMILLWLDIAAVFPPIYDPRMYSMETST 288  
QY 301 QLTREVYTDPLGAVNVSSIGSWTDKAPSGVIESSVIRPHVFDYITGLTVYTSRSISS 360  
Db 289 QLTREVYTDPI-SLSISNPGI-----GPSFSQMENTAIRTPHLVDYLDDELYITYSKYKAPS 343  
QY 361 ARY---IRHWAGHQISVHRVSRGSLNQ--MYCTNQNLHSTSTFDTNYDIYKTLSDAV 415  
Db 344 HEIQPDLFYSAHKVSF-KOSEQSNLYTTGIYKTSIGSYSSGAYSFNGNDIYRLAAPS 402  
QY 416 LLDIVPGYTYIIFGMPEVEFFMVNQLNTRKTLKYNVPVKDIIASTRDSLELPPTSD 475  
Db 403 ---VYIP-YTQ-NVGEQVEFYGVKGVHVRGDKYD-----LTYSDIDQLPPD--G 447  
QY 476 QPNYESYSHRLCHITSI-----PATGNTTGLVPVPSWTHRSADLNNIYSDKIQTIPAVK 531  
Db 448 EPIHEKYTHRLCHATAISKSTPDYDNAT--IPIFSWTHRSABEYNNRIYPNKITPIPAVK 505  
QY 532 WDLNPFVVPVKGPGHTGGDLQVNRSTGVTFLARYGLALEKAGKYRVLRYATD--A 589  
Db 506 YKLGDTSTVVKGPGTGGDLVK-RGNGYIGDI-KATVNSPLSQ--NYRVRYATVNSG 561  
QY 590 DIVLVNDAQIOMPK-----TNPGEDLSTKTPKVAADAITTLNLATDSSLALKHNLGED 643  
Db 562 QFNVYINDKITLQKQFQNTVETIGEGKDLTYSGFYIEYSTTIQFPDKPKITLHLS 621  
QY 644 PNSTLSGIVVVDRIETIPVDTEYEAQDLAAKAVNALNTKDGRLPGVTYEVNQAA 703  
Db 622 NNSSF-----YVDSIEFIPVDVNYDEKEKKAQKAVNTLFTEGRNALQKQVTDVTKVDQS 677  
QY 704 NLVECLSDLLYPNEKLLFDVAREAKLSARNLQDPDFQIEING--ENGWTAATGTEVI 761  
Db 678 ILVDCISGDLYPNEKELQNLVYAKLSYRNLLLDPTFDSINSSENGWYSGNLVIG 737  
QY 762 EGDALFKGRYLRLPGAREIDTETPTLYYQKVEEVLKPYTRYRLRGFGVSSQGLEIFTI 821  
Db 738 NGDFVPKGNLYIPSGTN--DTQ-YPTVLYQIDESKLKEYTRYKLGFISSQDLAYVI 794  
QY 822 RHQTNIRVKNVPPDLLPDSVPNSDGSINRCSEKQYVNSRLEVENRSGE----- 870  
Db 795 RYDAKHRTLDVSDNLLPDILPENTCGEPNRCAAQVLD-----ENPSSECSMDQDGLSD 849  
QY 871 AHFSPIDTGEIDYENAGIWWGFKITDPGEVATLGNLELVEEGLSGDALRELQREEQ 930  
Db 850 SHSFSNLIDIGSINHNLGIVLFWLSTLEGAKFNLEVIDGPPVIGALARKVKQET 909  
QY 931 QWKIQMTRREEDRRYMASQAVDRLYADYQDQQLNPDPVEITDLTAAQDLIQTPIPVYN 990  
Db 910 KWRNKLAQLTTETQATYTRAKQALDNLFANAQDHLKIDVTFAEIAAARKIVQSIREAYM 969  
QY 991 EMPPEIPGMNYTKFETELTDLQQAWSLYDORNAIPNGDFNGLSNWNATPGVEVQOINHT 1050  
Db 970 SWLSVPGVGNHPIFTELSERVQAFQLYDVNRVNRGRFLNGLSDMTVTSDBVKVQENGN 1029  
QY 1051 SVLVIPIPDWDSQOQFTVQPNORYLVRVTARKEGVNGVYISRDGNGQTETLTFASDYD 1110  
Db 1030 NVLVNNDWAQVLQNVKLYQDRGYILRVYARKIGIGEGYITITDEEGHTVQLRPTACEV- 1088  
QY 1111 TNGMYNTQVSNNTNGYNTNNAYNTOASSTNGYNANNMYNTOASNTNGYNTNSVYNDQTGYI 1170  
Db 1089 -----IDASNAP-----ISGYI 1100

QY 1171 TKVTFTFIPYTDQWMIEMSETEGTFYIESVELIV 1203  
Db 1101 TKSELPFPDTEKWHIEIGETEGIFLVESELFL 1133

RESULT 11  
C1BD\_BACTZ  
ID C1BD\_BACTZ STANDARD; PRT; 1231 AA.  
AC O92A25;  
DT 30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)  
 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pesticidal crystal protein cryIbD (Insecticidal delta-endotoxin  
 DE CryIb(d) (crystalline entomocidal protoxin) (140 kDa crystal protein).  
 GN CRYIbD OR CRYIb(D) OR CRYIaL OR CRYIeL.  
 OS Bacillus thuringiensis (subsp. wuhanensis).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=52024;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HD-525;  
 RX MEDLINE=20153386; PubMed=10688690;  
 RA Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;  
 RT "Cloning of two new cry genes from Bacillus thuringiensis subsp.  
 RT wuhanensis strain";  
 RL Curr. Microbiol. 40:227-232(2000).  
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
 CC EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PLUTELLA  
 CC XYLOSTELLA.  
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART  
 CC OF THE SPORE COAT.  
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE  
 CC N-TERMINUS.  
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.  
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 CC  
 CC ENBL; U70726; RAD10292.1; --  
 DR HSPSP; P02965; ICIX.  
 DR InterPro; IPR001178; Endotoxin.  
 DR Pfam; PF00555; endotoxin; 1.  
 KW Toxin; Sporulation.  
 SQ SEQUENCE 1231 AA; 139654 MW; 129A0371CDDBBE52 CRC64;  
 Query Match 37.3%; Score 2359.5; DB 1; Length 1231;  
 Best Local Similarity 41.1%; Pred. No. 6.1e-124;  
 Matches 525; Conservative 197; Mismatches 433; Indels 121; Gaps 26;  
 QY 1 MSPNNQNEYIIDATPSTSVSNDNRYPANETPALQMDYKYLKMSAGNASEYFQSP 60  
 DB 1 MTSNRKNEIINALSIPAVNSHSAQMDLSLDAR-----IEDSLCIAEGN-----NI 47  
 QY 61 EVLVSGQDAKAAIDIVKLLSGLVFPVGPVLSLYTQIDILWPSGKSOWEIFMEQVE 120  
 DB 48 NPLVSA-STVGTGNIAGRIIGLVGPVAGQASLYSFLVGLWELWESG-RDPWEIFLEHVE 105  
 QY 121 ELINQKIAEYARNKALSELGLGNQYLYLTALBEEWENPNNGSRALDRVNRFEILDSLF 180  
 DB 106 QLIRQVTEENTATARLEGLGRGYSYQQALETWLDNRNDARSIIERYVALELDI 165  
 QY 181 TOYMPSPVTVNPEVPLTVYMAANLHLLKDAISFGEWGWSTTTNNYIDRQMKLTA 240  
 DB 166 TTAIPLFRIRNEEVLPMVYAQAANLHLLLRDASLFGSEWGNASSDVNQYEQIRYTE 225  
 QY 241 EYSDHCWKWYETGLAKLGTSAKOWVDYNOQREMTLAVLDVVALFPNYDTFTYMETKA 300  
 DB 226 EYSNHCQWYNTGLNLRGTNAESWLRVYNQFRDUTGLVGLDVALFSPDYTKTYPINTSA 285  
 QY 301 QLREVVYDPLGANVSS----IGSWY-DKAPSGFVIESVIRPPHFVDFITGLTVYTSQR 356  
 DB 286 QLREIYVDPGRWTNAPSGFSTWNNFNNAPSAIEAAIFPPHLLDFPEQLTIYSASS 345  
 QY 357 SISSARYTRHWAGHQISYHRVSRGSLNQMYCTGNLHSTSTFTDPTNYDIYKTLSDAVL 416  
 DB 346 RWSSTQHNWYVWGHRLNFRPIGTTLNTSTQGLTNTNTSINPVTLOPTSRDVRVTESSAG-- 403

QY 417 LDIVYPGYTYIFF-----GMPEVEFPFVWQNLN-NTRKTLKYNPVSKDIIASTSDSELELP 470  
 DB 404 -----TNILFTFVNGVPWFNFNFQNIYERGATTYSQPYQGVQQLDFSETLP 455  
 QY 471 PETSDOPNYESYHRLCHITSIPATGNTTGLVPVFWSTHRSADLNNTIYSDKLTQIPAVK 530  
 DB 456 PETERPNYESYHRLSHIGLI--IGNTL-RAPVYSWHRSADRTWTIGNRIITQIPAVK 512  
 QY 531 CWDNLFPFV---PVVKGFGHTGGDLLOYNRSTGVSGLTFLARYGLALEKAG-KYRVRURYA 586  
 DB 513 G-----RFLFNGSVISGPGFTGGDVLRNNGNIQNRGVEVPIQFTSTSTRYRVRUYA 568  
 QY 587 TDADIVLHVN--DAQI---OMPTMMPGEDLTSTKTKVADAITLNLATSSALKKNLG 641  
 DB 569 SVTSELNVNLGNSSIFTNLTATAASLDNLQSGDFGYEINNNAFTSATGNIGAR---- 624  
 QY 642 EDNSTLSGLVYVDRIEFIPVDETAEAOLEAKAVNALFTNTKD-GLRPGVTDYEVN 700  
 DB 625 ---NFSANAEEVIIDRFEPVTFATFEAYDLERAQAVNALFTSTNPRUKTDVTDTHID 681  
 QY 701 QAANLVECLSDLLYPNEKRLLFDAVREAKELSEARNLLQDPDFQEING----- 748  
 DB 682 QVSNWACLSDDECLDEKRELFEKVKYAKELSDERNLLQDPNFTFISGQLSPASIDGQSN 741  
 QY 749 -----ENGWTAAGIIEVIGDALFKGYRLRPGAREIDTETYPYLYKQVEEGLKP 800  
 DB 742 FTSINELSEHGWSGSENVITQEGNDVFKENYVTLPGT---FNECYPNLYKQIGESLKA 798  
 QY 801 YTRYLRGFGVSSQGLEIFIRHQTNRIKVNVP--DLLP--DVSPVNSDGSINRCSEQK 856  
 DB 799 YTRYQLRGYIEDSQDLEIYLIRYNAKHETLDVPGTDSLWPLSVKSPIGRCGEPNRCAPHF 858  
 QY 857 YVNSRLREVENRSGE-----AHEPSIPIDTGEIDYDNENAGIWWGFKITDPGAYATLGNLEL 911  
 DB 859 EWNPDLDSCSDGECRCAHSHHFTLIDVCTDLHENLGVVWVFKIKTQSGYARLGNLEF 918  
 QY 912 VEEGLSGDALERLQREEQWKIQMTRRRETDERRRYNASKQAVDRLYADYQDQQLNPDVE 971  
 DB 919 IEEKPLIGEALSRVKRAEKKRDKREKLQLETKRVYTEAKETVDALFVDSHYNRLQADTN 978  
 QY 972 ITDLTAADLIQSIPIYVYNEMFPEIPGMNYTKETLTDRLQQAWSLYDQRNAIPNGDPN 1031  
 DB 979 IGMTHAADRLVHRHIEAYLPELPIPGINAVIPEELNRISTAFSLYDARVINKGDFNN 1038  
 QY 1032 GLSNWNAITPGVEVQIQIHNTSVLIPNWDQVSOFTVQPNQRYVLRVTARKEGVNGYVS 1091  
 DB 1039 GLSCWNVKGVHDVQOQSHRSDLVIPWEAEVSQAVRCPGEGYILRVYAYKEGEGCVT 1098  
 QY 1092 IRDGGNOTETLTSASDYDTNGMYNTQVSNYNTNGYNTNNAYNTOASTNGYNNANMYTQA 1151  
 DB 1099 IHEIENNTDELKF--KNCEEEVYPTDGTGNDYTAHQG---TAACNSRNAGYEDAYEV 1152  
 QY 1152 SNTNGYNTSVYNDQT-----GYITKTVTFTPYTQMWIEM 1187  
 DB 1153 DTTASVNYKPYTEBETVTVDRDNHCEYDRGVNYPVPAGYVTKLEYFPETDVTWIEI 1212  
 QY 1188 SETEGTFVIESVELIV 1203  
 DB 1213 GETEGKFIVDSVELLL 1228  
 RESULT 12  
 CLIBE\_BACTU  
 ID CLIBE\_BACTU STANDARD; PRT; 1227 AA.  
 AC 085805;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Pesticidal crystal protein cryIbE (Insecticidal delta-endotoxin  
 DE CryIb(e) (crystalline entomocidal protoxin) (139 kDa crystal protein).  
 GN CRYIbE OR CRYIb(E) OR 158C2B.  
 OS Bacillus thuringiensis.  
 OG Plasmid pMYC2383.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL B-18972 / PS1582C;  
 RA Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Stelman S.;  
 RT "Bacillus thuringiensis genes encoding lepidopteran-active toxins."  
 RL Patent number US5723758, 03-MAR-1998.  
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
 CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE  
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
 CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART  
 CC OF THE SPORE COAT.  
 CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE  
 CC N-TERMINUS.  
 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.  
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 CC  
 DR EMBL; AF077326; AAC32850.1; -  
 DR HSSP; P07130; 1DLC.  
 DR InterPro; IPR001178; Endotoxin.  
 DR Pfam; PF00555; endotoxin; 1.  
 DR Toxin; Sporulation; Plasmid.  
 KW TQXIN; Sporulation; Plasmid.  
 SQ SEQUENCE 1227 AA; 139084 MW; CBA847BEA0B34CD3 CRC64;

Query Match 37.2%; Score 2356.5; DB 1; Length 1227;  
 Best Local Similarity 41.5%; Pred. No. 8.9e-124;  
 Matches 526; Conservative 200; Mismatches 433; Indels 109; Gaps 23;

QY 1 MSPNNQNEYIIDATPTSTVSNSRNPFFANEPNTNALQNDYKDYKMSAGNASEYGPSP 60  
 DB 1 MTSNRKNEIINALSIPAVNSHAQ-----MNLSTDAIEDSLCIAEGNID----P 49  
 QY 61 EVLVSGDAAKAIDIVKLLSGLVGVPFGIVSLYLTQLDILWPSGKQWEIFMEQVE 120  
 DB 50 FVSAS---TVQTGINAGRLVLGVLPFGAGQIASFSLVGLMELPRG-RDPWEIFLSE 105  
 QY 121 ELNQIAEYARKALSELGLGNLYLTALTEWENPNRSGALRDVNRPRILDSLF 180  
 DB 106 QLRQQTENRTRTALRLOGLNSFRAYQOSLEDWLENRDDATRSVLTYQIALSLDP 165  
 QY 181 TQWPSFRVTNFEVFLTVYAMAANLHLLKDKASIFGEWGNSTTTNNYDRQMKLTA 240  
 DB 166 LNAMPLFAIRNQEVPLLMVYQAANLHLLLRDASLFGSEFGLTSQEIQRYERQVEKTR 225  
 QY 241 EYSDHCVKYETGLAKLGTSAKOWDYNQPRREMTLAVLDVVALFNYDTRTPMETKA 300  
 DB 226 EYSDYCARWNTGLNLRGTNAESWLRYNQPRDLTGLVDLVALFSDYDTRVPMNTSA 285  
 QY 301 QLTREVYDPLGANVSS---IGSWY-DKAPSGFVIESSVLRPPHVDYITGLTVYTSR 356  
 DB 286 QLTREIYDPIGRNAPSGFASFAIAEAAVLRPHLLDPFQQLIFSVLS 345  
 QY 357 SISRARIYRWAGHQISYHRVSRGNSLQOMYGTGNLHSTSTPFTNYDIYKTLSDAVL 416  
 DB 346 RWSNTQYMYWVGHRLE-SRTIRGLSTSTHGTNTSINPVTQLQTSRDVYRTESFAGIN 404  
 QY 417 LDIVYPGYTYIFPGMPVEBFPMVQNLNTRTKLYKNPVSKDIIASTRDSSELELPESDQ 476  
 DB 405 ILLTTP-----VNGVPWARENWRNPLNSLGSLLTYTYGTGVGQLFDSFETELPETTER 459  
 QY 477 PNYESYSHRLCHITSIPATGNTTGLVPVFSWTHESADLNNTIYSDKTOIPAVKCNWNL 536  
 DB 460 PNYESYSHRLNRLI---SGNTL-RAPVYSWTHRSADRTNTISSDIQIPLVKSFNLS 516  
 QY 537 FVPVVKPGFGHTGGDLLQYNRSTGSGVGLTFLARYGLALEKAGKYRVLRYATDADIVLHV- 595

DB 517 GTSVSVSGPGTGGDIIRTN-VANGSVLSMGLNFNNTSLQ---RYRVRVRYAASQTVMLRVT 572  
 QY 596 ----NDAQIQMPKTNPGEDLTSKTEKVDADITLNL--ATDSSLALKNLIGEDPNSTLS 649  
 DB 573 VGGSTTFDGGFPSTMSANESLTSQSFRPAEPFVGISASGSGTAGISISNAGRQ----- 626  
 QY 650 GIVYVDRIEPIFVDETYEABQDLAAKAVNALFTNTKD-GLRPGVTDYEVNQAANLVEVC 708  
 DB 627 -TFHPDKIEFIPITAFEAEDLERAQAVNALFTNTNPRRLKATGTYDHIDEVSNLVAC 685  
 QY 709 LSDDLVPNEKRLFLDAVREAKRLSEARNLLQDDPPOEIN-----G 748  
 DB 686 LSDEFCLDEKRELLEKVKYAKRLSDERNLLQDDPNFTSINKQDPFISTNEQSNFTSIEQS 745  
 QY 749 ENGWTASTGIEVEGALPKGYRLRPGAREIDTETPTLYOKVEGVLKPYTRVRLRG 808  
 DB 746 EHWGENSENITQEGNDVFKENVILPGT---FNECYPIYLYOKIGAEALKATRYQLSG 802  
 QY 809 FVGSSQGLFIFTIRHQTRIVKRVDPD-----LLPVSVPNSDGSINRCSEQKTVNRSLEV 864  
 DB 803 YIEDSQDLRIYLIRYNAKHETLDPGTESVWPLSVESPIGRCGEPNRCAPHFENWPDLC 862  
 QY 865 ENRSGE-----AHEPSIPIDTGBIDYNAGIWWGPKITDPEGYATLGNLELVEBGLSG 919  
 DB 863 SCRDEGKCAHSHHFSLDIDVGCIDLHENLGVWVVPKIKTQEGHARLGNLEFTEEPKLLG 922  
 QY 920 DALERLQREEQWKIQWTRRRRETRRYMASKOADRLVADYQDQQLNPDVEITDITAAQ 979  
 DB 923 EALSURVRAEKWRDKREQLQLETKRVTYTEAEAVDALFVDSQYDRLQADNTNIGMHAAD 982  
 QY 980 DLTSQSPYVYNEMFPIPGMNYTKFTELDRLOQAAVSLYDQARNALPNPDPRNGLSNWAT 1039  
 DB 983 KLVHRIEAVLSLSVPGVNAEIPFELEGRIITLALYDARNVKNDFNGLACWNVK 1042  
 QY 1040 PGVEVQOINHTSVLVPNDWDEQVSQFTVPQNYRVLRVYARKEGVNGVYVSRDGNQT 1099  
 DB 1043 GHVDVQSHRSVLVPEWEAEVSQAVRVCPGRGYLRTAYKEGYGEGCVTIEIENNT 1102  
 QY 1100 ETLTFSASDYDTNGMYNTQVSTNGYNTNAYNTQASSTNGYNNANNMYNTQASNTNGYNT 1159  
 DB 1103 DELKP-KNCEEBEYPTDTGTCDNYTAHQG-----TAACNSRNAGYEDAYEVDTTASVNY 1156  
 QY 1160 NSVYNDQT-----GYIKTVTFPIYTDQMIEMSETEGTFY 1195  
 DB 1157 KPTYEBEYTDVVRDNHCEYDRGVVYVPPVPGVAGYMTKELEFFETDKVWIEIGETGEKFI 1216  
 QY 1196 IESVELIV 1203  
 DB 1217 VDSVELLL 1224

RESULT 13  
 C7AA\_BACTU STANDARD; PRT; 1138 AA.  
 ID C7AA\_BACTU  
 AC Q03749;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Pesticidal crystal protein cry7Aa (insecticidal delta-endotoxin  
 DE CryVIIA(a)) (Crystalline entomocidal protoxin) (129 kDa crystal  
 DE protein).  
 GN CRY7AA OR CRYVIIA(A) OR CRYIIIC.  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92384571; PubMed=1514800;  
 RA Lambert B., Hofte H., Annys K., Jansens S., Soetaert P., Peferoen M.;  
 RT "Novel Bacillus thuringiensis insecticidal crystal protein with a  
 RT silent activity against coleopteran larvae."  
 RL Appl. Environ. Microbiol. 58:2536-2542 (1992).

CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
 CC EPITHELIAL CELLS OF COLEOPTERA. THIS PROTEIN IS NOT TOXIC IN ITS  
 CC NATURAL FORM. IT IS HIGHLY TOXIC TO COLORADO POTATO BEETLE LARVAE  
 CC AFTER AN IN VITRO SOLUBILIZATION AND TRYPSIN ACTIVATION STEP.  
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING  
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF  
 CC THE SPORE COAT.  
 CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-  
 CC TERMINUS.  
 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M64478; AAA22351.1; -;  
 CC DR EMBL; A07236; CAA00646.1; -;  
 CC DR HSP; P07130; IDLC.  
 CC DR InterPro: IPR001178; Endotoxin.  
 CC DR Pfam; PF00555; endotoxin; 1.  
 CC KW Toxin; Sporulation.  
 CC SQ SEQUENCE 1138 AA; 129391 MW; 69D8676D4F6A1FAC CRC64;  
 CC  
 CC Query Match 37.1%; Score 2348; DB 1; Length 1138;  
 CC Best Local Similarity 41.7%; Pred. No. 2.4e-123;  
 CC Matches 512; Conservative 211; Mismatches 385; Indels 120; Gaps 27;  
 CC  
 CC QY 1 MSPNNQNEYIIDATPSTSVNSDNRYPPFANPEPTNALQNDYKDYKMSAGNASEYPGSP 60  
 CC Db 1 MNLNLDGYE-----DSNRTLNLSNYPTQKALSPSLKNMNYQDFLSITERE-----QP 49  
 CC  
 CC QY 61 EVLVSGDAAKAIDIVKLLSGLVPGFVPIVSLYLTQIIDILWPSEKQWEIEMFQVE 120  
 CC Db 50 EALASGNTAINTVSVTGATLSALGVGASPTITNFYKIALGLWPENCKI-WDFEFTVE 108  
 CC  
 CC QY 121 ELINQKIAEYARNKALSELGLGNVYQLYLTAELEENENPNSPALRDVNRFEILDSLF 180  
 CC Db 109 ALIDQKIEEYVRNKALAEGLDGLSALDKYQKALADWLQKQDDPEALISVATEFRIIDLSF 168  
 CC  
 CC QY 181 TOTMPSFRVTNFEVPLTVYAMAANLHLLKQASIFEGEWGWSSTTINNYDROMKLT 240  
 CC Db 169 EFSMPSEKVTGYRIPLLTVAQAANLHALLRDLSTLYGDKWGTQNNIENYRQKRIS 228  
 CC  
 CC QY 241 EYSDHCKVETGLAKLGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDRTYPMETKA 300  
 CC Db 229 EYSDHCKVYNSGLSRLNGSTYEQWYNFRREMLMALDVLAVFPDPRYSMETST 288  
 CC  
 CC QY 301 QLTREYVYDPLGAVNVSSIGSWYDKAPSGFVIESSVIRPVPVYIYGLTYTQSRIS 360  
 CC Db 289 QLTREYVYDPLV-SSISN-----PDIGPSFQSMOAIARTPHLDVLDLYIYTSKYKAFS 343  
 CC  
 CC QY 361 ARY---IRHWAGHOISYHRVSRGSLNQ--MYGTQNMHLSTSTDFNYDIYTKLSKDAV 415  
 CC Db 344 HETQDPLFYSAHKVSEK-SEQSNLYTGYGKTSYSGAYSFGNDIYRTLAAPSV 402  
 CC  
 CC QY 416 LLDIVYGYTYIPFGMEVEFFWMYQNLNTRKTLKYNPVSKDIIASTRDSLELPPTSD 475  
 CC Db 403 ---VVTY-YYQ-NYGVQEVFYGKGVHVRGDNKYD-----LTVDSIDQLPPD--G 447  
 CC  
 CC QY 476 QPNYESVSHRLCHITSI-----PATGNTGLVPVSWTHRSADIANNTYSDKITOIPAVKC 531  
 CC Db 448 EPIHEKYTHRLCHATAIFKSTPDYDNAT--IPIFSWTHRSAYYNNYIPNKKITIPAVKM 505  
 CC  
 CC QY 532 WDNLPFPVVKPGCHTGDILQYNRSGVCTGLFLARYGLALEKAGYKRVRLVATD--A 589  
 CC Db 506 YKLDDPSTVVKPGFTGDLVK-RGSTYIGDI-KATVNSPLSQ--KIRVRYATVNSG 561  
 CC  
 CC QY 590 DIVLHVNDQIQMPK-----TWNPGDLTSKTFKVAADAITLMLATDSSLAKHNLGSD 643

Db 562 QFNVYINDKITLQTKFQNTVETIGEGKDIYSGFGVIEYSTTIQFPDEHPKITLHLSDL 621  
 QY 644 PNSTLSGIVVYVRIEIPVDETYEABQDLEAKAKAYNALFTNTKGLRGVTVDEYNQAA 703  
 Db 622 NNSSF---YVDSIEFIPVDVNVYAEKEKLEKAKAVNTLFTFEGRNALQKDVTDYKVDQS 677  
 QY 704 NLVECLSDDLIPNEKLLFDVAREAKRLSEARNMLLOPDPQFIEING--ENGWTASTGIEVI 761  
 Db 678 ILVDCISGDLIPNEKRLQNLVKYAKRLSVSRNLLDPTFDSINSSEENGWYSGNIVIG 737  
 QY 762 EGDALFKGYLRLPAGAREDTETYPYLYKQVEGVLKPYTVRLRGFVGSOGLEFTI 821  
 Db 738 NGDFVFKGNLYIPSGYN--DTQ-YPTLYLKIDESKLEYRYKLGKGFIESQDLAEYI 794  
 QY 822 RHQTRIVKXNPDLIPDVSPVNSDGINRCSQKTVNSRLEVENRS-----GEAHEFS 875  
 Db 795 RYDAKHTLDVSDNLLPDLIPENTCGEPNRCAAQVLDENPSPSCSMQDGLSDSHSFS 854  
 QY 876 IPIDTGEIDYENAGIWFQKIDTPEGYATLGNLEIVBEGPLSGDALERLQREEQWKIQ 935  
 Db 855 LNIIDTGSINHNENLGIWLFKISTLEGYAKFGNLEIVEDGPIVIGEALARKVROETKWRNK 914  
 QY 936 MTRREETERYMAKQAVDRLYADYQDQOLNPDVEITDLTAAQDLIOSIOPYVYNEMFPE 995  
 Db 915 LAQUTTOAIYTRAKQALNLFANAQDSHLKRDVTFAETAAARKIVQSIREAMSWLSV 974  
 QY 996 IPGMNTKTELTDLRQQAWSLYDQNAIPNGDFRNLGNWNAIPGVEVQOINHTSLVI 1055  
 Db 975 VFGVNHPIFTELSGRVQAFQLYDVNRVNRGFLNGLSDWIVTSVKVQEEGNVNLVL 1034  
 QY 1056 PNWDEQVSQOFTVOPNORYVLRVYRTARKEGVNGYVSIIRGNGNOTETLTTPSASYDTNGMY 1115  
 Db 1035 NNWDAQVLQNVKLYQDRGYILHTVARTAKIGIGEGYITTBEGHTDQLRFTACE----- 1087  
 QY 1116 NTOVSNYNGVNTNAYNTQASSTNGVNNMNTQASNTNGVNTNSVNDQTVITKTVT 1175  
 Db 1088 --EIDASNAF-----ISGYITKELE 1105  
 QY 1176 FIPVTQMMIEMSETEGTFVIESVELIV 1203  
 Db 1106 FFPDTEKVIETEGTGFVLESIELFL 1133  
 PRT; 1228 AA.  
 RESULT 14  
 ID\_C1BA\_BACTK STANDARD; PRT; 1228 AA.  
 AC F05517; Q45731;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Pesticidal crystal protein crylBa (Insecticidal delta-endotoxin  
 DE CrylB(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).  
 GN CRYIIB OR CRYIIB(A) OR CRYIAB.  
 OS Bacillus thuringiensis (subsp. kurstaki), and  
 OS Bacillus thuringiensis (subsp. entomocidus).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=29339, 1436;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.t.kurstaki; STRAIN=HD-2;  
 RX MEDLINE=88203216; PubMed=3362680;  
 RA Brizzard B.L., Whiteley H.R.;  
 RT "Nucleotide sequence of an additional crystal protein gene cloned  
 RT from Bacillus thuringiensis subsp. thuringiensis";  
 RL Nucleic Acids Res. 16:2723-2723 (1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.t.entomocidus; STRAIN=HD-110;  
 RA Soetaert P.;  
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT  
 CC EPITHELIAL CELLS OF INSECTS.  
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING



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CC or send an email to [license@ebi-sib.ch](mailto:license@ebi-sib.ch)).

|    |  |
|----|--|
| CC | EMBL; Z46442; CAA86568.1; --                         |
| DR | HSP; P02965; ICIY.                                   |
| DR | InterPro; IPR001178; Endotoxin.                      |
| DR | Pfam; PF00555; endotoxin; 1.                         |
| DR | Toxin; Sporulation.                                  |
| KW | SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64; |
| SQ |  |

Query Match 36.7%; Score 2321.5; DB 1; Length 1233;  
Best Local Similarity 40.6%; Pred. No. 8.1e-122;  
Matches 520; Conservative 200; Mismatches 431; Indels 131; Gaps 28;

**Qy**      1 MSPNQNEYIIDATPSTVSNDNRYPFANEPTNALQMWDYKYLKMSAGNASEYPGSP 60  
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dd**      1 MTSRKNEBTEINALSIPTVSNPSQT-----MKLSPDARIEDSLCVAEYNND----P 49

QY 61 EVLVSGDAKAAIDIVKLLSGLGVPPGVPIVSLYTOIIDILWPSEKSKSQWEIFMEQVE 120

Db 50 FVSAS---TVQTGNIAGRILGVLVPPAGQLASFYSLFVGLWELPVG--RDPWEIFLEHVE 105

**Qy**

121 ELINOKIAEVARNKALSLEGGNNYQLYLTALEEENPNPGRALDVRNRFILDSLP 180  
          :||::|||::|||||:|||::|||::|||::|||::|||::|||::|||:

**Dø**

106 QLIRQQVNTNRNTAIALLEGGRGYRSGYOQALETFLDNDRNDARSSTILERYVALELDI 165  
          :||::|||::|||||:|||::|||::|||::|||::|||::|||::|||:

|    |     |                                   |                          |     |
|----|-----|-----------------------------------|--------------------------|-----|
| Qy | 181 | TQYNPSFRVNFVEPFLTVVYAAANLHLLLLKDA | IFGESEGWSTTTINNTYDQMKLTA | 240 |
|    |     | :   :                             |                          |     |
|    |     | :   :                             |                          |     |
| Db | 166 | TTAIPLFRIRNEVPFLMVAQAANLHLLLRDASL | FGSEGWMASSDVNQYEQIRVTE   | 225 |

[illegible]

```

Qy 301 QLTREVTDPGAVNVAS---IGWY-DKASFGVISSVTRPPHVFYITGLTYTQSR 356
      |||||:||||:| | :|:| | | | | | | | | | | | | | | | | | | | | | |
      | | :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 286 QLTREITDPIGRNAPSGPASTWFWNNASFSAIEAAIFPPHLLDFPQLITYSASS 345
      |||||:||||:| | :|:| | | | | | | | | | | | | | | | | | | | | |
      | | :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```
Qy      357 SISA RYIRHWAGHQISVHRYSRGSNLQMVGYNQLHSTSPFTPNVDIKTSLSKDAVL 416
        ||:::||::|::||::||::||::||::||::||::||::||::||::||::||::||
Db      346 RWSSTQHMYWGHRLNFRPFGITLNTSTQGILTNNTSINPVLTQFTRSDRVRTESNAG-- 403
```

Qy 417 LDIYVPGTYIFF-----GMEVEFFVMYNQLN-NTRKTLKYNPUSKDIASRSELSLP 470

Db 404 -----TNILFTTPVNGVPEWARPNFNPQNIYERGATTYSQPQGVGIQLFDSETSLP 455

|     |   |     |
|-----|---|-----|
|     | PETSDQPNYESYSHRLCHITGIPATGNNTGLVPVSWTHRSADLNNITYSKDITOIPAVK | 530 |
| Qy  | :                           :                               | :   |
| 471 | :                           :                               | :   |
|     | PETTERPNYESYHSLSHIGLI--IGNTL-RAPVYSWTHRSADRNTTGPNRITQIPLVK  | 512 |
| Dd  |   |     |

**Qy**                : ||| |||| |:: ::||: :||: :||: ||| ||  
531 CWDLPFPVVKPGHGTGDDLQNRSFGSVGLTFLARYGLEALEKAGYRVLRVA---TD 588  
**D6**                : ||| |||| |:: ::||: :||: :||: ||| ||  
513 ALNLHGVTWVGPGFTGGDILR-RTNATGEDI---RLNNVPPLSQRYVRIRYASTTD 568

**QY**      :    :    :    :    :    :    :    :    :    :    :    :    :    :    :    :    :  
589 ADIVLHVNDAAIQM---PKTNWPGSBLFSTKFKVADATLTNLAATDSSALKLNHGEDPN 645  
  
**Dd**      :    :    :    :    :    :    :    :    :    :    :    :    :    :    :    :    :  
569 LQFFTRINGTTWNIGNFGRITWRNGDLBYRSFTAGFPFNFLNAQS---TFTLGASPF 625

QY 646 STLGGIVVDRIRFIPVDTEYEAOQLSAAKAKANVALFTNTKD -GLRFGVTDDYEVNQAN 704  
| : ||||| : | : ||||| : ||||| : ||||| : ||||| :  
Db 626 SNQE-- VYIDRFVEFPAEVTFEABYDLERQAQKANALFTSTNPRRLKTDDTVDYHIDQVSN 683

|    |  |     |  |     |
|----|--|-----|--|-----|
| QY |  | 705 | LVECSDDLYENREKLLDVAKEAKSEARNLLOPQFQELING<br>: :<br>: | 748 |
| Db |  | 684 | MVACUSDEFCIDEXRELPEKKVKIARLSDERNLLQPNTFFISGQLSFASIDGQNFPFSI  | 743 |
| O: |  | 749 | PACHMBS QNCSTNUXECRLT EVCZUOT NI DOA DEDIBEMUTUMUT VAVATIGCTATCAVMAY   | 804 |

QY 749 ----ENGWIASIGIEVIBGDAFAGKILUKLPARGSLDIETIFLIIJIANVEGVAFIIRI 804  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 744 NELSEHWGSGANVTIQEGNDVFKENZYTLPTOT---PNECYPNLYIKIGESELKAYTRY 800

[illegible]

Search completed: January 7, 2003, 05:14:40  
Job time : 34 secs

Search completed: January 7, 2003, 05:14:40  
Job time : 34 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 7, 2003, 05:03:13 ; Search time 83 Seconds  
(without alignments)  
2993.889 Million cell updates/sec

Title: US-10-032-717-2  
Perfect score: 6332  
Sequence: 1 MSPFNQNEYIIDATEPSTV.....MSRETEGFYIESVELIIVDVE 1206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTEMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_podent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match % | Length | DB ID | Description |
|------------|--------|---------------|--------|-------|-------------|
| 1          | 2440   | 38.5          | 1144   | 2     | Q45745      |
| 2          | 2342   | 37.0          | 1228   | 2     | Q93775      |
| 3          | 2332   | 36.8          | 1228   | 2     | Q93NM5      |
| 4          | 2184.5 | 34.5          | 1189   | 2     | Q9L877      |
| 5          | 2075.5 | 32.8          | 1180   | 2     | Q9S5V8      |
| 6          | 2070.5 | 32.7          | 1176   | 2     | Q45736      |
| 7          | 2068   | 32.7          | 1160   | 2     | Q93NF9      |
| 8          | 2055.5 | 32.5          | 1176   | 2     | Q9RC30      |
| 9          | 2054.5 | 32.4          | 1171   | 2     | Q06894      |
| 10         | 2048   | 32.3          | 1155   | 2     | Q9F296      |
| 11         | 2027   | 32.0          | 1177   | 2     | Q45735      |
| 12         | 2024   | 32.0          | 1155   | 2     | Q93T21      |
| 13         | 2021   | 31.9          | 1177   | 2     | Q03743      |
| 14         | 2020.5 | 31.9          | 1178   | 2     | Q9R826      |
| 15         | 2017.5 | 31.9          | 1178   | 2     | Q45768      |
| 16         | 2005   | 31.7          | 1174   | 2     | Q45749      |

|    |        |      |      |   |        |
|----|--------|------|------|---|--------|
| 17 | 1961.5 | 31.0 | 1176 | 2 | Q9S514 |
| 18 | 1902   | 30.0 | 1128 | 2 | Q9FDC0 |
| 19 | 1867   | 29.5 | 1280 | 2 | Q8VUK9 |
| 20 | 1860   | 29.4 | 1118 | 2 | Q9AM83 |
| 21 | 1823   | 28.8 | 1118 | 2 | Q9AM82 |
| 22 | 1793   | 28.3 | 1236 | 2 | Q939T3 |
| 23 | 1688.5 | 26.7 | 1118 | 2 | Q9AM81 |
| 24 | 1562.5 | 24.7 | 1254 | 2 | Q8VUL0 |
| 25 | 1523   | 24.1 | 1270 | 2 | Q8VUL1 |
| 26 | 1514   | 23.9 | 719  | 2 | Q93NJ5 |
| 27 | 1512   | 23.9 | 719  | 2 | Q8S796 |
| 28 | 1491   | 23.5 | 719  | 2 | Q9F0P8 |
| 29 | 1212.5 | 19.1 | 723  | 2 | Q9S4B5 |
| 30 | 1194.5 | 18.9 | 652  | 2 | Q9S6N9 |
| 31 | 1167   | 18.4 | 1155 | 2 | Q9AM80 |
| 32 | 1103.5 | 17.4 | 645  | 2 | Q9S603 |
| 33 | 1046.5 | 16.5 | 526  | 2 | Q32308 |
| 34 | 1028   | 16.2 | 558  | 2 | Q8VW63 |
| 35 | 1025   | 16.2 | 638  | 2 | Q87654 |
| 36 | 1012.5 | 16.0 | 620  | 2 | Q45720 |
| 37 | 966.5  | 15.3 | 618  | 2 | Q32306 |
| 38 | 962    | 15.2 | 618  | 2 | Q45737 |
| 39 | 955.5  | 15.1 | 558  | 2 | Q8VW61 |
| 40 | 937    | 14.8 | 607  | 2 | Q45721 |
| 41 | 933    | 14.7 | 660  | 2 | Q8RQU6 |
| 42 | 906.5  | 14.3 | 381  | 2 | Q45740 |
| 43 | 710.5  | 11.2 | 666  | 2 | Q8VW62 |
| 44 | 635    | 10.0 | 650  | 2 | Q8VNX2 |
| 45 | 624.5  | 9.9  | 688  | 2 | Q8VNX1 |

ALIGNMENTS

RESULT 1

Q45745 ID Q45745 PRELIMINARY; PRT; 1144 AA.  
AC Q45745;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Delta-endotoxin (Fragment).  
GN CRYIX GENE.  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
OC Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94085596; PubMed=8262221;  
RA Shevelev A.B., Svarinsky M.A., Karasin A.I., Kogan Y.N.,  
RA Chestukhina G.G., Stepanov V.M.;  
RT "Primary structure of the cryX\*\*the novel Delta-endotoxin-related  
RL gene from Bacillus thuringiensis ssp. galleriae.";  
RL FEBS Lett. 336:79-82(1993).  
DR EMBL; X75019; CAA52927.1; -.  
DR FSSP; P07130; IDLC.  
DR InterPro; IPR001178; Endotoxin.  
DR Pfam; PF00555; endotoxin; 1.  
FT NON\_TER 1  
SQ SEQUENCE 1144 AA; 129399 MW; 7D28594A19C4B065 CRC64;

Query Match 38.5%; Score 2440; DB 2; Length 1144;  
Best Local Similarity 44.0%; Pred. No. 6.6e-132; Indels 146; Gaps 25;  
Matches 534; Conservative 177; Mismatches 357;  
QY 42 YKDYLMKSNAGNASEYFGSPVELVSGQDAKAAADIVGKLSGLGVFPVPGIVSLYTOLID 101  
Db 20 YKDYLMKSGSDYIDSYINPGNVRTG---LQTGIDIVAVVVGALGGPVGGLTCLFLSLFG 76  
QY 102 ILWPSGEKSGQWELFMQVBEINQKIAEYARNKALSEGLEGNYYQIYLTALBEWENPN 161  
Db 77 FLWPSNDQAVWEAFIEQMEELIEQRIISDQVVRTALDLDLTGIONYYNQYLTALKEWERN 136

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QY 162 GSRALDRVRNRFEILDSLTOYMPSF-----RVTFVFPFLTVYMAANLHLLILKDSAP 217
Db 137 GVRA-NLVQRFEILHALFVSSMPSFGSGSQRFQQLLVYQAANLHLLILKDAEY 195
QY 218 GEBWGSTTTNNYDYROMKL-TAEYSDHCVKWYETGLAKGTSKOWVDYNOFRREMT 276
Db 196 GARWGLRESOIGNLYFNELOTRDRYTNHCNVANNGLAGLRTGTSABSWLKHQFRREAT 255
QY 277 LAVLDVVALPNTDTRYPMETKALREVYTDPLGAVNUSS-----IGSWYD-KAPS 328
Db 256 LMAMDLLALPPYNNRYPIAVNPQLREVYTDPLGVSESSLPPELRCURWQETSAMT 315
QY 329 FGVISSVIRPPHVFYDITGLTVVTOQRSIS-SARYIRHWAGHOISYHVRSGSN--LOQ 385
Db 316 FSNLENAIISPHLFDIINNLMITGVSFVHLTNQLEGWGHVSFSSLLASGTTVLRR 375
QY 386 MYGTNQLHSTSTPFDNYDIYTKLSK-----DAVLLDIV-----YPGVYIIFPGMPE 433
Db 376 NYGSTTSI--VNYFSFNDRDVYQINTRSHTGLGFQNAFLFGITRAQFYPGGT.----- 426
QY 434 VEFPMNQLNTRKTLKYNPVSKDIIASTRDSLELPETSDQPNYSYSHRLCHITS-- 491
Db 427 ----SVTORNALTCQYNSID-----ELPSLDNPEIRSHSYSHRLSHITSYL 470
QY 492 ----IPATGNTTGLVPVFSWTHRSADLNNTIYSDKITOIPAVKWCWNLPPVVPVKGPGH 546
Db 471 HRVLTIDGINIYSGNLTYVWTHRDVLTNTIADRITQLPLVKSFEIPAGTIVVRGPGF 530
QY 547 TGGDLQYNRSTGSGVTLFLARYGLALEKAGKYRRLRYA--TDADIIVLHVNDQI--- 601
Db 531 TGGDIL---RRTG-VGTFGTIRVTTAPLQRYRIRFRFASTTNLFIGIRVQDRQVNYFD 586
QY 602 MPKTMNPGEDLTSKTFKVAADAITLNLATDSSL-----ALKHNLGEDPNSTLSGVIYVDRI 657
Db 587 FGTMNRGDELRYESFATREFTTDFNFRQPOELISVFANAFSAGOE-----VYFDRI 638
QY 658 EFLPVDTEYAEQDLAAKAVNALFTNTKDLRPGVTDYEVNQAAANLVECLSDLLYPNE 717
Db 639 EILPVPNAREAKEDLEAKKAVASLFTTRDGLQVNVKDYQVDAQANLVCLSDBOQGYD 698
QY 718 KRLLFDVAREAKRLEARNLQDPDOEING--ENGWASTGIEVIEGDALEFKGKRYRLP 775
Db 699 KQMLLEAVRAAKRLEARNLQDPDFTINSTENGWAKASNGVITSEGGPPYKGRALQLA 758
QY 776 GAREIDTETPTLYOKVEEGVLKPYTRYLRGFGVSSQGLEIETIRHOTNRIKVNPD 835
Db 759 SAR-----ENPTYIYQKVDASELPYTRYRSDGFGVKSQDLEIDLIIHHKHVHLKVNPDN 814
QY 836 LLPDVSFVNSDGSNRCSEQKYVNSRLEVEN-----RSGEAHEFSIPIDTGEIDYNNEN 888
Db 815 LVSDTYDDSCSGINRCQEQVNAQALETETHHHPMDCCAAQTHEFSYIUTGDLNNSVD 874
QY 889 AGIWWGPKITDPEGYATLGNLEVEGSLGDALERLQREBQWKIQMTRREETDRRYM 948
Db 875 QGIWAIKVRTTDCGYATLGNLEVEGSLGESLEREQDNTKSAELGRKRAETDRVYQ 934
QY 949 ASKQAVDLVADYQDQNLNPDVEITDLTAQDLTQSIPIYVYNEMPEPEIPGMNYKFTLT 1008
Db 935 DAKOSINHLFVYDQDQNLNPEIGHADINDAQNLVASIDSVYSDAVLQIPGINIYRIYELS 994
QY 1009 DRLOQASVLDORNAIPNGDPFNGLSNWNATPGVEVQOINHTSVLVI PNWDEQVSQQFTV 1068
Db 995 NRLOQASVLTSRNAVQDGNGLSDNWNATAGASVQDQGNTHFLVLSHWDAQVSQFV 1054
QY 1069 QPNQRYVLRVARTARKEGVNGVYSIRDGNGQNETITLTFASDYDTNGMYNTQVSNNGYNTN 1128
Db 1055 QPNCKYVLRVTAEKVGVDGYVITRDGAHHTETLTFNACDIDNGTYT----- 1103
QY 1129 NAYNTQASSTNGYNNANMYNTQASNTNGYNTNSVNDQGTIITKTVPIPTDQWNIEMS 1188
Db 1104 -----DNT-YLTREVIPIYSHTHEMWEVN 1126
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QY 1189 ETEGTFYIESVELI 1202
Db 1127 ETEGAFHIDSIEFV 1140
RESULT 2
Q93T75 PRELIMINARY; PRT; 1228 AA.
ID AC Q93T75;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN CRY1BA2.
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria, Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RT "Characterization of cryIB gene and its flanking regions cloned from
RL Bacillus thuringiensis subsp. entomocidus HD-9.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1228 AA; 139621 MW; 3DA2A4DBF59C95C3 CRC64;
Query Match 37.0%; Score 2342; DB 2; Length 1228;
Best Local Similarity 42.1%; Pred. No. 3.3e-126;
Matches 533; Conservative 193; Mismatches 435; Indels 106; Gaps 26;
QY 1 MSPNNQNEYEIIIDATSTSVNSDNRYPFANEPNALQNDYKYLQMSAGNASEYPGSP 60
Db 1 MTSNRKNENIINA-----VSNHSAQ-----MDLLPDARIEDSLCIAEGNNID----P 44
QY 61 EVLVSGQDAKAADIVKGLSLGLVPPFVGPIVSLYLTQLDILWPSCKEQWELPMEQVE 120
Db 45 FVSAAS---TVQTGINIAGRILGVLPFAGQLASFYSFLVGLWPRG-RDQWEIPLSHVE 100
QY 121 ELINOKIATYARNKALSELEGLGNNYQLYLTALLEEENPNRGRALRDVNRPFILSLP 180
Db 101 QLNIQQTENARNALTALARIQLGDSFRAYQOSLEDMLNDRDDARTSRVLTHTQYIALSLDP 160
QY 181 TQWPSFRVTVNFEVPLTVYAMAANLHLLILKDAIPGEBWGSTTTNNYDYROMKLTA 240
Db 161 LNAMPLFAIRNQEVPLLMVYAQAANLHLLILKDAISLFGSEFGLTSQEIORYERQVETR 220
QY 241 EYSDHCVKWYETGLAKGTSKOWVDYNOFRREMTLAVLDVVALPNTDTRYPMETKA 300
Db 221 DYSYCVETVNTGLNSLRGTNAASWVRYNQFRRLDITGLVLDLVALFSDYTRTYPIINTSA 280
QY 301 QLREVTYDPLGA--VNVSSIGSWY-DKAPSGFVSISSVIRPPHVFYIITGLTVVTOQRS 357
Db 281 QLREVTYDPLGA--VNVSSIGSWY-DKAPSGFVSISSVIRPPHVFYIITGLTVVTOQRS 339
QY 358 ISSARYIRHWAGHOISYHVRSGSNLQNMGTNQLHSTSTFTDNYDYIYKLSKDAVLL 417
Db 340 WSNTRHMTYWRGHTIOSRPIGGGLNTSTHGATNTSNPV-TLRFASRDVYRTESYAGVLL 398
QY 418 DIVYPGYTIFFGMPVEVERPMVNLN-NTRKTLKYNPVSKDIIASTRDSLELPETSDQ 476
Db 399 ---WGILEPIHGVTFRVFNFTPNQISDRGTANYSPQESPGQLKQDSELPETTER 455
QY 477 PNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITOIPAVKWCWNL 536
Db 456 PNYESYSHRLSHIGIILQSRVN---VPVSWTHRSADRTNIGPNRITQIPMKWASELPQ 512
QY 537 FVPVVGPGHGTGDLQYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVN 596
Db 513 GTTVVRGFGTGGDILA-RTNTGGFGPIRVTVANGPLTQ---RYRIGPRYASTVDFDFVVS 568
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Db 981 LVHREAYSELPIVPGVNAEIPFEELEGHITAITSLDYARDNVVKNQGNGLTCWNVKG 1040
QY 1041 GVEVQOINHTSVLVIPNWDQVSOQFTVOPNORYVLRVYARKEGNGVGSIRDOGNQTE 1100
Db 1041 HVDVQOQHRSDDLVIPEWAEVSQAVRVCPCGGYILRVYARKEGNGVGSIRDOGNQTE 1100
QY 1101 TLTFASDYDNTGNTQVSTNGTNTNAYNTQASSTNGYNANMNTQASNTNGYNTN 1160
Db 1101 ELKE--KNREBEVPTDGTGTCNDYTAHQGTAGCADCACNSRAGYEDAYEDVTTASVNYK 1158
QY 1161 SVYNDOT-----GYITKVTFTFYPTDQMIEMSETEGTYI 1196
Db 1159 PVEEETVYDVRDNHCEYDRGVNYPVPAGYVTKLEYFPTDVTWIEIGTEGKPIV 1218
QY 1197 ESVELIV 1203
Db 1219 DSVLELL 1225

RESULT 4
ID Q9L877 PRELIMINARY; PRT; 1189 AA.
AC Q9L877;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Toxin Cry1Ca6.
GN CRY1Ca6.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2-F;
RA Yu J., Pang Y., Li J.;
RT "Cloning and sequence analysis of the cry1Ca6 gene from Bacillus
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF215647; AAF37224.1; -.
DR HSP; P02965; IC1Y.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1189 AA; 134685 MW; 98F8C1D978DF9451 CRC64;

Query Match 34.5%; Score 2184.5; DB 2; Length 1189;
Best Local Similarity 40.1%; Pred. No. 3.7e-117;
Matches 505; Conservative 190; Mismatches 435; Indels 129; Gaps 31;

QY 1 MSPNNQNEYEIIDATPSTSVSNDNRYPFAPEPTNALQNMIDYKDYLRMSAGNASPYGSP 60
Db 1 MEENNQOC-----IPYNCLSNPE----- 19
QY 61 EVLVSGQ--DRAKAIDIVKLSGLGVFPVGVISLVLTOLIDILWPSGEKSWQEIFMEQ 118
Db 20 EVLDGGERISTGNSIDISLSLVQFLVSNFY--PGGGFLVGLIDFVGVIGVPSQMDAPLVQ 78
QY 119 VEELINOKIAYARKALSELEGKNNYQVLTALAEENPENGSRALRDVNRPEILDS 178
Db 79 IEQLINERIAEFARNAALANLEGLGNFNIVVEAFKEWEEBPNPATRVIDRFRILDG 138
QY 179 LFTQMPFSFRVTFNPEVPLTYVYMAANLHLILLKLDASIFGEWGSTTTINNYDQMKL 238
Db 139 LLERDIPFSFRISGEVPLSVYAQAANLHLAILRDSVIFGERGWGVTINNVENYNLIRH 198
QY 239 TAEYSDDHCKVYETGLAKTKTSKQWVDVNOQFREMTELVLDVVALFPNDTRTYPMET 298
Db 199 IDEYADHCANTYRNLNLPKSTYQDMITYNRRLRDLTLVLDIAAFPNFYDNRPIQP 258
QY 299 KAOLTRVYDTPGLGVNVSSIGSWDKAPSGVIESSVIRPDPVDTLGTVYVYQSRSI 358
Db 259 VGQLTREYVTDPL--INFNPOLQSVQALPTFNWMESSAIRNPHLPDILNLTIFTDWFPSV 316

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QY 359 SSARYIRHWAGHOISYHRVSRGSLNQMGYNTQNQLHSTSTFTDFTNYDIYKTLSDAV-LL 417
Db 317 GRNFI---WGHREVISLIGGNTISPIYKREANQEBPRSFTE-NGPVFTLSNPTLRLL 372
QY 418 DIVVPGTYIIFPGMEVEFPFVWNLNTRTKLNPNVSKDIIIASTRDSELELPETSQOP 477
Db 373 QQMPAPPPNLRGVGEVEP-----STPTNSFTYRG-----RGTVDSLTELPPEDNSVP 420
QY 478 NYESYSHRLCHITSIPATGN---TTGLVPVFSWTHRSADLNNTIYSKTIQIPAVKWDN 534
Db 421 PREGYSHRLCHATFVQSRGTFPLTTGV--VFSWTHRSATLTNTIDPERINQIPUKGFRV 478
QY 535 LPFPVVKPGCHTGGDILQYNRSTGSGVTLFLARYGLALEKAGKYRVRLEYAT--DADIV 592
Db 479 WGGTSVITGPGFTGGDILREN---TEGDFVSLQVWINSPIQRYLRFRVASSRDARVI 534
QY 593 LHVNDA-----QIOMP---KTNWPGEDITSKTFKVADAITLTNLATDSSLALKHNLGE 642
Db 535 VLTGAASTGVGGQVSNMPLQKTMIEIGENTSRTFRYTFDSNPFSTRANPDII---GISE 591
QY 643 DP-----NSTLSGIYVDRIEPIPVDETYEABQDLAAKAVNALFTNTKO-GLRPGVTDY 697
Db 592 RPLFGAGSISGELYIDKIELIILADATFEABSLERAQKAVNALFTSSNQIGLKTVDY 651
QY 698 EYVQAANLVECLSDLLYPNBKRLFLDAVREAKRLSEARNLLQDPDFQFIN--GENGWAS 755
Db 652 HIDQVSNLVDCLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPDGRWRS 711
QY 756 TGIIEVIGDALFKGRYLRLPGAREIDTETPTVLYLYQKVEGVLPKYTRYRLRGVGSQ 815
Db 712 TDITIQQGDDVFKENYVTLFET--VD--ECPYTYLYQKIDESKLKAYTRYELRGVIESQD 768
QY 816 LEIFTIRHOTNRIVKVNDDP---LLPDVSPVNSDGSINRCSEKQKYNVSRLEVENRSGE- 870
Db 769 LEIYLIRYNAKHEIVNVPCTGSLWPLSAQSPICKGEPNRCAPHELNWPDCCSCROGEK 828
QY 871 ----AHEFSIPIDTGEIDYNENAGIIVGPKITDPPEGYATLGNLELVEEGPLSGDALRELQ 926
Db 829 CAHSHSHFTLIDIVGCTDLNEDLGVWVIFKIKTDQGHARLGNLELVEEGPLSGDALRELQ 888
QY 927 REEQWIKIOMTRREEDTRRYMASQAVDLADYDQOQLNPDEIETDLTAAQDLIOSIP 986
Db 889 RAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIAIHAADKRVHRIR 948
QY 987 VYVNEPPEIPGMNYTKFTLTDLQOAWSLYDORNAIPNGDPFRGLSNWNTATPGVEV-Q 1045
Db 949 EAYLPELSVIPGVNAALFELEGRIFTAYSLYDARNVIRKNGDFNNGLLCNWVKGHVDEE 1008
QY 1046 QINHTSVLIPNWDQVSOQFTVOPNORYVLRVYARKEGNGVGSIRDOGNQTEITLFS 1105
Db 1009 QNNHRSVLVPEWAEVSVQVRVCPGRGYILRVYARKEGNGVGSIRDOGNQTEITLFS 1068
QY 1106 ASDYDTNGMTATQVSTNGTNTNAY-NTQASSTNGYN---ANN-----MTN----- 1148
Db 1069 -NCVEEYVYNNVTTCNNYTGTEBEYEGTYSRRNQGYDEAFGNPNPSVPADYASYBESKY 1127
QY 1149 TQASNTNGYNTSVYNDOT---GYITKVTFTFYPTDQMIEMSETEGTYIYBSVELIV 1203
Db 1128 TDGERENPCESRGYGDYTPPLPAGYVTKDLEYFPTDQMIEMSETEGTYIYBSVELIV 1186

RESULT 5
ID Q9S5V8 PRELIMINARY; PRT; 1180 AA.
AC Q9S5V8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Bt84al crystal protein.
GN Bt84al.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.

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OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T84A1;
RA Nagamatsu Y.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=T84A1;
RA Ogo M., Yamada S., Kobayashi Y., Shibata J., Nagamatsu Y.;
RT "Nucleotide Sequence of the Lepidoptera-toxic Protein Gene of Bacillus
thuringiensis subsp. dendrolimus T84A1.";
RL J. Fac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=T84A1;
RA Nagamatsu Y., Itai Y., Hatanaka C., Funatsu G., Hayashi K.;
RT "A Toxic Fragment from the Entomocidal Crystall Protein of Bacillus
thuringiensis.";
RL Agric. Biol. Chem. 48:611-619(1984).
DR EMBL; AB026261; BAA77213.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1180 AA; 133489 MW; 1199E4A6D1DC62D CRC64;

Query Match 32.8%; Score 2075.5; DB 2; Length 1180;
Best Local Similarity 39.6%; Pred. No. 7e-111;
Matches 493; Conservative 179; Mismatches 441; Indels 131; Gaps 33;

QY 23 DSNRYPPANE--PTNALQNMDDYKDYLRKMSAGNASSEYFGSPVVLGGDAKAA---IDIV 77
DB 2 DNN--PNINEICYPNCLSN-----PEVEVLGGERIETGYTPIDIS 39

QY 78 GKLLSGLGVPVGVIGVSLYLTQILDLHPSPGKSEOWEIPMEQVEELINOKIAEYARNKALS 137
DB 40 LSTQFLLESEV-FCAGFVLGVLIIINGIFGSPQWDAPLVQIEQLINQRIEAPNQAIS 98

QY 138 ELEGLGNYYQLYLTALBEWENPNRGRALDRNRKFEILDLSFTQYMPSPRVTFVFPFL 197
DB 99 RLSEGLSNLYQIYAESFREWEDPTNPALREEMRIQFNDMSALITATPLFAVQYQVPLL 158

QY 198 TVYMAANLHLKLDASIFGEEGWSTTTINYYDQMKLTABYSCHVKWYETGLAKL 257
DB 159 SVTYQAANLHLVLSDVSVFQGRGPDAAATNSRYNDLTRLIGNYTDVAVRWYNTGLERV 218

QY 258 KGTSAKQWVDYQNRREMTLAVLDVVALFPNYDRTPTPMETKAQLTREYVYTDPLGAVNVS 317
DB 219 WGPDSRDWRVYNQPRRELTTLVDLVALFNSYDSRRYPRTVSQLTREIYTNP---VLEN 275

QY 318 SIGSWYDKAPSGFVIESSVIRPHVPDYITGLTVVTQSRSSSARYIRHWAGHOISYHRV 377
DB 276 FDGSGFRGAQR---IEQN-IKQPHLMDILNRITTYDVH-----RGFNWGHGQITASPV 326

QY 378 --SRGSLQOQMYGTNQLHSTSTFDFTNYDIYKTLSDKDAVLDDIVPGYTYIPFG----- 430
DB 327 GFSGPEAFPLFGNAGNAAPPVLVSLTGLGIFRTLS-----PLYRRIILSGGN 377

QY 431 -----MPEVEFFMYNQLNTRKTKYNPVSKDIIASTRDSLELPPTSDQNPVTSYSHR 485
DB 378 QELFVLGDTGFSPASLTNLPSTI-YRQ-----RGTVDSLDVIPPQDQNSVPPRAGFSHR 430

QY 486 LCHTTSIPATGNT--TGLVPVPSWTHRSADLNNTYSKTIQIIPAVKCDNLPFPVPVVK 543
DB 431 LSHVTMLSOAAGAVYTLRAPFTSWQHSABFNIIIPSSQITQIPLTKSTNLGSGTSVVVK 490

QY 544 PGHTGGDLQVNRSTGVTGLFLARYGLALEKAGKRYRVLRYATDADIVLHVN-DA----- 598
DB 491 PGFTGGDLR-RTSPGQISTL---RVNITAPLSQRYRVRIRYASTNQLQFHTSIDGRPIN 546

QY 599 QIQMPKTNPNPQEDLTSKTFKQVADAITTLNLTADGSL-----ALKHNLGSDPNSTLSGIYV 654
DB 547 QGNFSATMSSGSLQSGSFRVTGVTTPFPNFGSGSVFTLSARVNSGNE-----VYI 598

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QY 655 DRIEPIVDVETYEAEQDLAAKAVNALFTNTKD-GLRPGVTDYEVNQANLVCELSDDL 713
DB 599 DRIEFPVPAEVTPEAYDLERAQKAVNELFTSSNQIGLTKDVTDTYHIDVSNLVCELSDEF 658

QY 714 YPNEKLLPDAVREAKRLSEARNLLQDPDFQIEING--ENGWTAETAGIEVIEGALPKGRY 771
DB 659 CLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDTITIGGGDDVPKENV 718

QY 772 LRPLPGAREIDTETPYLVYQVKEGVLPKYRVRRLRGFGVSSQGLSEIFTRHQTNRIVKN 831
DB 719 VTLLGTFD---ECYPTLVYQKIDESKLKAYTRYQLRGYTEDSODLSIYLRYNAKHETVN 775

QY 832 VPDD-----LLPDSVPNSDGSINRSEQKYVNSRLSEVENRSGE-----AHEFSIPIDTGE 882
DB 776 VPGTGLMPLSAQSPICKGCEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDVGC 835

QY 883 IDYNEAGIWWGKIYTDPEGYATLGNLELVESGPLSGDALERLQREBQOQWKIOWTRREE 942
DB 836 TDLNEDLGVMVIFKIKTQDGHARLGNLEFLLEKPLVGEALARKVAKKWRDKREKLEWE 895

QY 943 TDRRYMASKQAVDLVADYQDQOLNPDPVEITDLTAQDLIQSIPIYVNVNEMFPIPGHNYT 1002
DB 896 TNIVYKEAKESVDALFVNSQYDRLOQADTNJAMTHAADKRVHSIREAYLPELSVIPGVNAA 955

QY 1003 KFTELTDLRQAAWSLYDQRNAIPNGDFRNGLSNNNATPGVEV-QQINHTSVLVPINWDEQ 1061
DB 956 IFBELEGRIPTAFSLYDARNVKNKGDFNGLSCMNKGVHDVEEQNNHRSVLVVPWEAE 1015

QY 1062 VSQOFTVQPNQRVLRVTKRKGVGNGYVSIROGGNQGTETLTFSS-----AS 1107
DB 1016 VSQEVRCPCRGYILRVTKYKEGYGEGCVTIHEIENNTDELKFSNCVBESEVYNNVTVCN 1075

QY 1108 DYD-TNGMY-NTQVSNVTNGYNTNAYNTQASSTNGYNA--NNMYNTQASNTGNTNTSVY 1163
DB 1076 DYTATOEYEGTTSNRGY--DCAYESNSVADYASAYEEKAYTDRDRDNPCESNRGY 1133

QY 1164 NDQT---GYITKTVPIPTVQDMWMIEMSETEGTFYIESVELIV 1203
DB 1134 GDYTPLAGVITKLEYFPETDKVWIEIGETGTFIVDSVELLL 1177

RESULT 6
Q45736 PRELIMINARY; PRT; 1176 AA.
AC Q45736;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Insecticidal crystal protein.
GN CRYIA(A).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FU-2-7;
RC Kondo S., Tamura N., Kunitate A., Hattori M., Akashi A., Ohmori I.;
RT "Cloning and nucleotide sequencing of two insecticidal delta-endotoxin
genes from Bacillus thuringiensis var. kurstaki HD-1 DNA.";
RL Agric. Biol. Chem. 51:455-463(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FU-2-7;
RX MEDLINE=94289859; PubMed=7764972;
RA Udayasuriyan V., Nakamura A., Mori H., Masaki H., Uozumi T.;
RT "Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain
FU-2-7 and analysis of chimaeric CryIA(a) proteins for toxicity.";
RL Biosci. Biotechnol. Biochem. 58:830-835(1994).
DR EMBL; D17518; BAA04468.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.

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DR Pfam; PF00555; endotoxin; 1.  
FT CONFLICT 77 77 L -> P (IN REF. 1).  
FT CONFLICT 965 965 S -> F (IN REF. 1).  
SQ SEQUENCE 1176 AA; 133075 MW; AA4135B49A289F85 CRC64;  
  
Query Match 32.7%; Score 2070.5; DB 2; Length 1176;  
Best Local Similarity 39.4%; Pred. No. 1.4e-110;  
Matches 492; Conservative 176; Mismatches 440; Indels 137; Gaps 33;  
  
QY 23 DSNRYPPANE--PINALQNDYKDYLMKSNAGNASEYPGSPVLYSGQDAKAA---TDIV 77  
DB 2 DNN--PINECIPNCLSN-----PEVVLGGERIETGTPIDIS 39  
  
QY 78 GKLLSGLVGPEVGVISLYTOLIDILWPSGKESQWEIFMEQVEBELINOKIAEYARNKALS 137  
DB 40 LSLTQFLSERV-PGAGFVLGLVDIIWIGIFGPSQWDAPLVQIEQLINQRIEFARNQAS 98  
  
QY 138 ELEGIGNYQIYLTALBEEWENPGSRALRDVRNFEILDSLFQYMPSPFVTPVPEPPL 197  
DB 99 RLEGLNLYQIYAESFREWEADPTNPALREEMRIQFNDMSALATTAIPLLAVQYQVPELL 158  
  
QY 198 TVVMAANLHLLKADSIKGEWGSMTTINNYDROMKLTAEYSDHCVKWYETGLAKL 257  
DB 159 SVYVQANLHLSVLRDVSFGQRGWGFDAATINSYNDLTRIGNYTDYAVRWYNTGLERV 218  
  
QY 258 KGTSAKQWVDYNQRRMTLAVLDVALFPNYDTRTPMETKAQLTREVYTDPLGAVNVS 317  
DB 219 WGPDSRDWRVYNQRRRLTLVLDIVAFSNYDSRRPIRVSQLTRITVNP---VLEN 275  
  
QY 318 SIGSWYDKAPSGFVIESVIRPPHFVDYITGLTVYTSQSRISARYIRHWAGHQISYHRV 377  
DB 276 FDGSGFRGMAQR---IEQN-IRQPHLMDILNSITVDVH-----RGFNWYSGHQITASP 326  
  
QY 378 --SRGSLNQMYGYNQNLHSTSTFDNYDIYKYLKSDAVLLDIVPGYTIFFG----- 430  
DB 327 GFSGPEFAPFLFGNAGNAAPVLSVLTGLGIFRTLS-----PLYRRIILGSGFNN 377  
  
QY 431 ----MPEVEFFMVNQLNTRKTLKYNPVSKDIIASTRDSLELPPETSDOPNYESYSHR 485  
DB 378 QELFVLDTGTEFSFASLTNLPSTI-YRQ-----RGTVSDLDVIPPQDNVSPRAGFSHR 430  
  
QY 486 LCHITSIPATGNT--TGLVPVFSWTHRSADLNNTYSDKITQIPAVKCDNLPPFVVPVKG 543  
DB 431 LSHVTMLSQAAAGAVYTLRAPTFSGHRSAPENNIIPSSQITQIPLTSTNLGSGTSVYKG 490  
  
QY 544 PGHTGGDLQVNRSTGVTGLFLARYGLALEKAGKYRVLRYATDADIVLHVN-DA----- 598  
DB 491 PGFTGGDILR-RTSPGQISTL---RVNITAPLSQRYRIRIYASTTNLQFHTSIDGRPIN 546  
  
QY 599 QIQMPKTMNPGEDLTSKTFKVADAITTLNLTATDSL---ALKENLGEDPNSTLSGIYVY 654  
DB 547 QGNFSATMSSGNSNLOSGSFRTVGTTFNFSGNSGVFTLSAHVNSGNE-----VYI 598  
  
QY 655 DRIFIPVDETYEAOBLEAKKAVNALFTWKD-GLRPGVTDYEVNQANLVECLSDDL 713  
DB 599 DRIFVFAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDVTHIDQVSNLVECLSD 658  
  
QY 714 YPNEKRLFLDAVREAKLSEARNLLOPDPFOEING--ENGWASTGIEVIEGDALPKRY 771  
DB 659 CLDEKQELSEKVKHAKLSDBRNLLQPNFRGIRNQRDRGRGSTDITIQGGDDVFKENY 718  
  
QY 772 LRLPGAREIDTETPTLYLQKVEGVLLKPYTRYRLRGVPGSSQGLEIFTIRHOTNRIVKN 831  
DB 719 VTLGTFD---ECYPTLYQKIDSKLAKYTRYQURGYEDSQLELYLRYNAKHETVN 775  
  
QY 832 VPDD-----LLPDSVPVNSDGSINRCSEQKYVNSRLEVENRSGE-----AHFSPIDTGE 882  
DB 776 VPGTGLWPLSAQSPFGKGBPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSIDVGC 835  
  
QY 883 IDYENAGIWWGFKITDPEGVATIGNLEVEEGLPSGDALRERLOREQOQWIKQWTRREE 942  
DB 836 TDLNEDLGWVWIFIKIQDQGHARLGNLEFLKEKPLVGBALARVKRAEKKWDRKLEWE 895

QY 943 TDRRYMASKQAVDLRYADYQDQOQLNPDVETIDLTAAQDLIQSIPIVYVNMFPPIPGNMT 1002  
DB 896 TNIVYKEAKESVDALFVNSQYDQLQADTNLAMIHAADKRVHSIRREAYLPSELSVIPGNAA 955  
  
QY 1003 KFTFELTRLOQASWLYDQRNAIPNGDFRGLSNWNAATPGVEV--QQINHTSVLVIPNWD 1061  
DB 956 IFBELEGRISTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQNNQSRSLVVPWEAE 1015  
  
QY 1062 VSOQFTVQPNQVRVLARTARKGNGVYISRDGNGOTETLTES-----AS 1107  
DB 1016 VSOEVRVCPGRGILRTAYKEGYGEGCVTHIEINTDELKFCVCEBIEIYNNVTVCN 1075  
  
QY 1108 DYDTN-----GMTNTQVSTNGYNTNAYNTQASSTNGYNNANNMNTQASNTGYNTNSV 1162  
DB 1076 DYTQVQBEYGGAY---TSRNGY--NEAPSPADYASVYEKSY--TDCRRNPCENRG 1128  
  
QY 1163 YNDQT-----GYTKVTVPFIPYTDQMIEMSETEGTFFIESVELIV 1203  
DB 1129 YRDYTPLPVGYVTKELEYFPETDKWIEIGETGTFIVDSVELLL 1173  
  
RESULT 7  
Q93TF9 PRELIMINARY; PRT; 1160 AA.  
AC Q93TF9;  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)  
DE Insecticidal crystal protein.  
GN CRYIDB.  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
OC Bacillaceae; Bacillus.  
OX NCBI\_taxid=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B-PR-88;  
RA Li C., Zhang J., Huang D., Li G.;  
RL "A crystal endotoxin from Bt strain B-PR-88";  
DR Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF358662; AAK48937.1; -  
DR InterPro; IPR001178; Endotoxin.  
DR Pfam; PF00555; endotoxin; 1.  
SQ SEQUENCE 1160 AA; 130952 MW; B18B04193D87695E CRC64;  
  
Query Match 32.7%; Score 2068; DB 2; Length 1160;  
Best Local Similarity 39.4%; Pred. No. 1.8e-110;  
Matches 482; Conservative 189; Mismatches 425; Indels 126; Gaps 29;  
  
QY 33 PTNALQNDYKDYLMKSNAGNASEYPGSPVLYSGQDAKAAIDIVGKLLSGLGVPPVGP 92  
DB 11 PYNCLN---PDAILDA-----ERLETGNTVADISGLINFLYSNP-VPGGGPI 56  
  
QY 93 VSLYTOLIDILWPSGKESQWEIFMEQVEBELINOKIAEYARNKALSLEGLNNYQIYLT 152  
DB 57 VG---LLELGVGVPQWEIPLAQIEQLISQRIEFARNQAIISLEGLSNVEIYET 112  
  
QY 153 LEWEEENPGSRALRDVRNFEILDSLFQYMPSPFVTPVPEPFLTYVMAANLHLLK 212  
DB 113 FRAMEKDPSPALREEMRTQFNVMNSALIAAIPLLRVRYEVALLSVYQAAANLHLSVL 172  
  
QY 213 DASIFGEWGSMTTINNYDROMKLTAEYSDHCVKWYETGLAKGTSAKQWVDYNOFR 272  
DB 173 DVSVIGQMGFDPATVNSRYSDTLRIHVITDHCVDYTDNDGLKNLGRSLSDWVYNNRFR 232  
  
QY 273 REMTLAVLDVALFPNYDTRTPMETKAQLTREVYTD-PLGAVNVSISGSWYDKAPSGFV 331  
DB 233 RLITISVLDIIAFPNYDIEAYPIQATASQLTRVYLDLPVNETLSPASV----PTFSA 298  
  
QY 332 IESVIRPPHFVDYITGLTVYTSQSRISARYIRHWAGHQISYHRVSRGSLN--QQMYGT 389  
DB 289 AESAIRSRPHLVDFLNSFTIYTD--SLASVAY--WGHVLVNSFRGTGTTNLRSPLYGR 343

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QY 390 NQNLHSTSTPFT-NYDIYKTLKDAVLLDIVVPGYTIYP-----GMPEVEFFM 438
DB 344 EGTERPVTISASPSVPIFRTLS-----YFTGLNNNPVAGIBGVF-- 385
QY 439 VQNLNTRKTLKYNPVSKDIIASTR--DSELELPETSDQPNYESYSHRLCHITSIATG 496
DB 386 -----QNTISRSYRKSGBPDSFSELPPQDVSVPASIGYSHRLCHATFLERIS 433
QY 497 NTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKWCNDLPPVPVKGPGHGTGGDLQYNR 556
DB 434 GPRIAGTVFWSWTHRSASPINEVSPSRITQIPWKAHTLASCASVKGPGGTGGDLTRN- 492
QY 557 STGSVGLFLIARYGLALEKAGKYRRLRYATDADIVLHVNDQA-----IQMPKTMNPGED 611
DB 493 SMGDLGALRVTFTRGLPQ---SYVIRPRYASVANRSCTFRYSQPPSYGISPPKTMADAGEA 549
QY 612 LTSKTFKVADAITNLATDSSLAKNLGCDPNSTLSGIYVYDRIRFIPVDETYEABQD 671
DB 550 LTRSRP-----AHTTLPPIFTSRA-----QEEFDLYIQSGYIIDRIEFIPVDATFESEIN 600
QY 672 LEAAKAVNALFTNTKD-GLRPGVTDYEVNOANLVECLSDLYPNKRLLEDAVREAKR 730
DB 601 LERAQAVNALFTSTQGLKHTVTDTHIDQVSNLVECLSDPECLDEKRELSKVRHAKR 660
QY 731 LSEARNLLODPDFOEIN--GENGWTAETGIEVIEGDALFKRGLRFLRPFAGREIDTETPTY 788
DB 661 LSDERNLLODPENFGINRQPDGRWGRTDITIQQGDDVFKENYVTLGTFD---ECYPTY 717
QY 789 LYQKVEGLVKPTRRLRGLRFGVSSQGLEIFPTRHQNRNIVKVNPPD-----LLPDVSPVN 844
DB 718 LYQKIDESKLYKATRYOLRGYIEDSOBLEIYLIRYNKAKHEIVNVPGTGSLWPLSVQSPIG 777
QY 845 SDGSINRCSQKYNRSLEVENESGE-----AHEFSIPIDTGEIDYNNENAGIWWGFKITD 899
DB 778 KCGEPRNRCAPHEWNPDLDCSDEEKCASHHSHFSLDIDVGCITDLMEDLGVWIFIKT 837
QY 900 PEGYATLGNLEVEGLPLSGDALERLQREQOMKIQWTRREEREDRRYMASKOAVDRLYA 959
DB 838 QDGHARLGNLEPLEEKLPLVGEALARVKAESKWRDKREKLELTNIIVYKEAKESVDALFV 897
QY 960 DYQDQOLNPVVEITDLTAAQDLTOSIPYVNEPPEIPGMNYTKFTBLTRLOQOASLYD 1019
DB 898 NSQYDQOLQADTNTAMTHAADKRVHSIREAYLPELSVIFPGVNAIGFEBELEGRIETAVSLYD 957
QY 1020 QRNAIPNGDFRNLGNWNAFPGEV-QQINHTSVLVPNDDEQVSOQFTQPNQRYVLR 1078
DB 958 ARNVIKNGDFNGLSGCNWVKGHVDVSEQNHRSVLVVPWEAEVSOBRVCPGGRGYTLRV 1017
QY 1079 TARKEGVNGYVIRDGNGQNTETLTFSASDYDNGMTQVNTNGYNTNNAVNTQASST 1138
DB 1018 TAYKEGVGECVTHIEVDNNTDELK--SNCEKEQVYPGNTVACNDYKXKHGANACSSRN 1075
QY 1139 NGYNANNNMT-----QASNTNGYNTN-SVND-----QTYIYTKVTFPIPYTD 1181
DB 1076 RGYDESYENSSIPADYAPYVEBEAYTDQGNPSEFNRGHTPLPAGYVTAELIYFPETD 1135
QY 1182 QMIWMESETGTFYIESVELIV 1203
DB 1136 TWVEIGETEGTFIVDSVELLL 1157

RESULT 8
Q9RC30
ID Q9RC30 PRELIMINARY; PRT; 1176 AA.
AC Q9RC30;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 135 kDa insecticidal protein.
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
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[1]
RN SEQUENCE FROM N.A.
RP STRAIN=HD-1-02;
RA Hou B.K., Chen Z.H.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF154676; RAD55382.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1176 AA; 133010 MW; FCEE069D0B81D8C4 CRC64;

Query Match 32.5%; Score 2055.5; DB 2; Length 1176;
Best Local Similarity 39.4%; Pred. No. 9.9e-110;
Matches 491; Conservative 175; Mismatches 442; Indels 137; Gaps 33;

QY 23 DSNRYFANE--PTNALQWMDYKDYKMSAGNASEYPGSPVULVSGQ---DAAKAAIDIV 77
DB 2 DNN--FNINECIPYNCLSN-----PEVELGGRIETGYTPIDIS 39
QY 78 GKLLSGLGVPFVCGPIVSLYLTQLDIILWPSGEKSQWEIFMEQVEELINOKIAEYARNKALS 137
DB 40 LSTQFLLSEFV-PGAGFVLGLVDIIIGFSGQWDTFLVQIEQLINORIEEFARNOAIS 98
QY 138 ELEGLGNNYQLYLTALEEWEENPNGSRALDRVNRPFILDSLFTQYMPSPRVTFNFFVPL 197
DB 99 RLEGLSNLYQIYAESPFEWEADPTNPALREEMRIQFNDAWSALTATPALLAVQNYQVPLL 158
QY 198 TVYMAANLHLLLLKDAISIFGBEWGSTTTNNYDRQMKLTAEYSDCHCVKWTETGLAKL 257
DB 159 SVYVQAANLHLSLRVDSVFGQWGPDAATINSRYNDLTRIGNYTDYAVRWNTGLERV 218
QY 258 KGTSAQWVDYQNFREMTLAVLDVVALPNDYTRYPMETKAQLTRVYTDPLGAVNVUS 317
DB 219 WGDSDRWYRQNFRELTLTVLDIVALSNDYDRRYPIRTVSQLTREIYTNP---VLEN 275
QY 318 SIGSWDKAPSEGVIBSSVIRPPHVDYITGLTVYVFSWTHRSADLNNTIYSDKITQIPAVKWCNDLPPVVK 377
DB 276 FDGSPRGAQR---ISQN-IRQPHLMDILNSITIIYTDVH-----RGFNWMSGHOITASPV 326
QY 378 --SRGNLQOMGTQNLHSTSTFTDFNTVDIVYKTLKDAVLLDIVVPGYTIYPFG----- 430
DB 327 GFSGPEFAPFPLFGNAGNAAPPVLVSLTGLGIFRTLS-----PLYRRIILGSGPNN 377
QY 431 -----MPEVEFFMVNQLNTRKTLKYNPVSQKDIATSTRSELELPETSDQPNYESVSHR 485
DB 378 QELFVLDGTGTFSPASUTTLNLPSTI-YRQ-----RGTVDSLDVIPPQDINSVPPRAGFSHR 430
QY 486 LCHITSIPATGNT--TGLVPVFSWTHRSADLNNTIYSDKITQIPAVKWCNDLPPVVK 543
DB 431 LGHVWLSQAAGAVYTLRAPTFSWHRSFAFNIIIPSSQITQIPLTKSTNLGSGTSVVK 490
QY 544 PGHTGDLLOYNRSTGSGVTFLIARYGLALEKAGKYRRLRYATDADIVLHVNDQA----- 598
DB 491 PGFTGDLIR-RTSPQIISTL---RVNITAPLSQRYVRIRVYASTTNLQFHTSIDGRPIN 546
QY 599 QIQMPKTMNPGEDLTSKTFKVADAITNLATDSSL-----ALKHNLGDPNSTLSGIYV 654
DB 547 QGNFSAIATSGSNLQSGSPRTVGTFTPPFNSGSSVFTLSAHVFNSGNE-----VYI 598
QY 655 DRIEFIPVDETYEAEQDLEAAKAVNALFTNTKD-GLRPGVTDYEVNOANLVECLSDDL 713
DB 599 DRIEFVPAEVTPEAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHDQVSNLVECLSD 658
QY 714 YNEKRLLPDAVREAKRLSEARNLLODPDFOEIN--ENGWTAETGIEVIEGALPKRY 771
DB 659 CLDEKQELSEKVKHAKRLSDERNLLODPNFRGINRQLDGRWGRTDITIQQGDDVFKENY 718
QY 772 LRLPGAREIDTETPTYLYQKVEGLVKPTRVRLRGLRFGVSSQGLEIFPTRHQNRNIVK 831
DB 719 VTLGLTFD---ECYPTYLYQKIDESKLYKATRYOLRGYIEDSOBLEIYLIRYNKAKHETVN 775
QY 832 VPDD-----LLPDVSPVNSDGSINRCSQKYNRSLEVENESGE-----AHEFSIPIDTGE 882
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Db 776 VFGTGLWPLSAQSPGKGEFNRCAHLEWNPDLDCSDRGCEKCAHHSHFSLDIDVGC 835
Qy 883 IDYNENAGIWWGFKITDPBGATLGNLEVEGPISGDALEROREQOWKIOMTFRREE 942
Db 836 TDLNEDLGWVIFKIKTQDCHARLGNLEFELEKPLVGEALARKVIAKRWDRKRELEW 895
Qy 943 TDRRYWASKQAVDRLYADYQDQOLPNVBEITDLTAQDLIQSIPIVYNEMFPEIGMNYT 1002
Db 896 TNIIVYKEAKESVDALFVNSQYDQLOADTNIAHIAADKRVHSIREAYLPELSVPGVNA 955
Qy 1003 KPELTDLRLOQAWSLYDQNAIPNGDFRGLSNWNAIPGVEV-QQINHTSVLVIWDEQ 1061
Db 956 IPEELEGRIFTAFSLYDARNVTKNGDFNGLSCWNVYKHVDVEEQNQRSVLVWPEWAE 1015
Qy 1062 VSQQTFOQPNORYVLRVARTARKEGVNGYVSIIRDGNQOTLTFS-----AS 1107
Db 1016 VSQEVVCPGCGYILRTAYKGYGEGCVTHIEIENNTDELKFSNCVBEIYNNVTVCN 1075
Qy 1108 DYDTN-----GMYNTQVSNNGYNTNAYNTQASSTNGYNANNMYNTQASNTNGYNTSV 1162
Db 1076 DYTVMQEEYGGAY---TSNRGY--NEAPSVPADYASVVEEKSY--TDGRRENPCFNRG 1128
Qy 1163 YNDQT-----GYTKVTFTPYTDQMWIEMSETEGTPIYESVELIV 1203
Db 1129 VRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTPIVDSVELLL 1173

RESULT 9
ID O06894 PRELIMINARY; PRT; 1171 AA.
AC O06894;
AT 01-JUL-1997 (TremBrel. 04, Created)
DT 01-JUL-1997 (TremBrel. 04, Last sequence update)
DT 01-DEC-2001 (TremBrel. 19, Last annotation update)
DE CryEa4.
GN CryEa4.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LBIT-147;
RA Barboza-Corona J.E.; Lopez-Meza J.E.; Ibarra J.E.;
RT "Cloning and expression of the cryEa4 gene of Bacillus thuringiensis
and the comparative toxicity of its gene product.";
RL World J. Microbiol. Biotechnol. 14:437-441(1998).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=LBIT-147;
RC Ibarra J.E.; Barboza-Corona J.E.;
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; U94323; AAD04732.1; -.
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00555; endotoxin_1;
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN 1.
SQ SEQUENCE 1171 AA; 133310 MW; 333603A1A782523A CRC64;

Query Match 32.4%; Score 2054.5; DB 2; Length 1171;
Best Local Similarity 38.9%; Pred No. 1,le-109;
Matches 483; Conservative 193; Mismatches 431; Indels 135; Gaps 33;

Qy 20 VSNDNRYPFANEPTNALQNDYDKYLKMSAGNASEYPGSPVLVSGDAAKAAIDIVGK 79
Db 4 VNNQOCVPY-----NCLNPE-NEILDERSNSTV-----ATNIALEISRL 44

Qy 80 LLSGLGVFVGPIVSLYTLIDILPSPGSKSQWEIFMEQVEBLINQKIAEYARNKALS 139
Db 45 LASAT-----PIGGILLGLFDIAIGSIPGSQWDLFLQIEILLIDKIEFARNQAISRL 98

Qy 140 EGLGNYQLYLTALBEWEENPNGRALRDVRNRFELDSLFTQYMPSTFVTFVPLTV 199

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Db 99 EGISLYGIYEAFAREWADPTNPALKEEMTQFNDMNSILVTAIPLFSVQYQVPLSV 158
Qy 200 YAMAANLHLLLKDASIPGEWGHSTTTNNYDROMKLTAEYSDHCWKVYETGLAKG 259
Db 159 YVOAANLHSLVRDVSFQWAGFDIATINSYRNDLTRILPIYTDYAVRWNTYGLDLPR 218
Qy 260 TSA-KOWYDYNQFRREMTLAVLDVVVALFPNPDYTPMETKAQLTREYVTPDPLGAVNVS 318
Db 219 TGGLENWARFQNFRELTSVLDIISFRNVDLSRLPIPTSSQLTREYVTPDV--INTD 276
Qy 319 IGSWYDKAPSGVIESSVIRPPHVDYITGLVYVYQSSISARSYIRHWAGHQISYHRVS 378
Db 277 ---YRVGSPENIENSARSPLHMLFNLNLTDT-----DLIRGVHWAGHRVTSH--F 325
Qy 379 RGSN---LQOMYNTGNLH-----STSPDFNTYDIYKLSKDAVLLDIVPGYIIFG 430
Db 326 TGSQVITTPQYGNSONAPRRTIAPSTFGLNL-FYRTLSNP-----FPR 370
Qy 431 MPEVEFFWVNLNTRKTLKYN-----PVSKDIIASTR---DSELELPPETSDQPN 478
Db 371 RSE-----NITPLGINVVGVGFIQPNNAEVLIRSGVTVDLSNELP--IDGENS 418
Qy 479 YESXSHRLCHITSIPATGNT--TGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCDNLP 536
Db 419 LVGYSHRLSHVLTLSLNTNITSL-PTFWTHHSATNTINPDIITQIPLVKGFRGG 477
Qy 537 FVPVVGPGHGTGDLLOVNRSTGVTGLFLARYGLALEKAGKRVRLRYAT--DADIYH 594
Db 478 GTSVIKGPFGTGDILRRN---TIGBEVSLQVNSIPITQRYLRFRYASSRDARITVA 533
Qy 595 VND---AQIQMPKTMNCEDELTSKTFKADAITLNLATDSSLAKKNLGDPNSTLSGI 651
Db 534 IGGQIRVDMTLEKTEWIGESLTSRTFSYTNFSPFRANPDII---RIABE-LPIRGGE 589
Qy 652 VYDRIEIPVDETYEARQDLAAKAVNALFTNTKD-GLRPGVTYDEVNQAANLVECLS 710
Db 590 LYIDKIELIADATFEEYDLEAKAVNALFTSTNQLGKTDVTDHIDQVSNLVECLS 649
Qy 711 DDLFPNEKRLFPDARENRKLSERNLLQDPDPQORIN--GENGWASTAGIEVIEGDAIFK 768
Db 650 DEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQDPDRGWRGSTDITIQGDDVFK 709
Qy 769 GRYLRLPGAREIDETPTLYLQKVEGVLPKPYRRLRGVFGSSQGLEIETIRHQTWRI 828
Db 710 ENYVTLPGTFD---ECYPTIYQKIDSKLKAYTRYELRGYIEDSQDLEILIRYNAKHE 766
Qy 829 VKNVPDD---LLPDVSPVNSDGSINRCSEQKYNSRLSEVENRSGE-----AHEPSIPID 879
Db 767 TVNVPGTGSLWPLSAQSPIGKGEFNRCAHLEWNPDLDCSDRGCEKCAHHSHFSLDID 826
Qy 880 TGEIDYNENAGIWWGFKITDPBGATLGNLEVEGPISGDALEROREQOWKIOMTFR 939
Db 827 VGCTDLNEDLGWVIFKIKTQDCHARLGNLEFELEKPLVGEALARKVIAKRWDRKRE 886
Qy 940 REETDRRYWASKQAVDRLYADYQDQOLPNVBEITDLTAQDLIQSIPIVYNEMFPEIGM 999
Db 887 EWETNIVYKEAKESVDALFVNSQYDRLQADTNIAHIAADKRVHSIREAYLPELSVPGV 946
Qy 1000 NYTKFTLTDLRLOQAWSLYDQNAIPNGDFRGLSNWNAIPGVEV-QQINHTSVLVIW 1058
Db 947 NAAIFEELEGRIFTAFSLYDARNVTKNGDFNGLSCWNVYKHVDVEEQNQRSVLVWPEW 1006
Qy 1059 DEQVSQQTFOQPNORYVLRVARTARKEGVNGYVSIIRDGNQOTLTFS-----ASDY 1109
Db 1007 EAEVSQEVVCPGCGYILRTAYKGYGEGCVTHIEIENNTDELKFSNCVBEIYNNVT 1066
Qy 1110 DTNGHYNTQVSNNGYNTNAYNTQASSTNGYNANNMYN-----TOASNTNGYNTSVND 1165
Db 1067 TCNNYTATQEHGTYTSRNRGYDEAYESNSVHASVVEEKSYTDRRENPCSNRNGYGD 1126
Qy 1166 QT----GYITKVTFTPYTDQMWIEMSETEGTPIYESVELIV 1203

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db 1127 YTPLPAGVTTKELEYFPETDKWIBIGETEGTFIVDSVELLL 1168

## RESULT 10

Q92926 PRELIMINARY; PRT; 1155 AA.

1D Q9F296  
AC Q9F296;  
ID 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Delta endotoxin.  
DE Bacterium thuringiensis.  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
OC Bacillaceae; Bacillus.  
NCBI\_TaxID=1428;  
RN [1]  
RX SEQUENCE FROM N.A.  
RA Meza-Basas L.A., Theoduloz C.;  
RT "Cloning and expression of a delta endotoxin gene from a Chilean  
RT native Bacillus thuringiensis strain.";  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U94191; AAG16877.1; -.  
DR HSSP; P02965; 1CIY.  
DR InterPro; IPR0011178; Endotoxin.  
DR Pfam; PF00555; endotoxin.1  
DR  
SQ SEQUENCE 1155 AA; 130557 MW; 5D69E3E2F527749D CRC64;

Query Match 32.3%; Score 2048; DB 2; Length 1155;  
Best Local Similarity 38.9%; Pred. No. 2.6e-109;  
Matches 480; Conservative 192; Mismatches 426; Indels 136; Gaps

QY 23 DSNRYPPANE--PTNALQNDYKDYLKMSAGNASEYPGSEVLVSGQDAAKAA---IDIV 77  
DB 2 DNN--PNINPCIPNCLSN-----PEVLGGERIETGYTPIDIS 39  
QY 78 GKLLSGLGVPFVGIVSLYQLIDILMPSGCKSQWELFMBOVELLNOKIAEYARNKALS 137  
DB 40 LSLTQFLLSFV--PGAGFVGLVDLIINGIIFGPQWDAPFVQIQLNQRIEFAFNQALS 98  
QY 138 ELBGLGNYYQLYTALBEBENPNNGSRLADVRNRFEILDLSFTQYMPFRVTFVPEPL 197  
DB 99 RLEGLSLYQIYAESPFEWEDPTNPALREEMRIQFNDMNSALTATPLFAVQNYQVPLL 158  
QY 198 TVYMAANLHLILLKQASIFGEEGWSTTTINNYDQMKLTAEYSDHCVKWYETGLAKL 257  
DB 159 SVTVQAAHLHLVLDVSVFGQWGFDAATNGKYNLDRLIGNYTDHVRWNTGLERV 218  
QY 258 KGTSAKQWDYNQPRREMTLAVLDVVALFFNYDTRTPYMETKAQLTRVYTDPL----- 312  
DB 219 WGPDSRDWRYNQPRRELTTLVLDIVSLFFNYDSRTVPITVVSQLTREIYTNPVLNFDG 278  
QY 313 AVNVSSITGSWYDKAPSGVGLSESVIRPHVFDITGLTVYVTSQSRSSARYIRHWAGHOI 372  
DB 279 SFRGSAQ-----IEGS--IRSPHLMQILNSTIYTDH-----RGEYVNSGHQI 321  
QY 373 SYHRV--SRGSNLQOQYGTQNLHSTSF--DFTNYDIYKTLSDKAVLLDVIYVGYTYIF- 428  
DB 322 MASPVGFSGEFTPLXGTWGAAPQORIVAQLGQGYRTLSSTL-----YRPPN 372  
QY 429 FGMPEVEFFVWNLNTRKTLKNYPVSKDIIASTROSELELPETSQDPNYESYHRLCH 488  
DB 373 IGINNQQLSVLDGTEFAYGTSNNLPSAVYRKSGVTVDLSDEIIPQNNVPPRQGFSHRLSH 432  
QY 489 ITSIPATGNMTGL-----VPFVPSWTHRSADLNNTYSDKITQIIPAVKCDNLPPVPVVKGP 544  
DB 433 VSMFRSGFSNSVSIIRAPMFSWTHRSAEFNNIIPSSQITQIPLTKSTNLGSGTGVKGP 492  
QY 545 GHTGGDLLQNRSTGSGVTGLFLARYGLALEKAGKYRVLRYATADADIVLHVN-DA----- 599  
DB 493 GFTGGDILR-RTSPGOISTL---RVNITAPLSQRYRVIRYASTNLOFTSIDGRPINQ 548  
QY 600 IQMPKTNVPGEDLTSTKTFKVADAITTLNLTADSSL-----ALKHNLGSDPNSTLGIVYVD 655

[illegible]

## RESULT 11

|        |   |      |          |
|--------|---|------|----------|
| Q45735 | PRELIMINARY;  | PRT; | 1177 AA. |
| AC     | Q45735;   |      |          |
| DT     | 01-NOV-1996 (TREMBLRel. 01, Created)  |      |          |
| DT     | 01-NOV-1996 (TREMBLRel. 01, Last sequence update)                             |      |          |
| DT     | 01-DEC-2001 (TREMBLRel. 19, Last annotation update)                           |      |          |
| DE     | Delta-endotoxin.  |      |          |
| OS     | Bacillus thuringiensis.   |      |          |
| OC     | Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;                 |      |          |
| OC     | Bacillaceae; Bacillus.  |      |          |
| OX     | NCBI_TaxID=1428;  |      |          |
| RN     | [1]   |      |          |
| RP     | SEQUENCE FROM N.A.  |      |          |
| RX     | MEDLINE=91197102; PubMed=2014985;   |      |          |
| RA     | von Tersch M.A., Robbins H.L., Jany C.S., Johnson T.B.;                       |      |          |
| RT     | "Insecticidal toxins from <i>Bacillus thuringiensis</i> subsp. <i>kenya</i> ; |      |          |
| RT     | cloning and characterization and comparison with <i>B. thuringie</i>          |      |          |
| RT     | subsp. <i>kurstaki</i> CryIA(c) toxins.";                                     |      |          |
| RL     | Appl. Environ. Microbiol. 57:349-358 (1991).                                  |      |          |
| DR     | EMBL; M35524; AAA22338.1; -   |      |          |
| DR     | HSP; P02965; ICIY.  |      |          |
| DR     | InterPro; IPR001178; Endotoxin.   |      |          |
| DR     | Pfam; PF00555; endotoxin; 1.  |      |          |
| SO     | SEQUENCE 1177 AA; 133114 MW; C81F76D03F38CCB5 CRC64;                          |      |          |

Query Match 32.0%; Score 2027; DB 2; Length 1177;  
Best Local Similarity 39.4%; Pred. No. 4.4e-108;  
Matches 494; Conservative 186; Mismatches 419; Indels 156

|    |      |  |      |
|----|------|--|------|
| Qy | 23   | DSNRYFPANE--PTNALQNDYKDYKMSAGNASEYPCSPFVLSVGQDAAKAA---IDIV     | 77   |
| Db | 1    |  |      |
| Db | 2    | DNN--FNINECIPYNCLSN-----PEVELGGERITEGTPTIDIS                   | 39   |
| Qy | 78   | GKLLSGLGVPFVGPVSVLTQIDILWPSEKGSOMEIPEWQVEELINOKIAEYARNKALS     | 137  |
| Db | 40   | LSUTQFLLSEFV--PGAGFVLGLVDIIWIGFGSQDWAFLVQIEQLINQRIEEFARNQAIS   | 98   |
| Qy | 138  | ELEGLGNNTQLYLTALLEEENPNPGRSALRDVVRNFEILDSLFTQYMPSPRVTNFEPFPL   | 197  |
| Db | 99   | RLEGLSNLQIYAESPFEWEADPTPALREEMKRIQFNDMSALTTAIPLAVQNYQVPELL     | 158  |
| Qy | 198  | TVYAMAANLHLLLLKDAASIPGEBGWSTTTINNYDROMKLTAEYSDHCVKWETGLAKL     | 257  |
| Db | 159  | SVTVQAAHLHLSVLRDVSFVGQWGFDAATINSRYNDLTRLIGNYTDHAEVNTYGLERV     | 218  |
| Qy | 258  | KGTSAKQWDVYNQFREMTLAVLDVVALPPNYDERTYPMETKAOLTREVTYDPL----      | 312  |
| Db | 219  | WGPDSDMWRYNQFRELTTLTVLDIVALEFPNYSRRYPIRTVSQUTREIYNPVLNFDG      | 278  |
| Qy | 313  | AVNVSSIGSWYDKAPSGFVIESVIRPPHFVFIITGLTVYTTQSRISISSARYIRHWAGHQI  | 372  |
| Db | 279  | SFRGSAQ-----IERS-IRSPHMLDILNSIITYDAH-----RGYYWSGHQI            | 321  |
| Qy | 373  | SYHRV--SRGSNN-QQWGTNQNLHSTSTF--DFTNYDIIYKTLSKOAVLLDIVPGYTYTIFP | 429  |
| Db | 322  | MASPFVSGFSGPEFTPLFYLTWGNAAPOORIVAOLQGQVYRTLSS-----TFY          | 367  |
| Qy | 430  | GMPEVEFFMYNQLNNTR-----KTLKYNVPKXDIITASTDSELELPETSDOPN          | 478  |
| Db | 368  | RRP-----FNIG-1NNQOLSVLGDTEPAYGTSNLSFSAVVRKSGTVDSUDEIYPPONNVPP  | 422  |
| Qy | 479  | YESYSHRLCHITIPATGNTTGL----VPVFSWTHRSADLANNITYSDKITQIIPAVKCDWN  | 534  |
| Db | 423  | ROGFSHRLSHV--SMFSGSSSVSIIRAPMFWSIHRSAEFNNIATSDSIITQIPAVK--GN   | 479  |
| Qy | 535  | LPP-VPVKGPGHGTGDLLOYNRSTGSGVTGLFLARYGLALEKAG-KYRVLRYATDADIV    | 592  |
| Db | 480  | FLFNGSVISGPGTGGDLVRLNLSGNNIQNRGYIEVPIHFPFSTSTPRVRYRVASVTPIH    | 539  |
| Qy | 593  | LHVN--DAQI---QMPKTMNPGEDITSKT---FKVADAIITLNLATDSSLAKHNLGEDP    | 644  |
| Db | 540  | LNVNWNSSIFSNTVPATATSLDNLOQSSDFGYFESANAFTS-----SLGNIIVGRVN      | 590  |
| Qy | 645  | NSTLSGIVYDRIEFIPDTEYAEAOEAAKAYNALFTNTKD-GLRPGVTYDEVNQAA        | 703  |
| Db | 591  | FSGTAGVI-IDREFIPVTATLEAYENLERAOKAYNALFTSTNLQGLKTNVTDHIDQVS     | 649  |
| Qy | 704  | NLVECLSDDLYPNEKLLFDVAAREKRLSEARNLLODPDPOEIN--GNGWMTASTGIEVI    | 761  |
| Db | 650  | NLVTCLSDFCLDEKSELKVKHAKHLSDERNLQDSNFKDINRQPERGWGSGTGITIQ       | 709  |
| Qy | 762  | EGDALPKGRVLRLPAGAREIDTETYPYLYOKVEEGLKPYTRYRLRPGVSGSGGLEIFTI    | 821  |
| Db | 710  | GGDDVFKENVTUTLSGTFD---ECYPYLYOKIDESLKAPTRYQLRGYIEDSODLEIYLI    | 766  |
| Qy | 822  | RHQTNRIVKXVPDD----LLPDVSPVNSDGSINRCSQKYNSRLSEVENRSGE-----AH    | 872  |
| Db | 767  | RYNAKHETVNVPGTSLWPLPSAQSPICKGCEPNRPAPHLEWNPDLDSCRDGEKCAHSH     | 826  |
| Qy | 873  | EFSIPIDTGBEIDYENAGIWWGKFTDPEGYATLGNLELVBEGPLSGDALERLOREQQW     | 932  |
| Db | 827  | HFSLIDIVGCTDLNEDLGVMYVFIKIQDQGHARLGNLFELEBKPLVGEALARVRAEKKW    | 886  |
| Qy | 933  | KIQWTRRRETDRRYNASKQAVDRLYADYQDOOLNPDVEITDLTAAQDLIOSIPYVYNEM    | 992  |
| Db | 887  | RDKREKLEWETNITVYKEAKESVDALFVNSQYDOLQADTNAMIHAADKRHSIREALYPE    | 946  |
| Qy | 993  | FPETPGMNYTKFTELDRLOQAWSLYDORNAIPNGDFRNLGNSNNWATPGVEV-QQINHTS   | 1051 |
| Db | 947  | LSVIPGVNAAIFEELEGRIFTAEFLYDARVNIKNGDFNGLSCMNWKGVHDVEGNNQRS     | 1006 |
| Qy | 1052 | VLVIPNWDQVSQQTVPQNRYVLRVLTARKEGVNGVYVSRIDGGNQOTETLTFSS-----    | 1105 |

|    |      |   |      |
|----|------|---|------|
| Db | 1007 | VLVPPWEAEVSOEVRVCPGRGYILLRVAYKEGYGEGCVTHIEIENNTDELKFSNCVVEE | 1066 |
| Qy | 1106 | -----ASDYDTN-----GMYNTQVSTNGYNTNAYNTQASSTGYNNANNMYNTQAS     | 1152 |
| Db | 1067 | IYPNNVTTCNDYTVQOEYGGAY--TSERNGY--NEAPSPADYASVYEKSY--TDGR    | 1119 |
| Qy | 1153 | NTNGYNTNSVYNDQT-----GYTKVTVPITPDQWIMSEMSETGTFVIESVELIV      | 1203 |
| Db | 1120 | RENPCFENRGYRDYPLPVGYYVTKLEYFPETDKVWIEIGETGTFIVDSVELLL       | 1174 |

  

|           |  |
|-----------|--|
| RESULT 12 |  |
| Q93T21    | PRELIMINARY; PRT; 1155 AA.   |
| ID        | Q93T21   |
| AC        | Q93T21;  |
| DT        | 01-DEC-2001 (TrEMBLrel. 19, Created)                                   |
| DT        | 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)                      |
| DT        | 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)                    |
| DE        | Crystal protein CryIAB6.   |
| GN        | CryIAB6.   |
| OS        | Bacillus thuringiensis (subsp. israelensis).                           |
| OC        | Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;          |
| OC        | Bacillaceae; Bacillus.   |
| OX        | NCBI_TaxID=1430;   |
| RN        | [1]  |
| RQ        | SEQUENCE FROM N.A.   |
| RA        | STRAIN=4Q7;  |
| RC        | Yu J., Tan L., Wu D., Pang Y.;   |
| RT        | "Molecular characterization of a silent gene encoding a 130-kilodalton |
| RT        | crystalline protein from Bacillus thuringiensis subsp. israelensis.";  |
| RL        | Submitted (MAY-2001) to the ENBL/GenBank/DBJ databases.                |
| DR        | ENBL; AF375608; AAK55546.1; -  |
| DR        | Interpro; IPR001178; Endotoxin.  |
| DR        | Pfam; PF00555; endotoxin; 1.   |
| SQ        | SEQUENCE 1155 AA; 130747 MW; 7FC98E0100C7698 CRC64;                    |

| Query Match | Score 2024 | DB 2 | Length |
|-------------|------------|------|--------|
|             | 32.0%      |      |        |



```
Db 767 RYNAKHETVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSH 826
Qy 873 EFSIPIDTGEIDYNENAGIIVGVFKITDPEGVATIGNLEVEEGPLSGDALERLQREBQW 932
Db 827 HFSLDIDVCGTDLNEDLGVMVIFIKITQDGHARLGNLEFLEKPLVGEALARKRAEKW 886
Qy 933 KIOWTRREEDRRYMAKQAVDRLYADYQDQQLNPVVEITDLTAAQDLIOSIPVYNEM 992
Db 887 RDKREKLEWETNIVYKAKESVDALFVNSQYDQQLADTNIAHIAADKRVHSIREAYLPE 946
Qy 993 FPEIPGMNNTKFTLTDLRLOQAWSLYDORNAIPNGDFRNGLSNNATPGVEV-QQINHTS 1051
Db 947 LSVIPGVNAALFELEGRIPTAFSLYDARNVKNQDFNGLSCNNVKGHVDFVEQNNQRS 1006
Qy 1052 VLVIPNDEQVSOQFTVOPNORYVLRVARTARKEGVNGVSVIRDCGNQTEITFS----- 1105
Db 1007 VLVVPEAEVSOBRVCPGRGYILRVYAYKEGYGEGCVTHIENNTDELKFSNCVEE 1066
Qy 1106 -----ASDYDTN-----GMNTQVSNNTNGYNTNAYNTQASSTNGYNANNMYTQAS 1152
Db 1067 IYPNNTVTCNDYTVNOEYGGAY---TSRNRGY--NEAPSPADYASVYEKSY--TDGR 1119
Qy 1153 NTNGYNTSNVNDQT---GYITKVTTFIPYTDQWIMSETEGTFYIESVELIV 1203
Db 1120 RENPCFNRGYRDYTPLPVGVYTKLEYFPETDKWIEBIGTEGTFIVDSVELLL 1174

RESULT 14
Q9R826 PRELIMINARY; PRT; 1178 AA.
ID Q9R826;
AC Q9R826;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE Crystal toxin protein.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Makhdoom R., Riazuddin S.;
RT "Sequence of a novel gene from a variant of Bacillus thuringiensis.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ130970; CAAL0270.1; -.
DR HSP; P02965; IC1Y.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1178 AA; 133270 MW; B6C016781EB3F0F4 CRC64;

Query Match 31.98; Score 2020.5; DB 2; Length 1178;
Best Local Similarity 39.18; Pred. No. le-107;
Matches 491; Conservative 186; Mismatches 423; Indels 155; Gaps 36;

Qy 23 DSNRYPRANE--PTNALQNDYKDYLKMSAGNASEYPGSPVLSYGQDAKAA---IDIV 77
Db 2 DNN--PNINECIPNCLN-----PEVELGGERIETGYTPIDIS 39
Qy 78 GKLSGLGVPPVPGTIVSYLTQIDILWPSGKSQWEIPMEQVEELINQIAEYARNKALS 137
Db 40 LSLTOFLLESEFV-PGAGVPLGLVDIIWIGIFGPSQWDAFLVQIEQLINRIEFAFNAQIS 98
Qy 138 ELEGIGNYQLYLTALBEEWENPNRSRALRDVRNREFILDSLFQYMPSPRVTFEVPPL 197
Db 99 RLEGLSNLYQIYAESFREFWEADPTNPALRBEEMIQFNDMNSALTATPALLAVQNYQVPLL 158
Qy 198 TVYAMAANLHLLKDAISIFGEEGWSSTTTNNYVDRQMKLTAEYSDRHCVKWYETGLAKL 257
Db 159 SVYVOAANLHLSVLRDVSFQGRWGFDAAATNSRNDLTRIGNYTDYAVRWYNTGLERV 218
Qy 258 KGTSAKQWVDYNQFRREMTLAVLDVVALFPNYPYTDRTYPMETKAQLTRVYVDPL-----G 312
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```
Db 219 WGPDSRDWVRYNQFRELTLTVLDIVLALFPNYSRRYPRTVSQLTREIYTNVLENFDG 278
Qy 313 AVNVSSIGSWYDKAPSGVTESSVIRPVPFVDTGLTVYTQSRSSISSARYIRHWAGHOI 372
Db 279 SFGSAQG-----IERS-IRSPHMLDILNSITTYTDAH-----RGYTWSHQOI 321
Qy 373 SYHRV--SRGSNLQOMYGNTQNHLSTSTP-DFTNYDIYKTLSDKDAVLDDIVVPGYVTFP 429
Db 322 MASPVGSGPEFTFPLYGTMGNAAPQORIVAQLQGVYRTLSS-----TFY 367
Qy 430 GMEVEFFFMVNLNTR-----KTLKYNPVSKOIIASTRSELELPELTPETSQPN 478
Db 368 RRP-----FNIIG-INNOQLSVLDCTEPAYGTSNLPBAVYRKSGTVDSLDIPQNNVPP 422
Qy 479 YESYSHRLCHITISIPATGNTTGL-----VPVFSWTHESADLNNTIYSDKITOIIPAVKWDN 534
Db 423 RQGFSHRLSHVSMFRSGSSNSVSIIRAPMFSWIHSABFNIIIASDSITQIIPAVK--GN 480
Qy 535 LPF--VPVVGPGHGTGDLLOYNRSTGSGVTFLFARVGLALEKAG-KYRVRLRYATDADIV 592
Db 481 FLFNGSVISGPGTGGDLVRLNSSGNNIQNRGYIEVPIHPFSTSTRYRVRYASVTPPIH 540
Qy 593 LHYN--DAQI---QMPKTMNPGEDLTSTK---PKVADATITLNLATDSSLSLAKHNLGEDP 644
Db 541 LNVNMGNSSIFSNTVPATATSLDNLQSSDFGYPESANAFTS-----SLGNIQVGRN 591
Qy 645 NSTLSGIVYVDRIEFIPVDTEYAEODLEAAKAVNALFTNTKD-GLRPGVTDYEVNOAA 703
Db 592 FSGTAGVI-IDREFIPVTATLEAEYNLEKRAKAVNALFTSTNQLGKTNVTVDYHIDQVS 650
Qy 704 NLVECLSDDLLYPNEKRLLLFDVAEREKRLSEARNLLQDPPQIEIN--GENGWTASTTGIEVI 761
Db 651 NLVTYLSDFECLDEKRELSEKVKHAKRLSDERNLQDSNPKDINRQPERGCGSGTGITQI 710
Qy 762 EGDALEKGRVLRPGAREIDTETPTLYLYQKVEEVLKPYTRYRLRGLGFGVSSQGLEIFTI 821
Db 711 GGDVFKENYVTLSTGTFD---ECYPTLYQKIDESKLKAFTRYQLRGYIEDSQLEIYLI 767
Qy 822 RHQTNRIKVNPPD---LLPDVSPVNSDGSINRCSEQKYVNSRLEVENRSGE-----AH 872
Db 768 RYNAKHETVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSH 827
Qy 873 EFSIPIDTGEIDYNENAGIIVGVFKITDPEGVATIGNLEVEEGPLSGDALERLQREBQW 932
Db 828 HFSLDIDVCGTDLNEDLGVMVIFIKITQDGHARLGNLEFLEKPLVGEALARKRAEKW 887
Qy 933 KIOWTRREEDRRYMAKQAVDRLYADYQDQQLNPVVEITDLTAAQDLIOSIPVYNEM 992
Db 888 RDKREKLEWETNIVYKAKESVDALFVNSQYDQQLADTNIAHIAADKRVHSIREAYLPE 947
Qy 993 FPEIPGMNNTKFTLTDLRLOQAWSLYDORNAIPNGDFRNGLSNNATPGVEV-QQINHTS 1051
Db 948 LSVIPGVNAALFELEGRIPTAFSLYDARNVKNQDFNGLSCNNVKGHVDFVEQNNQRS 1007
Qy 1052 VLVIPNDEQVSOQFTVOPNORYVLRVARTARKEGVNGVSVIRDCGNQTEITFS----- 1105
Db 1008 VLVVPEAEVSOBRVCPGRGYILRVYAYKEGYGEGCVTHIENNTDELKFSNCVEE 1067
Qy 1106 -----ASDYDTN-----GMNTQVSNNTNGYNTNAYNTQASSTNGYNANNMYTQAS 1152
Db 1068 IYPNNTVTCNDYTVNOEYGGAY---TSRNRGY--NEAPSPADYASVYEKSY--TDGR 1120
Qy 1153 NTNGYNTSNVNDQT---GYITKVTTFIPYTDQWIMSETEGTFYIESVELIV 1203
Db 1121 RENPCFNRGYRDYTPLPVGVYTKLEYFPETDKWIEBIGTEGTFIVDSVELLL 1175

RESULT 15
Q45768 PRELIMINARY; PRT; 1178 AA.
ID Q45768;
AC Q45768;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
```

01-DEC-2001 (TreeBLrel. 19, Last annotation update)  
DE Gene, complete cds.  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
OC Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=PS85A1;  
RC Feitelson J.S.;  
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.  
DR EMBL; N73249; AA73077.1; --  
DR HSRF; P02965; IC1Y.  
DR InterPro; IPR001178; Endotoxin.  
DR Pfam; PF00555; endotoxin; 1.  
SQ SEQUENCE 1178 AA; 133296 MW; 1336524F410E8863 CRC64;

Query Match 31.9%; Score 2017.5; DB.2; Length 1178;  
Best Local Similarity 39.3%; Pred. No. 1.5e-107;  
Matches 489; Conservative 187; Mismatches 434; Indels 135; Gaps 34;

QY 23 DGNRYPPANE--PTNALQNDYKYLKMSAGNASEYPGSEVLVSQDAKAA---IDIV 77  
DB 2 DNN--PINECPYCLSN-----PEVLGGERIETGYTIDIS 39  
QY 78 GKLLSGLGVFPVGVPIVSLYQLTIDILWPSEKESQWIFMEQVEELINQIAEYARNKALS 137  
DB 40 LSLTQFLLEFV-PCGAGVGLVDLIINGIFGPGQDAFLVQIQELINQIEBEARNQALS 98  
QY 138 ELKGLNNYQLYLTALKEEHPNPGSRALRDVNRREILDSLTQVMPFRVNTFVPL 197  
DB 99 RLEGLSNLYQIYAESPREWEADPTNPALEEMRIQFNDMNSALTTPALLAVQNYQVPLL 158  
QY 198 TVYMAANLHLILLKXASIFGREGWSTTTINNYDROMKLTAEYSDHCXKXVETGLAKL 257  
DB 159 SVYQAANLHLSVLRDVSFPGRWGDAATINSRYNDLRLIGNYTDYAVRWYNTGLERV 218  
QY 258 KGTSAKQVYDQFREMFLAVLDVVALFPNYDTRYPMETRAQLTREVYTDPL-----G 312  
DB 219 WGPDSRDVRYNQFREELTVDLIDVALFPNYDSRYPIRTVSQLTREIYTNVPLENFDG 278  
QY 313 AVNVSIGSWYDKAPSGFVIESVIRPPHVDYITGLTVYQTSRSISSARYIRHWAGHQI 372  
DB 279 SFRGSAQG-----IERS-IRSPHLMIDLNSITITVDAAH-----RGYYNSGHQI 321  
QY 373 SYHRV--SRGSNLQMGVGNLHSTFP-DPTNYDIYKLSKDAVLIDIVPGYIYIP- 428  
DB 322 MASPVGSGPEFTFPLYGTMGNAAPQORIVAQLGQGYRTLSSTL-----YRRPFN 372  
QY 429 FGMPEVEFFPMQNLNTRKTLKYNPVSKDIIASTRDSLELPPETSDOPNYESYSHRLCH 488  
DB 373 IGINNQQLSVLDGTEPAYGTSSNLPRAVYRKSGTVSDLSDEIPPQNNVPPRQGFSHRLSH 432  
QY 489 ITSIPATGNTTGL-----VPVFSWTHRSADLNNTIYDKITQIPAVKCDNLPF-VPVVKG 543  
DB 433 VSMFRSGFNSVSVIIIRAPMFWIHSABENIIASDSITQIPAVK--GNFLPNSGVISG 490  
QY 544 PGHTGGDLLOYNRSTGVTGLFLARYGLALEKAG-KYRVLRYATADIVLWV--DAQI 600  
DB 491 PGFTGGDLVRIANSNGNINQNGRYEIPPIHPSTSTRYRVRYASVTPPIHLNVNWNSSI 550  
QY 601 ---QMPKTNWPGEDLTSKT---PKVADAITLNLATDSSLAKHLNIGEDPNSTLSGIVVY 654  
DB 551 PNTVPATATSLDNLQSDFGYFESNAFTS-----SLGNIVGVNRFSGTAGVI-I 600  
QY 655 DRIFIPVDTEYAEQDLEAKAKAVNALPTNTKD-GLRPGVTDYEVNQANLVCELSDDL 713  
DB 601 DRFEIPVTATLEAEYNLERAKAVNALPTSTNQLGKTNVTDYHIDQVSNLVYLSDEF 660  
QY 714 YNPKELLFDVAEAKRLSEARNLQDDPQIEIN--GENGWTAISTGIEVIEGDALEPKRY 771  
DB 661 CLDEKRELSEKVKHAKRLSDERNLQDSNPKDINRQPERGWGGSTGITIQGGDDVFKENY 720

QY 772 LRLPGAREIDTETPTLYLYQKVEGVLPKPYTRYLRGPFVSGSQGLEIFTIRHQTNRIVKN 831  
DB 721 VTLSTGTFD---ECPTYLYQKIDESKLKAFTRYQLRGYIEDSODLEIYLIRYNAKHETVN 777  
QY 832 VPDD-----LLPDVSPVNSDGSINRCSEQKYNSRLEVENRSGE-----AHBESIPIDTGE 882  
DB 778 VPGTSLMPLSAQSPIGKGBFNRCAPHLEWNPDLDCSRDGEKCAHSHHFSLDIDVGC 837  
QY 883 IDYNENAGIWTGFKITDPGKATLGNLSELVEGLPSGDALERLQREEQOWKIQTMTRRRE 942  
DB 838 TDLNEDLGVWIFKIKTODGHARLGNLEFLEKPLVGEALARVKAEEKWRDKREKLEWE 897  
QY 943 TDRRYMASQAVDRLYADYQOQLNPDVEITDLTAAQDLSIOSIPVYNNEMFPEIPGMNT 1002  
DB 898 TNIVYKEAKESVDALFVNSQYDQLQADTNIAHIAADKRVHSIREAYLPESLVIQGVNAA 957  
QY 1003 KFTELTDLQOAWSLYDORNAIPNGDFNGLSNWNAITPGVEV-QQINHTSVLVIWNDEQ 1061  
DB 958 IPEELGRIPTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNQRSVLVVPWEAE 1017  
QY 1062 VSQOFTVOPNORYLVRVTARKEGVNGVYSIRDGNQOTETLTFSS-----AS 1107  
DB 1018 VSQEVRCVPCRGYILIRVTAYKEGYEGCVTHEIENNTDELKFSNCVEEIIYPNNVTTCN 1077  
QY 1108 DYDTN-----GMVNTQVSNVTNGYNTNAYNTQASSTNGYNANNMYNTQASNTNGYNTNSV 1162  
DB 1078 DYTVAQEEYGGAY---TSRNRGY--NEAPSPVADYASVVEEKSY--TDCRRNPPCEFNRG 1130  
QY 1163 YNDQT-----GYTKVTVPYTDQMWIEMSETEGTFYIESVELIV 1203  
DB 1131 YRDYTPLPVGYVTKELFPPETDKVIBIGETEGTFIVDSVELLL 1175

Search completed: January 7, 2003, 05:16:23  
Job time : 90 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 7, 2003, 03:35:28 ; Search time 69 Seconds  
(without alignments)  
2328.989 Million cell updates/sec

Title: US-10-032-717-2

Perfect score: 6332

Sequence: 1 MSPNNQNEYIIDATPSTSV.....MSETEGTYIESVELVDVE 1206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_101002.\*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
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10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
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12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
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16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------|
| 1          | 6332   | 100.0       | 1206   | 23 | AAU99255    |
| 2          | 5673   | 89.6        | 1210   | 23 | AAU99256    |
| 3          | 4959.5 | 78.3        | 1169   | 17 | AAW06417    |
| 4          | 3951.5 | 62.4        | 1157   | 13 | AAK28900    |
| 5          | 3950.5 | 62.4        | 1157   | 13 | AAK28997    |
| 6          | 3950.5 | 62.4        | 1157   | 14 | AAK33768    |
| 7          | 3950.5 | 62.4        | 1157   | 17 | AAW06418    |
| 8          | 3943.5 | 62.3        | 1157   | 13 | AAK27343    |
| 9          | 3940.5 | 62.2        | 1157   | 14 | AAK44208    |
| 10         | 3511   | 55.4        | 669    | 23 | AAU99259    |

|    |        |      |      |    |          |                    |
|----|--------|------|------|----|----------|--------------------|
| 11 | 3511   | 55.4 | 669  | 23 | AAU99262 | Bacillus thuringie |
| 12 | 3502   | 55.3 | 667  | 23 | AAU99257 | Bacillus thuringie |
| 13 | 3499   | 55.3 | 673  | 23 | AAU99260 | Bacillus thuringie |
| 14 | 3499   | 55.3 | 673  | 23 | AAU99265 | Bacillus thuringie |
| 15 | 3499   | 55.3 | 673  | 23 | AAU99271 | Bacillus thuringie |
| 16 | 3485.5 | 55.0 | 670  | 23 | AAU99266 | Bacillus thuringie |
| 17 | 3485.5 | 55.0 | 670  | 23 | AAU99273 | Bacillus thuringie |
| 18 | 3246.5 | 51.3 | 1167 | 23 | AAU0281  | Bacillus thuringie |
| 19 | 3229   | 51.0 | 616  | 23 | AAU99264 | Bacillus thuringie |
| 20 | 3217   | 50.8 | 620  | 23 | AAU99268 | Bacillus thuringie |
| 21 | 3217   | 50.8 | 620  | 23 | AAU99269 | Bacillus thuringie |
| 22 | 3217   | 50.8 | 620  | 23 | AAU99272 | Bacillus thuringie |
| 23 | 3203.5 | 50.6 | 617  | 23 | AAU99270 | Bacillus thuringie |
| 24 | 3203.5 | 50.6 | 617  | 23 | AAU99274 | Bacillus thuringie |
| 25 | 3021   | 47.7 | 1149 | 14 | AAK32354 | Coleoptera toxin f |
| 26 | 3021   | 47.7 | 1149 | 15 | AAK51692 | B.thuringiensis se |
| 27 | 2852   | 45.0 | 673  | 23 | AAU99263 | Bacillus thuringie |
| 28 | 2821   | 44.6 | 667  | 23 | AAU99258 | Bacillus thuringie |
| 29 | 2601.5 | 41.1 | 1157 | 20 | AAW84585 | Amino acid sequenc |
| 30 | 2600.5 | 41.1 | 1157 | 20 | AAW84586 | Amino acid sequenc |
| 31 | 2600.5 | 41.1 | 1157 | 20 | AAW84576 | Amino acid sequenc |
| 32 | 2599.5 | 41.1 | 1157 | 20 | AAW84582 | Amino acid sequenc |
| 33 | 2599.5 | 41.1 | 1157 | 20 | AAW84567 | Amino acid sequenc |
| 34 | 2599.5 | 41.1 | 1157 | 20 | AAW84569 | Amino acid sequenc |
| 35 | 2598.5 | 41.0 | 1157 | 20 | AAW84584 | Amino acid sequenc |
| 36 | 2598.5 | 41.0 | 1157 | 20 | AAW84572 | Amino acid sequenc |
| 37 | 2598.5 | 41.0 | 1157 | 20 | AAW84575 | Amino acid sequenc |
| 38 | 2598.5 | 41.0 | 1157 | 20 | AAW84577 | Amino acid sequenc |
| 39 | 2598.5 | 41.0 | 1157 | 20 | AAW84578 | Amino acid sequenc |
| 40 | 2597.5 | 41.0 | 1157 | 20 | AAW84592 | Amino acid sequenc |
| 41 | 2597.5 | 41.0 | 1157 | 20 | AAW84573 | Amino acid sequenc |
| 42 | 2596.5 | 41.0 | 1157 | 20 | AAW84586 | Amino acid sequenc |
| 43 | 2596.5 | 41.0 | 1157 | 20 | AAW84579 | Amino acid sequenc |
| 44 | 2595.5 | 41.0 | 1157 | 15 | AAK48678 | Insecticidal proto |
| 45 | 2595.5 | 41.0 | 1157 | 20 | AAW84588 | Amino acid sequenc |

#### ALIGNMENTS

#### RESULT 1

AAU99255  
ID AAU99255 standard; Protein; 1206 AA.

XX AC AAU99255;

XX DT 07-OCT-2002 (first entry)

XX DE Bacillus thuringiensis Cry1218-1 protein sequence.

XX KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;

XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;

XX KW insect target range; endotoxin; Cry1218.

XX OS Bacillus thuringiensis.

XX PN WO200234774-A2.

XX PD 02-MAY-2002.

XX PF 24-OCT-2001; 2001WO-US45468.

XX PR 24-OCT-2000; 2000US-242838P.

XX PR 23-OCT-2001; 2001US-0032717.

XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.

XX PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;

XX XX WPI; 2002-519178/55.

XX DR N-PSDB; ABK87234.

XX PT New isolated pesticidal polypeptide useful for impacting insect pest



PT e.g. Colorado potato beetle -

PS Claim 4; Page 96-98; 176pp; English.

XX The present invention relates to a new pesticidal polypeptide. The  
CC invention is useful for impacting an insect pest by applying the  
CC the molecules of the invention to the environment of the insect pest by  
CC spraying, dusting, broadcasting, or seed coating, where the insect pest  
CC is selected from Colorado potato beetle, western corn rootworm or  
CC southern corn rootworm. The invention is also useful for increasing  
CC insect target range and for producing transgenic microorganisms and  
CC plants that express the pesticidal polypeptide. The invention is also  
CC useful for producing transformed plants and in transforming any organism  
CC to produce the pesticidal polypeptide of the invention. The present  
CC amino acid sequence represents a *Bacillus thuringiensis* wild-type  
CC Cry1218 endotoxin protein.

XX Sequence 1206 AA;

Query Match 100.0%; Score 6332; DB 23; Length 1206;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPNNQNEYEIIIDATPTSVSNDSNRYPFANEPTNALQNDYKDYLMKMSAGNASEYFGSP 60  
DB 1 MSPNNQNEYEIIIDATPTSVSNDSNRYPFANEPTNALQNDYKDYLMKMSAGNASEYFGSP 60  
QY 61 EVLYSGQDAKAAADIIVGKLLSGIGVPGVPIVSLYTQIIDILWPSGKSWEIFMEQVE 120  
DB 61 EVLYSGQDAKAAADIIVGKLLSGIGVPGVPIVSLYTQIIDILWPSGKSWEIFMEQVE 120  
QY 121 ELINQIAEYARNKALSEGLEGNQYQLYLTALBEWENPNGSRALRDVNRPFILSLF 180  
DB 121 ELINQIAEYARNKALSEGLEGNQYQLYLTALBEWENPNGSRALRDVNRPFILSLF 180  
QY 181 TOYMPSFRVTNFEVFPFLTVYAMAANLHLLLDKASIFGEEWGSSTTTNNYDQMKLTA 240  
DB 181 TOYMPSFRVTNFEVFPFLTVYAMAANLHLLLDKASIFGEEWGSSTTTNNYDQMKLTA 240  
QY 241 EYSDHCVKWYETGLAKLGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDRTYPMETKA 300  
DB 241 EYSDHCVKWYETGLAKLGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDRTYPMETKA 300  
QY 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGFVIESVIRPPHVFYITGLTVYTOSRSISS 360  
DB 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGFVIESVIRPPHVFYITGLTVYTOSRSISS 360  
QY 361 ARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFTDFTNYDIYKTLSDAVLLDIV 420  
DB 361 ARYIRHWAGHQISYHRVSRGSLNQMYGTNQNLHSTSTFTDFTNYDIYKTLSDAVLLDIV 420  
QY 421 YPGYTYIFFGMPVEFFPMVGNLNTRKTLKYNPYSKDIIASTRSELELPETSDQPNYE 480  
DB 421 YPGYTYIFFGMPVEFFPMVGNLNTRKTLKYNPYSKDIIASTRSELELPETSDQPNYE 480  
QY 481 SYSHRLCHITSIPTAGNTTGLVPVFSWTHRSADLNNTIYSKTIQIPAVKCDNLFPVFPV 540  
DB 481 SYSHRLCHITSIPTAGNTTGLVPVFSWTHRSADLNNTIYSKTIQIPAVKCDNLFPVFPV 540  
QY 541 VKGPGHTGGDLLQNRSTGSGVTFLFARYGLALEKAGYRVLRYATDADIVLHVNDQAI 600  
DB 541 VKGPGHTGGDLLQNRSTGSGVTFLFARYGLALEKAGYRVLRYATDADIVLHVNDQAI 600  
QY 601 QMPKTMNPGEDLTSTKTFKVAADAIITLNLATDSSIALKHNKGEDPNSTLSGIVYVDRIEPI 660  
DB 601 QMPKTMNPGEDLTSTKTFKVAADAIITLNLATDSSIALKHNKGEDPNSTLSGIVYVDRIEPI 660  
QY 661 PVDETYEAOQLEAAKAVNALFTNTKDLRPGVTDYEVNQAAANLVECLSDLYPNEKRL 720  
DB 661 PVDETYEAOQLEAAKAVNALFTNTKDLRPGVTDYEVNQAAANLVECLSDLYPNEKRL 720  
QY 721 LFDVAVREAKRLSEARNLLQDPDFQIEINGENGWTAETGIEVGDALEFKGRYLRLPGAREI 780  
DB 721 LFDVAVREAKRLSEARNLLQDPDFQIEINGENGWTAETGIEVGDALEFKGRYLRLPGAREI 780

DB 721 LFDVAVREAKRLSEARNLLQDPDFQIEINGENGWTAETGIEVGDALEFKGRYLRLPGAREI 780  
QY 781 DTETYPYLYOKVEEGLVKEPYRYLRGPFVGSOGLEIFTRHOTNRIYKGNVDPDLLPDV 840  
DB 781 DTETYPYLYOKVEEGLVKEPYRYLRGPFVGSOGLEIFTRHOTNRIYKGNVDPDLLPDV 840  
QY 841 SPVNSDGSINRCSEQKYVNSRLVENRSGEAHFFSIPIDTGEIDYNNAGIYWGFKITDP 900  
DB 841 SPVNSDGSINRCSEQKYVNSRLVENRSGEAHFFSIPIDTGEIDYNNAGIYWGFKITDP 900  
QY 901 EGVATIGNLVBEGPLSGDALRLOREBEQOWKIOMTRREEDTDRRYMASKQAVDRLYAD 960  
DB 901 EGVATIGNLVBEGPLSGDALRLOREBEQOWKIOMTRREEDTDRRYMASKQAVDRLYAD 960  
QY 961 YQOQQLNPVDEIITDLTAAQDLIOSIPVYVNMPEPIPGMNYTKFTELTDRLOQAWSLYDQ 1020  
DB 961 YQOQQLNPVDEIITDLTAAQDLIOSIPVYVNMPEPIPGMNYTKFTELTDRLOQAWSLYDQ 1020  
QY 1021 RNAIPNGDFRNLGSLNNWNPATPGVEVQIQINHTSVLIVPNWDEQVSOQFTVQPNQRYVLRVTA 1080  
DB 1021 RNAIPNGDFRNLGSLNNWNPATPGVEVQIQINHTSVLIVPNWDEQVSOQFTVQPNQRYVLRVTA 1080  
QY 1081 RKEGVNGYVSIIRDGNGQTETLTFSASDYDTNGMYNTQVNTNGYNTNNAYNTQASSTNG 1140  
DB 1081 RKEGVNGYVSIIRDGNGQTETLTFSASDYDTNGMYNTQVNTNGYNTNNAYNTQASSTNG 1140  
QY 1141 YNANNMYNTQASNTNGYNTNSVYNDQGYITKTFTPTPYTDQMWIEMSETEGTYIESVE 1200  
DB 1141 YNANNMYNTQASNTNGYNTNSVYNDQGYITKTFTPTPYTDQMWIEMSETEGTYIESVE 1200  
QY 1201 LIVDVE 1206  
DB 1201 LIVDVE 1206  
RESULT 2  
AAU99256  
ID AAU99256 standard; Protein; 1210 AA.  
XX  
AC AAU99256;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE *Bacillus thuringiensis* Cry1218-2 protein sequence.  
XX  
KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;  
KW Colorado potato beetle; western corn rootworm; southern corn rootworm;  
KW insect target range; endotoxin; Cry1218.  
XX  
OS *Bacillus thuringiensis*.  
XX  
PN WO200234774-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 24-OCT-2001; 2001WO-US45468.  
XX  
PR 24-OCT-2000; 2000US-242838P.  
PR 23-OCT-2001; 2001US-0032717.  
XX  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
XX  
PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;  
XX WPI; 2002-519178/55.  
DR N-PSDB; ABK87235.  
XX  
PT New isolated pesticidal polypeptide useful for impacting insect pest  
PT e.g. Colorado potato beetle -  
XX  
PS Claim 4; Page 103-105; 176pp; English.  
XX  
CC The present invention relates to a new pesticidal polypeptide. The

invention is useful for impacting an insect pest by applying the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm. The invention is, also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present amino acid sequence represents a *Bacillus thuringiensis* wild-type Cry1218 endotoxin protein.

Sequence 1210 AA;

Query Match 89.6%; Score 5673; DB 23; Length 1210;

Best Local Similarity 89.2%; Pred. No. 0;

Matches 1095; Conservative 33; Mismatches 61; Indels 38; Gaps 7;

Qy 1 MSPNNQNEYIIDATPSTSVSDNSRNPANETNALQNDYKDYLMGAGNASEYPGSP 60  
 Db 1 MSPNNQNEYIIDATPSTSVSDNSRNPANETNALQNDYKDYLMGAGNASEYPGSP 60  
 Qy 61 EYLVSGQDAKAAIDIVGKLSGLGVFPVGPPIVSLVTQLIDILMPSGKSWEIFMEQYE 120  
 Db 61 EYLVSGQDAKAAIDIVGKLSGLGVFPVGPPIVSLVTQLIDILMPSGKSWEIFMEQYE 120  
 Qy 121 ELINQKIAFYARNKALSELEGLNNYQLYLTALAEENPNPNSRALRDVRNRFELIDSLF 180  
 Db 121 ELINQKIAFYARNKALSELEGLNNYQLYLTALAEENPNPNSRALRDVRNRFELIDSLF 180  
 Qy 181 TOYMSPRVNTEVEVPLTVYMAANLHLLLLKDAISFGBEWGSTTTINNYDROMKLT 240  
 Db 181 TOYMSPRVNTEVEVPLTVYMAANLHLLLLKDAISFGBEWGSTTTINNYDROMKLT 240  
 Qy 241 EYSDHCVKWYETGLAKTSAQWVDYVQPREMTLAVLDVVALPNDYDTRTPMETKA 300  
 Db 241 EYSDHCVKWYETGLAKTSAQWVDYVQPREMTLAVLDVVALPNDYDTRTPMETKA 300  
 Qy 301 QLTREYTDPLGANVSSIGSYDKAPSGVIESVIRPPHVPDYITGLTVYTQSRSS 360  
 Db 301 QLTREYTDPLGANVSSIGSYDKAPSGVIESVIRPPHVPDYITGLTVYTQSRSS 360  
 Qy 361 ARYIHWAGHQISYHRVSGSNLQMGYGNQNLHSTSTDFPDNYDIYKTLSDKAVLLDIV 420  
 Db 361 ARYIHWAGHQISYHRVSGSNLQMGYGNQNLHSTSTDFPDNYDIYKTLSDKAVLLDIV 420  
 Qy 421 YPGYTYIPGMEVEFPFMVQNLNNTKTLKYNPVSKDIIASTEDSELEPPETSDQPNYE 480  
 Db 421 YPGYTYIPGMEVEFPFMVQNLNNTKTLKYNPVSKDIIASTEDSELEPPETSDQPNYE 480  
 Qy 481 SYSHRLCHITSPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-- 538  
 Db 481 SYSHRLCHITSPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-- 538  
 Qy 539 ----PVVKGPGHTGDLQYNSRSGVGTFLFARYGLALEKAGK-YRVLRYATDADIVL 593  
 Db 541 GPNNTVSGPGFTGGGIIVKRN-----GVIIHMEVKISDINKYSMRIRVASANTTF 595  
 Qy 594 HYNDQIQM-----PKTMNPGEDLTSTKTKVADAITTLNLTADSSLALKENLGEDPNSTLS 649  
 Db 596 YINPSEENVKSHQAQTMNKGALTYNKNFYA-TLPPIKFTT-----TEPPITLG 643  
 Qy 650 GI-----VYVDRIEFPVDETYEARQDLLEAKKAVNALFTNTKGLRPGVTDYEV 699  
 Db 644 ALPEAEEDFLGIEAYIDRIEFPVDETYEARQDLLEAKKAVNALFTNTKGLRPGVTDYEV 703  
 Qy 700 NOANALVECLSDDLVYNEKRLLFDAVREAKRLSEARNLLQDPDFQINGENGWGTASTGIE 759  
 Db 704 NOANALVECLSDDLVYNEKRLLFDAVREAKRLSEARNLLQDPDFQINGENGWGTASTGIE 763  
 Qy 760 VIEGDALFKGRVLRLEPCAREIDTETPTVLYQKVEGVLPKPYTRYRLRFGVSSQGLEIF 819  
 Db 764 VIEGDALFKGRVLRLEPCAREIDTETPTVLYQKVEGVLPKPYTRYRLRFGVSSQGLEIF 823

Qy 820 TIRHQTNRIVKNVPDDLLPDVSPVNSDGSINRCSQKYVNSRLEVENRSGEAHEFSIPID 879  
 Db 824 TIRHQTNRIVKNVPDDLLPDVSPVNSDGSINRCSQKYVNSRLEVENRSGEAHEFSIPID 883  
 Qy 880 TGEIDYNNAGIWWGPKITDPEGYATLGNLELVEGPIISGDALERLQREEQWQKIQMTR 939  
 Db 884 TGEIDYNNAGIWWGPKITDPEGYATLGNLELVEGPIISGDALERLQREEQWQKIQMTR 943  
 Qy 940 REETDRRYWASKQAVDRLYADYQDQQLNPDVBEITDLTAAQDLIQSIPIVYNNMFPEIPCM 999  
 Db 944 REETDRRYWASKQAVDRLYADYQDQQLNPDVBEITDLTAAQDLIQSIPIVYNNMFPEIPCM 1003  
 Qy 1000 NYTKFTELTDLQQAWSLYDQRNAPNGDFRNLGNLSNNWATPGVEVQOQINHTSVLIPNWD 1059  
 Db 1004 NYTKFTELTDLQQAWSLYDQRNAPNGDFRNLGNLSNNWATPGVEVQOQINHTSVLIPNWD 1063  
 Qy 1060 EQVSQOFTVQPNQRYVLYVTARKEGVNGYVIRGGNQOTELTTFASDYDNGMYNTOV 1119  
 Db 1064 EQVSQOFTVQPNQRYVLYVTARKEGVNGYVIRGGNQOTELTTFASDYDNGMYNTOV 1123  
 Qy 1120 SNTNGYNTNNAVNTQASSTNGYNANNMYNTQASNTNGYNTNSVYNDQTYITKTVTFIPY 1179  
 Db 1124 SNTNGYNTNNAVNTQASSTNGYNANNMYNTQASNTNGYNTNSVYNDQTYITKTVTFIPY 1183  
 Qy 1180 TDQMIEMSETEGTFYIESVELIVDVE 1206  
 Db 1184 TDQMIEMSETEGTFYIESVELIVDVE 1210

# RESULT 3

AAW06417  
 ID AAW06417 standard; Protein; 1169 AA.

XX AC AAW06417;

XX DT 28-JAN-1997 (first entry)

XX DE Antiscarab pest toxin 50C(b).

XX KW Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae; pest control;  
 larval stage insect; grain; tuberous crop; white grub; chafer grub;  
 cyclocephala; popillia.

XX OS *Bacillus thuringiensis* strain kumamotoensis.

XX FN US5554534-A.

XX PD 10-SEP-1996.

XX PF 30-SEP-1994; 94US-0315468.

XX PR 01-FEB-1993; 93US-0014941.

XX PR 16-DEC-1991; 91US-0808316.

XX PR 30-JAN-1992; 92US-0828430.

XX PR 30-SEP-1994; 94US-0315468.

XX PA (MYCO ) MYCOGEN CORP.

XX PI Foncerrada L, Michaels TE, Narva KE;

XX DR WPI; 1996-424659/42.

XX PT N-PSDB; AAT43221.

XX PT New nucleic acid encoding *B.thuringiensis* toxin active against  
 scarab(s) - also related toxin and transformed microbes, effective  
 against adult pests and their larvae

XX PS Claim 2; Column 29-36; 24pp; English.

XX CC AAW06417-W06419 represent toxins that are active against scarab pests.

XX CC The DNA encoding this sequence was isolated from the *Bacillus*  
*thuringiensis* strain kumamotoensis. Insects in the family Scarabaeidae

CC constitute a serious pest control problem, especially when destructive  
 CC larval stage insects infest high value turf found in golf courses,  
 CC playing fields and lawns. The larvae of many species also attack grains,  
 CC tuberous crops, and ornamentals. The larvae are known as white grubs, or  
 CC chafer grubs, and can be found in decaying organic matter, or in the soil  
 CC where they consume plant roots. In Europe and the U.S. populations of  
 CC these larvae and adults have developed resistance to chemical  
 CC insecticides such as the organochlorines and DDT. These toxin sequences,  
 CC and intact cells that are capable of expressing these proteins, can be  
 CC used to control many pests of the family scarabaeidae, such as species of  
 CC Cyclocephala, and Popillia. The toxins are active against larvae  
 CC (present in soil) and against adults.

xx SQ Sequence 1169 AA;

Query Match 78.3%; Score 4959.5; DB 17; Length 1169;  
 Best Local Similarity 79.8%; Pred. No. 0;  
 Matches 967; Conservative 68; Mismatches 128; Indels 49; Gaps 8;

Qy 1 MSPNNQNEYEIIDATPSTVSNDNSRYPFANEPTNALQNDYKDYLMKMSAGNASRYPGSP 60  
 Db 1 MSPNNQNEYEIIDATPSTVSNDNSRYPFANEPTNALQNDYKDYLMKMSAGNASRYPGSP 60

Qy 61 EVLVSGDAAKAIDIVGKLLSGVFPVGPVIVSLYTQILIDILWPGSKSQWEIFMEQVE 120  
 Db 61 EVLVSGDAAKAIDIVGKLLSGVFPVGPVIVSLYTQILIDILWPGSKSQWEIFMEQVE 120

Qy 121 ELINOKIAEYARKKALSEGLEGNVQVLYLTALKEENPNSGRALDRVNRFEILDSLF 180  
 Db 121 ELINOKIAEYARKKALSEGLEGNVQVLYLTALKEENPNSGRALDRVNRFEILDSLF 180

Qy 181 TOYMPSFRVTNEVPFLTYVMAANLHLLKDDASIFGEWGMSTTTINNYDROMKLTA 240  
 Db 181 TOYMPSFRVTNEVPFLTYVMAANLHLLKDDASIFGEWGLSTSTINNYNRQMKLTA 240

Qy 241 EYSDHCWKYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALLPNDYTRTPMETKA 300  
 Db 241 EYSDHCWKYETGLAKLGTSAKQWVDYNOFRREMTLAVLDVVALLPNDYTRTPMETKA 300

Qy 301 QLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESSVIRPPHVDYITGLTVYQSRSSIS 360  
 Db 301 QLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESSVIRPPHVDYITGLTVYQSRSSIS 360

Qy 361 ARYIRHWAGHQISYHRVSRGSLNQMYGTGNQNLHSTFDFNTYDIYKTLSDKAVLLDIV 420  
 Db 361 DRYMYWAGHQISYKHIGYSSFTQMYGTGNQNLQSTSNFDFNTYDIYKTLSDKAVLLDIV 420

Qy 421 YPGYTYVIFPGMEVEPFMVNQLNTRKTLKYNPVSQDIITASTRDSSELELPETSDQPNYE 480  
 Db 421 YPGYTYVIFPGMEVEPFMVNQLNTRKTLKYNPVSQDIITASTRDSSELELPETSDQPNYE 480

Qy 481 SYSHRLCHLTSIPATGNTGLVPVSWTHRSADLNNTIYSDKLTQIPAVKCDNLPFPVPV 540  
 Db 481 SYSHRLCHLTSIPATGNTGLVPVSWTHRSADLNNTIYSDKLTQIPAVKCDNLPFPVPV 540

Qy 541 VKPGHGTGDLQYNRSTGSGVTLFLARYGLALEKAGKVRVRLRYATDADIVLHV---N 596  
 Db 541 VKPGHGTGDLQYNRSTGSGVTLFLARYGLALEKAGKVRVRLRYATDADIVLHV---N 596

Qy 597 DAQIQMPKT-MNPGE-DLTSKTPKVAADAITLNLATDSSLAKKHNLGEDPNSTLSGIVYV 654  
 Db 597 DAQIQMPKT-MNPGE-DLTSKTPKVAADAITLNLATDSSLAKKHNLGEDPNSTLSGIVYV 654

Qy 655 DRIEFTPVDETVEAEODLEAKKANVALFNTKQGLRPGVTDYEVNQANLVECLSDLLY 714  
 Db 655 DRIEFTPVDETVEAEODLEAKKANVALFNTKQGLRPGVTDYEVNQANLVECLSDLLY 714

Qy 715 PNEKRLLFDAVREAKLSBARNLLQDPDFQEIENGEGWTASTGIEVTEGDALFKGYRL 774  
 Db 715 PNEKRLLFDAVREAKLSBARNLLQDPDFQEIENGEGWTASTGIEVTEGDALFKGYRL 774

Qy 775 PGAREIDTETPTLYLQKVEGVLKPYTRYRLRGFVGSSQGLBIFTRHQTNRIVKNVPD 834  
 Db 775 PGAREIDTETPTLYLQKVEGVLKPYTRYRLRGFVGSSQGLBIFTRHQTNRIVKNVPD 834

Db 770 PGAREIDTETPTLYLQKVEGVLKPYTRYRLRGFVGSSQGLBIFTRHQTNRIVKNVPD 829  
 Qy 835 DLLPVPVNSDGSINRSEOKYVNSRLEVENRSGEAHEFSPIDTGEIDYNNENAGIWWG 894  
 Db 830 DLLPVPVNSDGSINRSEOKYVNSRLEVENRSGEAHEFSPIDTGEIDYNNENAGIWWG 889  
 Qy 895 FKITDPEGVATLGNLELVEEGPLSGDALERLQREEQWQKIOMTRREETDRRYMASKQAV 954  
 Db 890 FKITDPEGVATLGNLELVEEGPLSGDALERLQREEQWQKIOMTRREETDRRYMASKQAV 949  
 Qy 955 DRLYADYQDQQLNPVETDLTAAQDLIQSIPYVYVNEPPEIPGMNYTKFTLTDLQQA 1014  
 Db 950 DRLYADYQDQQLNPVETDLTAAQDLIQSIPYVYVNEPPEIPGMNYTKFTLTDLQQA 1009  
 Qy 1015 WSLYDQRNAIPNGDFRNLGNLSNWNATPGVEVQOINHTSVLVIENWDEQVSSQFTVQPNORY 1074  
 Db 1010 WSLYDQRNAIPNGDFRNLGNLSNWNATPGVEVQOINHTSVLVIENWDEQVSSQFTVQPNORY 1069  
 Qy 1075 VLRVTARKEGVNGVYVIRDDGNQGTETLTFSASDYDTNGMYNTQVSNYNTNGYNTNAYNQ 1134  
 Db 1070 VLRVTARKEGVNGVYVIRDDGNQGTETLTFSASDYDTNGMYNTQVSNYNTNGYNTNAYNQ 1108  
 Qy 1135 ASSTGYNNANNMYNTQASNTNGYNTNAYNQGTETLTFSASDYDTNGMYNTQVSNYNTNGYNTNAYNQ 1194  
 Db 1109 -----MYDTQASNTNGYNTNAYNQGTETLTFSASDYDTNGMYNTQVSNYNTNGYNTNAYNQ 1157  
 Qy 1195 YIESVELIVDVE 1206  
 Db 1158 YIESVELIVDVE 1169

# RESULT 4

AAR28900  
 ID AAR28900 standard; Protein; 1157 AA.  
 XX  
 AC AAR28900;  
 XX  
 DT 01-APR-1993 (first entry)  
 XX  
 DE Toxin 50C.  
 XX  
 KW Endotoxin; acarides; pest; Two Spotted Spider; mite;  
 KW phytophagus.  
 XX  
 OS Bacillus thuringiensis kumamotoensis PS50C.  
 XX  
 PN WO9219106-A.  
 XX  
 PD 12-NOV-1992.  
 XX  
 PF 30-APR-1992; 92WO-US03546.  
 XX  
 PR 30-APR-1991; 91US-0693210.  
 PR 13-SEP-1991; 91US-0759248.  
 PR 30-SEP-1991; 91US-0768141.  
 XX  
 PA (MYCO ) MYCOGEN CORP.  
 XX  
 PI Bagley AL, Cannon RJC, Payne JM;  
 XX  
 DR WPI; 1992-398411/48.  
 DR N-PSDB; AAQ30821.  
 XX

PT New Bacillus thuringiensis isolates and toxins - used for  
 PT controlling acarid pests of livestock, fowl, stored prods. and  
 PT plants

PS Claim 16; Page 53 + 49-51; 62pp; English.

XX Gene sequences encoding a toxin which is active against acarides and  
 CC is obtainable from B. thuringiensis isolates PS17a, PS17b, 33f2,  
 CC PS2A1, PS69D1, PS86A1 and PS50C are given in AAQ30803-07 and  
 CC AAQ30820-21 respectively. The toxin is a delta-endotoxin active against

cc acarid pests, including the Two Spotted Spider mite. The isolates can  
 CC be used against non-phytophagous mites such as acarid pests of livestock,  
 CC fowl and stored prods. The genes can be cloned and used to  
 CC transform other hosts, which can be used to control mites, or in  
 CC the case of transgenic plants, be resistant to mites.

xx  
 SQ Sequence 1157 AA;

Query Match 62.4%; Score 3951.5; DB 13; Length 1157;  
 Best Local Similarity 65.5%; Pred. No. 2e-256;  
 Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

QY 1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTNALQMDYKYLKMSAGNASPYGSP 60  
 DB 1 MSPNNQNEYIIDATPSTSVSNDNRYPFANEPTDALQNMNYKDYKMSGGNPELFGNP 60  
 QY 61 EYLVSGDAKAAADIVKLLSGLGVPFVGPVIVSLYITQIIDILMPSGKSOWEIPMEOVE 120  
 DB 61 EYFIS-SSTIGTIGIVGRILGALGVPPASQIASFYSPFVIGQLWPSKSDVINGEIMERVE 119  
 QY 121 ELINOKIAEYARNKALSELEGLGNNYQLYLTALBEEENPNPGRALDRVRNREFILDSLP 180  
 DB 120 ELVDOKIEKYVDKALAEKLGKALDVIYQOSLEWLENRDARTSRVSVNQFALDLP 179  
 QY 181 TQYMPFRVTFVFFLYVAANLHLLLLKODASIPGEEMGWSTTTINNYDRQMKLTA 240  
 DB 180 VSSIPSPAVSGHEVLLAVYAQAANLHLLLRDASIPGEENGFTPGCISRFNRQVQLTA 239  
 QY 241 EYSDHCWVYETGLAKLGTSAKQWYDYNQFRRENTLAVLDVVALFPNDYTRTPMETKA 300  
 DB 240 EYSDYCVKWKYIGLKLKGTTSKWLNFHQRRENTLVLVLDVLPNDYTHYPIETTA 299  
 QY 301 QLREVTYDPLGAVNVSSIGSWYDKAPSGV- ---IGSSVIRPPHVRDYITGLTVYTOSR 356  
 DB 300 QLREVDYDPLAFNIVTSTGFCNPMWTHSGILFYEVENNVRPPLFDILLSVEINT-SR 358  
 QY 357 ---SISARYIRHWAGHOISYHRVSRGSLAQMYGTQNLHSTSTFTDNYDIYKLSKD 413  
 DB 359 GGITLNDAYINYSGHLYKYRYTA-DSTVITYTANYGRITSEKNSFALEDRIPEINSTV 417  
 QY 414 AVLDDIVPGYTYTFPGMEVEFPVNVQNNRKTLYKNPVSKDIIASTR--DSELELPP 471  
 DB 418 ANLANYTQKAY- ---GVPGSFHFMVKRGTSSTAYLYSKHTALQCGCTQVYESSDEIPL 472  
 QY 472 ETSQPNVYESYSHRLCHITSIPATGNTT- ---GLVPVFWTHRSADLNNTIYSDKITQIPA 528  
 DB 473 DRT-VPAVESYSHRLSHITSFSKNGSAYSGSPFVFWTHTSADLNNTIYSDKITQIPA 531  
 QY 529 VKCWDNLFPV- ---PVVKGPGHGGDLLOYNRSTGSGVTGLFLARYGLALEKAGKYRVLRYA 586  
 DB 532 VK- ---GDMLYLGGSVVQSGFGTGGDILK- ---RTNPSILGTFAVTNGSLSQ- ---RYRVRIYA 585  
 QY 587 ---TDADIVLHVDA- ---QIQMPKTNWPGBDLTSKTPKVAADAITLNL- ---ATDSSLAK- ---H 638  
 DB 586 STTDFEFTLYLGTIEKNRPNKNDMGASLTETPKPASFITDFQFRETQDKILLSMGDF 645  
 QY 639 NLGSDPNSTGLSVVYVDRIEIPVDTEAEQDLEAKKAVNALFTNTKGLRPGVTIYE 698  
 DB 646 SSGQE- ---VYIDRIEIPVDTEAEQDLEAKKAVNALFTNTKGLRPGVTIYE 697  
 QY 699 VNQAANLVECLSDDLIPNEXKLLFDVAREAKRLSEARNLLQDPDQFENGNGWTASTGI 758  
 DB 698 VNQAANLVECLSDDLIPNEXKLLFDVAREAKRLSEARNLLQDPDQFENGNGWAATGI 757  
 QY 759 EVIGSDALFKGYRLRPGAREIDTETPTLYLYQKVEBGLPYTYRYLRGFGVSSQGLEI 818  
 DB 758 EIVEGDVAFKGYRLRPGAREIDTETPTLYLYQKVEBGLPYTYRYLRGFGVSSQGLEI 817  
 QY 819 FTIRHQTNRIVKNVDDLLDPVSPVNSDGSINRCSEQYVNSRLFEVNSGEAHEFSLPI 878  
 DB 818 YTIIRHQTNRIVKNVDDLLDPVSPVNSDGSINRCSEQYVNSRLFEVNSGEAHEFSLPI 877  
 QY 879 DTGBIDYNNAGIWWGPKITDPEGVATLGNLELVEEGLSGDALERLQREEQWQKIOMTR 938

DB 878 DIGELDYNNAGIWWGPKITDPEGVATLGNLELVEEGLSGDALERLQREEQWQKIOMTR 937  
 QY 939 RRETDTRYWASKQAVDRLYADYQDQQLNPDVEITDLTAAQDILLQSIPIYVYNNFPEIPG 998  
 DB 938 RRETDTRYWASKQAVDRLYADYQDQQLNPDVEITDLTAAQDILLQSIPIYVYNNFPEIPG 997  
 QY 999 MNYTKFTELDRLOQAWSLYDORNAIPNGDFRNLGSNNWNPATPGVEQOINHTSVLVIPNW 1058  
 DB 998 MNYTKFTELDRLOQAWSLYDORNAIPNGDFRNLGSNNWNPATPGVEQOINHTSVLVIPNW 1057  
 QY 1059 DEQVSQOFTVQPNQRYVLRVYARKEGNGVYSIRDGNGNQETELTFSASDYDTNGMYNQ 1118  
 DB 1058 DEQVSQOFTVQPNQRYVLRVYARKEGNGVYSIRDGNGNQETELTFSASDYDTNGM- --- 1113  
 QY 1119 VSNVTNGVNTNAYNTQASSTNGVNNANNMYTQASNTNGVNTNSVYNDOTGYITKTVTIPI 1178  
 DB 1114 - ---YNDQTYITKTVTIPI 1129  
 QY 1179 YTDQMWIESETEGTFYIESVELIVDVE 1206  
 DB 1130 YTDQMWIESETEGTFYIESVELIVDVE 1157

# RESULT 5

AAR25997  
 ID AAR25997 standard; Protein; 1157 AA.  
 XX AAR25997;  
 AC AAR25997;  
 XX 27-JAN-1993 (first entry)  
 DT Delta-endotoxin.  
 DE B.t.P550C; colorado potato beetle; Leptinotarsa decemlineata;  
 KW Pseudomonas; expression vector.  
 XX Bacillus thuringiensis.  
 OS EF498537-A.  
 PN 12-AUG-1992.  
 PD 16-JAN-1992; 92EP-0300366.  
 PF 16-JAN-1991; 91US-0642112.  
 PR (MYCO ) MYCOGEN CORP.  
 XX Foncerrada L, Payne JM, Sick AJ;  
 PI WPI; 1992-270497/33.  
 XX P-PSDB; AAR25997.  
 DR New insecticidal Bacillus thuringiensis strain NRRL B-18746 - and  
 PT toxin, DNA encoding it, vectors and transformed cells, effective  
 PT against Coleoptera  
 XX Claim 6; Page 11-14; 16pp; English.

CC The sequence given is an approx. 130 kD protien known as Bacillus  
 CC thuringiensis PS50C (B.t.P550C). This novel delta-endotoxin has been  
 CC shown to be active against the Colorado potato beetle (Leptinotarsa  
 CC decemlineata). The gene encoding this toxin can be transformed into  
 CC suitable hosts such as Pseudomonas, which can then be applied to the  
 CC environment of coleopteran insects where they will proliferate and be  
 CC ingested by the insects. This DNA sequence can be inserted into an  
 CC expression vector which contains a promoter/operator region, a ribosome  
 CC binding site, polyadenylation signals, etc. This will allow  
 CC transcription and translation of the cells in the appropriate host.  
 XX Sequence 1157 AA;

Query Match 62.4%; Score 3950.5; DB 13; Length 1157;  
Best Local Similarity 65.5%; Pred. No. 2.4e-256;  
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

QY 1 MSPNNQNEYIIDATPSTSVSDSNRYPPFANETNALQNMNDYKYLKMSAGNASYEGPSP 60  
DB 1 MSPNNQNEYIIDATPSTSVSDSNRYPPFANETDALQNMNDYKYLKMSAGNENPFGNP 60

QY 61 EVLVSGODAAKAAIDIVGKLLSGLVPGVPISVLYTOLIDLWPSGKESQWEIFMEQVE 120  
DB 61 ETFIS-SSTIQTGTGIVGRIIGALGVPFASQIASFYISVQLWPSKSVDTWGEIMERVE 119

QY 121 ELINQKIAEYARNKALSEGLEGNYYQLYLTALBEEENPNPNSALRDRVRNFILDSLF 180  
DB 120 ELVDQKIEKYDKALAEKLGALDVYQOSLEDWLENRNDARTSVSVNQFIALDNP 179

QY 181 TQYMPSTVTFNPFVFFITVYMAANLHLLKLDASIFGEEWGSTTTNNYYDROMKLT 240  
DB 180 VSSIPSPAVSGHEVLLAVYAQAANLHLLLDASIFGEEWGSTTPEISRYNROVQLTA 239

QY 241 EYSDHCYKWTETGLAKLGTSAKOWDYNOFRREMTLAVLDVALFNYDRTYPMETKA 300  
DB 240 EYSDYCKWYKIGLDKLGKGTSSWLNHQPFRREMTLLVLDLVALFNYDTHYPIETTA 299

QY 301 QLTREVYTDPLGAVNVSSIGSWYDKAPSGV-IESSVIRPPHVFDYITGLTVYTSR 356  
DB 300 QLTREVYTDPIAFNIVTSGFCNPSWTHSGILFYEVENNVIRPPHFDILSSVEINT-SR 358

QY 357 ---SISARYIRHWAGHOISYHRSVRSNLOQMYGTGNLHSTSTFDFTNYDIYKLSKD 413  
DB 359 GGITLNDAYINWSGHTLKYYRTA-DSTVYTYANYGRITSEKNSFALEDRIEINSTV 417

QY 414 AVLLDIVVPGVYTIFFGMPVEVEFWMVQLNTRKTLKYNPVSKDIIASTR--DSELELPP 471  
DB 418 ANLANYQKAY-----GVPGSWFHWKRGTSSTAYLSKTHKALQCTQVYESDSEIPL 472

QY 472 ETSQPNYESYSHRLCHITSPATGNTT---GLVPVFSWTHRSADLNNIYSDKITOIPA 528  
DB 473 DRT--VPAVESYSHRLSHITSHSPKNGSAYYGSFPVFWTHTSADLNNIYSDKITOIPA 531

QY 529 VKWDLNPFV--PVVKGPGHTGBLLQVNRSTGVTGLFLARYGLALEKAGKYRRLRYA 586  
DB 532 VK--GDMLYLGGSVVQPGFTGGDILK--RTNPSILGTFAVTVNGSLSQ--RYRVRIRYA 585

QY 587 --TDADIVLHVDA--QIQMPKTNPGEDLTSTKFKVADAITLNL-ATDSSLALK---H 638  
DB 586 STTDFEFTLGLDGTIEKNRKNKTNDNGASLTFTYFKFASFITDFQFRETQDKILLSGDF 645

QY 639 NLGDEPNSTLSGIVVDRIEPIVDETYEABQDLAAKAVNALFTNTKGLRPGVTDYE 698  
DB 646 SSGQE-----VIIDRIEPIVDETYEABQDLAAKAVNALFTNTKGLRPGVTDYE 697

QY 699 VNOAANLVECLSDLLYPNEKELLFVAREAKRLSEARNLLQDPPFOEINGENGTASTGI 758  
DB 698 VNOAANLVECLSDLLYPNEKELLFVAREAKRLSGARNLLQDPPFOEINGENGTASTGI 757

QY 759 EVIEGDALFKGRIYLRLEAREIDTETPTLYYQKVERGLKPYTRYRLRGVSSQGLEI 818  
DB 758 EIVEGDVAFKGRYLRLEAREIDTETPTLYYQKVERGLKPYTRYRLRGVSSQGLEI 817

QY 819 FTIRHOTNRIVKVPDILLPVPVNSDGSINRSCQKYVNSRLEVENRSGEAHEFSIPI 878  
DB 818 YTIHOTNRIVKVPDILLPVPVNSDGSINRSCQKYVNSRLEGENRSGDAHEFSIPI 877

QY 879 DTGEIDYNENAGIWWGFKITDPEGYATLGNLELVEEPLSGDALERLOREQQWKIOWTR 938  
DB 878 DIGELDYNENAGIWWGFKITDPEGYATLGNLELVEEPLSGDALERLOREQQWKIOWTR 937

QY 939 RRETDTRYWASKOAVDRLYADYQDQQLNPVEITDLTAADQLIQSIPYVYNNEMFPPIPG 998  
DB 938 RRETDTRYWASKOAVDRLYADYQDQQLNPVEITDLTAADQLIQSIPYVYNNEMFPPIPG 997

QY 999 MNTYKTFELTDLRLOQAWSLYDQNAIPNGDFRNLGNLNNWATPGVEVQOQINHTSVLIPNW 1058

DB 998 MNTYKTFELTDLRLOQAWSLYDQNAIPNGDFRNLGNLNNWATPGVEVQOQINHTSVLIPNW 1057

QY 1059 DEQVSOQFTVQPNQRYVLRVTARKEGVGNGYVIRDCGNQETLTTFSASDYDNGMYNTQ 1118  
DB 1058 DEQVSOQFTVQPNQRYVLRVTARKEGVGNGYVIRDCGNQSETLTTFSASDYDNG----- 1112

QY 1119 VSNITNGYNTNAYNTQASSTNGYNANNMYNTQASNTNGYNTNSVYNDOTGYITKTVTFIP 1178  
DB 1113 -----VYNDOTGYITKTVTFIP 1129

QY 1179 YTDQMIMSETEGTFFYIESVELIVDVE 1206  
DB 1130 YTDQMIMSETEGTFFYIESVELIVDVE 1157

RESULT 6  
AAR33768  
ID AAR33768 standard; Protein; 1157 AA.  
XX  
AC AAR33768;  
XX  
DT 15-JUL-1993 (first entry)  
XX  
DE Bt isolate Ps50C.  
XX  
KW Lepidopteran-active; toxin; Ti; Ri; plant; cell; Bt.  
XX  
OS Bacillus thuringiensis.  
XX  
PN WO9304587-A.  
XX  
PD 18-MAR-1993.  
XX  
PF 11-SEP-1992; 92WO-US07697.  
XX  
PR 12-SEP-1991; 91US-0758020.  
PR 09-SEP-1992; 92US-0941650.  
XX  
PA (MYCO) MYCOGEN CORP.  
XX  
PI Bradfish GA, Uyeda KA;  
XX  
DR WPI; 1993-100566/12.  
DR N-PSDB; AAQ38653.  
XX  
PT Controlling lepidopteran pests - using compan. of Bacillus  
PT thuringiensis strains or plants or microorganisms transformed  
XX  
PS Claim 12; Page 22-25; 38pp; English.  
XX  
The sequences given in AAR33768-70 represent lepidopteran-active toxins.  
The DNA encoding these sequences were used within a Ti or Ri plasmid,  
to transform plant cells. Whole plants can then be regenerated from  
the transformed cells. The toxin may also be produced by cloning  
Bacillus thuringiensis (Bt). It may then be applied directly to  
the plant locus.

QY 1 MSPNNQNEYIIDATPSTSVSDSNRYPPFANETNALQNMNDYKYLKMSAGNASYEGPSP 60  
DB 1 MSPNNQNEYIIDATPSTSVSDSNRYPPFANETDALQNMNDYKYLKMSAGNENPFGNP 60

QY 61 EVLVSGODAAKAAIDIVGKLLSGLVPGVPISVLYTOLIDLWPSGKESQWEIFMEQVE 120  
DB 61 ETFIS-SSTIQTGTGIVGRIIGALGVPFASQIASFYISVQLWPSKSVDTWGEIMERVE 119

Query Match 62.4%; Score 3950.5; DB 14; Length 1157;  
Best Local Similarity 65.5%; Pred. No. 2.4e-256;  
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;







```
Db 300 QLTRDVYTDPIAFNIVTSTGFCNPSWTHSGILFYEVENNVRPHLPDILSSVEINT-SR 358
Qy 357 ---SISARVIRHWAGHOISYHRVSRGSLNQMGYTNQNLHSTSTFTPTNYDIYKTLISKD 413
Db 359 GGITLNDALINWAGHTLKYRRTA-DSTVITYANYGRITSKNSPALEDRDIFEINSTV 417
Qy 414 AVLLDIIYVPGTYIFFGMEPEVPPMVNQLNNTKLYKNPVSKDIIIASTR--DSELELPP 471
Db 418 ANLANYQKAY-----GVPGSWFHWKRVSTSTAYLYSKHTHALQGCCTQVYESSDEIPL 472
Qy 472 ETSQDPNYESYSHRLCHITSTPATGNTT---GLVPVSWTHRSADIANNTIYSDKITQIPA 528
Db 473 DRT-VPVAETYSHRLSHITSHSFKNGSAYYGSPFVFWTHTSADLNNIYSDKITQIPA 531
Qy 529 VKCWDNLFPV--PVKPGHGTGGDLLOVNRSTGVSGLTFLARYGALAKGKGYRVLRYA 586
Db 532 VK--GDMLYIGSVVQPGFGTGGDLK--RTNPSILGTFAVTNGSLSQ--RYRVRIRYA 585
Qy 587 --TDADIVLHVND--QIOMPKNPGBEDLTSKFKVADAITLNL-ATDSSLAK---H 638
Db 586 STTDPFTLVLDITKRNFKNTWDNGASLTVEYFKFASPTTDFQFRETQDKILLSMGDF 645
Qy 639 NLGSDPNSTLSGIVYDRIBFIPVDETYEARQDLEAKKAVNALFTNTKQGLRPGVTDYE 698
Db 646 SSGQE-----VYIDRIEIPVDETYEARQDLEAKKAVNALFTNTKQGLRPGVTDYE 697
Qy 699 VNOQANLVECLSDDLYPNEKELLDAVREAKRLSEARNLLODPDQFQINGENGWASTGI 758
Db 698 VNOQANLVECLSDDLYPNEKELLDAVREAKRLSGARNLLQDPDQFQINGENGWASTGI 757
Qy 759 EVIEGDLFKGRYLRLPGAREIDETETPTLYQKVEGVLKPYRYRLRGVSGSQGLEI 818
Db 758 EIVEGDAVFKGRYLRLPGAREIDETETPTLYQKVEGVLKPYRYRLRGVSGSQGLEI 817
Qy 819 FTIRHQRNIRVKNVPDILLPVSPVNSDGSINRCSEQKYVNSRLSEVENRSGEAHEFSIPI 878
Db 818 YTIHQNRIRVKNVPDILLPVSPVNSDGSINRCSEQKYVNSRLSEGENRSGDAHEFSIPI 877
Qy 879 DTGEIDYENAGIWWGFKITDPEGVATLGNLELVEEGPLSGDALERLOREOQWKIOMTR 938
Db 878 DIGELDYENAGIWWGFKITDPEGVATLGNLELVEEGPLSGDALERLOREOQWKIOMTR 937
Qy 939 RREBTRRYNASKOAVRLYADYQDQQLNPQVEITDLTAAQDLIQSIPIVYNMFPPEIPG 998
Db 938 RREBTRRYNASKOAVRLYADYQDQQLNPQVEITDLTAAQDLIQSIPIVYNMFPPEIPG 997
Qy 999 MNYTKFTLDRLOQAWSLYDORNAIPNGDFRNLGNLNNNATPGVEVQOINHTSVLVI PNW 1058
Db 998 MNYTKFTLDRLOQAWSLYDORNAIPNGDFRNLGNLNNNATPGVEVQOINHTSVLVI PNW 1057
Qy 1059 DEQVSOQFTVQPNORYLRLVTRARKEGNGVYSIRDGNGOTETLTFSSADYDTNGMYNQ 1118
Db 1058 DEQVSOQFTVQPNORYLRLVTRARKEGNGVYSIRDGNGOSETLTFSSADYDTNG----- 1112
Qy 1119 VSNNGYNTNAYNTQASSTNGYNANNMYNTQASNTNGYNTSVNDOTGYITKVTTFIP 1178
Db 1113 -----VNDQGTGYITKVTTFIP 1129
Qy 1179 YTDQWMIEMSETGTFYIESVELIVDVE 1206
Db 1130 YTDQWMIEMSETGTFYIESVELIVDVE 1157

RESULT 9
AAR44208
ID AAR44208 standard; Protein; 1157 AA.
XX
AC AAR44208;
XX
DT 09-DEC-1995 (first entry)
XX
DE Bacillus thuringiensis crystal protein PS50C.
XX
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KW Crystal protein; delta endotoxin; acaricide; pesticide;
KW biological control agent; transgenic plant; crop improvement.
OS Bacillus thuringiensis var. kumamotoensis (isolate PS50C).
XX
XX US5262158-A.
XX
XX 16-NOV-1993.
XX
XX 30-APR-1991; 91US-0693210.
XX
XX 30-APR-1992; 92US-0876280.
XX 30-APR-1991; 91US-0693210.
XX 13-SEP-1991; 91US-0759248.
XX 30-SEP-1991; 91US-0768141.
XX
XX (MYCO ) MYCOGEN CORP.
XX
XX Bagley AL, Cannon RJC, Payne JM;
XX
XX WPI; 1993-377387/47.
XX
XX N-PSDB; AAQ51704.
XX
XX Controlling acaride pests e.g. two spotted spider mite - utilising
XX Bacillus thuringiensis delta-toxins cloned into microbe hosts.
XX
XX Disclosure; Column 71-76; 42pp; English.
XX
XX DNA encoding the insecticidal toxin can be cloned into baculo
XX viruses and transferred to other host microbes, preferably E. coli
XX NM522 (pMYC 2320) NRRL B-18769, to control acaride pests, or to
XX plants which become resistant to the acaricide pests.
XX Specifically, the two-spotted spider mite (Tetranychus urticae) is
XX controlled.
XX
XX Sequence 1157 AA;
XX
XX Query Match 62.2%; Score 3940.5; DB 14; Length 1157;
XX Best Local Similarity 65.4%; Pred. No. 1.le-255;
XX Matches 803; Conservative 119; Mismatches 213; Indels 93; Gaps 19;
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Qy 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPNALQNDYDKYLMKAGNASEYPCGP 60
Db 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPNALQNDYDKYLMKAGNASEYPCGP 60
Qy 61 EVLVSGQDAKAAIDIVKLLSGLVGVPFVPIVSLYQLDILWPSEKKSOWEIFMEQVE 120
Db 61 ETVFIS-SSTIQTGIGIVGRILGALGVFPASQIASFYFIVGQLWPSKSVDIWGEIMERVE 119
Qy 121 ELINOKIAEYARNKALSEGLEGNVQLYLTALFEWENPNRSLRDLVRNRFELDSL 180
Db 120 ELVDQKLEKVKDKNAELKGLGNALQVQOSLEDWLENDRNDATRSVVSQFALDLNF 179
Qy 181 TQYMFSPRVTFVFPFLTVYAMAANLHLLKLDASIFGEEWGNSTTTNNYDROMKLTA 240
Db 180 VSSIPSAVSGHEVLLAVYAQAQVNLHLLLRDASIFGEEWGNSTTTNNYDROMKLTA 239
Qy 241 EYSHCVKWTETGLAKLGTSAKOWDYQNPFRREMTLAVLDVVALFPNYDTRTPYMETKA 300
Db 240 EYSDYCVKWKYIGLDKLGTTSKSLNLYHQFRRMTLLVLDVVALFPNYDTRTPYMETKA 299
Qy 301 QLTREVTYDPLGAVNVSSIGSWYDKAPSGV-----IESSVIRPPHVPDYITGLTVYTOSR 356
Db 300 QLTREVTYDPLGAVNVSTIGFCNPSWTHSGILFYEVENNVRPHLPDILSSVEINT-SR 358
Qy 357 ---SISARVIRHWAGHOISYHRVSRGSLNQMGYTNQNLHSTSTFTPTNYDIYKTLISKD 413
Db 359 GGITLNDALINWAGHTLKYRRTA-DSTVITYANYGRITSKNSPALEDRDIFEINSTV 417
Qy 414 AVLLDIIYVPGTYIFFGMEPEVPPMVNQLNNTKLYKNPVSKDIIIASTR--DSELELPP 471
Db 418 ANLANYQKAY-----GVPGSWFHWKRVSTSTAYLYSKHTHALQGCCTQVYESSDEIPL 472
```



QY 541 VKPGHTGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRVLRYATDADIVLHVNDQI 600  
 DB 541 VKPGHTGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRVLRYATDADIVLHVNDQI 600  
 QY 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSLAKHNLGDPNSTLSGIYVVDRIEPI 660  
 DB 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSLAKHNLGDPNSTLSGIYVVDRIEPI 660  
 QY 661 PVDETYEAE 669  
 DB 661 PVDETYEAE 669

RESULT 11  
 AAU99262 standard; Protein; 669 AA.

AC AAU99262;

DT 07-OCT-2002 (first entry)

XX Bacillus thuringiensis Cry1218-1A truncated protein sequence.

XX Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;  
 KW Colorado potato beetle; western corn rootworm; southern corn rootworm;  
 KW insect target range; endotoxin; Cry1218.

XX Bacillus thuringiensis.

XX WO200234774-A2.

XX 02-MAY-2002.

XX 24-OCT-2001; 2001WO-US45468.

XX 24-OCT-2000; 2000US-242838P.

PR 23-OCT-2001; 2001US-0032717.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

PI Abad AR, Duck NB, Peng X, Flannagan RD, Kahn TW, Sims LB;

XX WPI; 2002-519178/55.

DR N-PSDB; ASK87241.

XX New isolated pesticidal polypeptide useful for impacting insect pest

PT e.g. Colorado potato beetle

XX Claim 4; Page 125-127; 176pp; English.

XX The present invention relates to a new pesticidal polypeptide. The  
 CC invention is useful for impacting an insect pest by applying the  
 CC the molecules of the invention to the environment of the insect pest by  
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest  
 CC is selected from Colorado potato beetle, western corn rootworm or  
 CC southern corn rootworm. The invention is also useful for increasing  
 CC insect target range and for producing transgenic microorganisms and  
 CC plants that express the pesticidal polypeptide. The invention is also  
 CC useful for producing transformed plants and in transforming any organism  
 CC to produce the pesticidal polypeptide of the invention. The present  
 CC amino acid sequence represents a Bacillus thuringiensis wild-type  
 CC Cry1218 endotoxin protein.

XX Sequence 669 AA;

XX Query Match 55.4%; Score 3511; DB 23; Length 669;

XX Best Local Similarity 100.0%; Pred. No. 3.5e-227;

XX Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPNNQNEYIITDPTSVSNDNSRYPANETNALQNDYKDYLMKSNAGNASEYFGSP 60

DB 1 MSPNNQNEYIITDPTSVSNDNSRYPANETNALQNDYKDYLMKSNAGNASEYFGSP 60

QY 61 EYLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYTQIIDLWPSEKSKQWEIFMEQVE 120  
 DB 61 EYLVSGQDAKAAIDIVGKLLSGLGVPFVGPVIVSLYTQIIDLWPSEKSKQWEIFMEQVE 120  
 QY 121 ELINOKIAEYARNKALSEGLEGNNYQLYLTALBEEWENPNGSRALRDVRRNPEILDSLF 180  
 DB 121 ELINOKIAEYARNKALSEGLEGNNYQLYLTALBEEWENPNGSRALRDVRRNPEILDSLF 180  
 QY 181 TOYMPSFRVTNFPVPLTVYAMAANLHLLKDAISFGEWGWSTTTNNYVDROMKLT 240  
 DB 181 TOYMPSFRVTNFPVPLTVYAMAANLHLLKDAISFGEWGWSTTTNNYVDROMKLT 240  
 QY 241 EYSDHCVKWYETGLAKGTSKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKA 300  
 DB 241 EYSDHCVKWYETGLAKGTSKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKA 300  
 QY 301 QLTREVTYDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVFYITGLTVYTQSRSS 360  
 DB 301 QLTREVTYDPLGAVNVSSIGSWYDKAPSGVIESVIRPPHVFYITGLTVYTQSRSS 360  
 QY 361 ARYIRHWAGHOISYHRVSRGNSLQOMYGTNOLHSTSTFDFTNYDIYKTLSDAVLLDIV 420  
 DB 361 ARYIRHWAGHOISYHRVSRGNSLQOMYGTNOLHSTSTFDFTNYDIYKTLSDAVLLDIV 420  
 QY 421 YPGYTYIIFGMEVEFFMVNQLNTRKTLKYNPVSVDIIASTRDSELELPPTSDQPNYE 480  
 DB 421 YPGYTYIIFGMEVEFFMVNQLNTRKTLKYNPVSVDIIASTRDSELELPPTSDQPNYE 480  
 QY 481 SYSRLCHITSIPATGNTTGLVPVSWTHRSADLNNTIYSDKITQIPAVKCDNLPFPVPV 540  
 DB 481 SYSRLCHITSIPATGNTTGLVPVSWTHRSADLNNTIYSDKITQIPAVKCDNLPFPVPV 540  
 QY 541 VKGPGHTGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRVLRYATDADIVLHVNDQI 600  
 DB 541 VKGPGHTGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRVLRYATDADIVLHVNDQI 600  
 QY 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSLAKHNLGDPNSTLSGIYVVDRIEPI 660  
 DB 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTATDSSLAKHNLGDPNSTLSGIYVVDRIEPI 660  
 QY 661 PVDETYEAE 669  
 DB 661 PVDETYEAE 669

RESULT 12

AAU99257

ID AAU99257 standard; Protein; 667 AA.

XX AC AAU99257;

XX DT 07-OCT-2002 (first entry)

XX DE Bacillus thuringiensis Cry1218-1 truncated protein sequence.

XX KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;

XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;

XX KW insect target range; endotoxin; Cry1218.

XX OS Bacillus thuringiensis.

XX PN WO200234774-A2.

XX PD 02-MAY-2002.

XX PF 24-OCT-2001; 2001WO-US45468.

XX PR 24-OCT-2000; 2000US-242838P.

XX PR 23-OCT-2001; 2001US-0032717.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;  
 XX WPI; 2002-519178/55.  
 DR N-PSDB; ABK87236.  
 XX New isolated pesticidal polypeptide useful for impacting insect pest  
 PT e.g. Colorado potato beetle -  
 XX Claim 4; Page 108-109; 176pp; English.  
 XX The present invention relates to a new pesticidal polypeptide. The  
 CC invention is useful for impacting an insect pest by applying the  
 CC the molecules of the invention to the environment of the insect pest by  
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest  
 CC is selected from Colorado potato beetle, western corn rootworm or  
 CC southern corn rootworm. The invention is also useful for increasing  
 CC insect target range and for producing transgenic microorganisms and  
 CC plants that express the pesticidal polypeptide. The invention is also  
 CC useful for producing transformed plants and in transforming any organism  
 CC to produce the pesticidal polypeptide of the invention. The present  
 CC amino acid sequence represents a *Bacillus thuringiensis* wild-type  
 CC Cry1218 endotoxin protein.  
 XX Cry1218 endotoxin protein.  
 XX Sequence 667 AA;  
 SQ

Query Match 55.3%; Score 3502; DB 23; Length 667;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-226;  
 Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNM DYKDYLMKMSAGNASYPPGSP 60  
 Db 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNM DYKDYLMKMSAGNASYPPGSP 60

Qy 61 EYLVSGQDAKAAIDIVGKLLSGLVPPGPIVSLYLTQIDILWPSEKSGOWEIFMEQVE 120  
 Db 61 EYLVSGQDAKAAIDIVGKLLSGLVPPGPIVSLYLTQIDILWPSEKSGOWEIFMEQVE 120

Qy 121 ELINOKIAEYARNKALSEGLEGNNGYQLYLTALBEEENPNSGRALDRVRNRFEL 180  
 Db 121 ELINOKIAEYARNKALSEGLEGNNGYQLYLTALBEEENPNSGRALDRVRNRFEL 180

Qy 181 TOYMSFRVTNEVPPLTYVYAAANLHLLLDKADSTFGBEWGSTTTINNYDRQMKLTA 240  
 Db 181 TOYMSFRVTNEVPPLTYVYAAANLHLLLDKADSTFGBEWGSTTTINNYDRQMKLTA 240

Qy 241 EYSDHCWKVETGLAKLKTSAQWVDYNQPREMTLAVLDVVALPNDYTRTYMETKA 300  
 Db 241 EYSDHCWKVETGLAKLKTSAQWVDYNQPREMTLAVLDVVALPNDYTRTYMETKA 300

Qy 301 QLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESSVIRPPHVFDTYITGLTVTQSRSSIS 360  
 Db 301 QLTREYVTDPLGAVNVSSIGSWYDKAPSGVIESSVIRPPHVFDTYITGLTVTQSRSSIS 360

Qy 361 ARYIRHWAGHQISYHRVSRGSLQMQYGTGNLHSTSTFTDNYDIYKTLKSDAVLLDIV 420  
 Db 361 ARYIRHWAGHQISYHRVSRGSLQMQYGTGNLHSTSTFTDNYDIYKTLKSDAVLLDIV 420

Qy 421 YPGYTYIFPGMEVEFFPMYNLNTRKTLKYNPVSVDIIASTRDSLELPPESTDPNVE 480  
 Db 421 YPGYTYIFPGMEVEFFPMYNLNTRKTLKYNPVSVDIIASTRDSLELPPESTDPNVE 480

Qy 481 SYSHRLCHTITSPATGNTTGLVPVSWTHRSADLNNTIYSDKITQIPAVKCDNLPFPVPV 540  
 Db 481 SYSHRLCHTITSPATGNTTGLVPVSWTHRSADLNNTIYSDKITQIPAVKCDNLPFPVPV 540

Qy 541 VKGPHTGDLQYNRSTSGVTGLFLARYGLALEKAGKYRVLRYATDADIIVLHVNDQI 600  
 Db 541 VKGPHTGDLQYNRSTSGVTGLFLARYGLALEKAGKYRVLRYATDADIIVLHVNDQI 600

Qy 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTADSSLAKHNLGDPNSTLSGIVVVDRIEPI 660  
 Db 601 QMPKTMNPGEDLTSKTFKVADAITTLNLTADSSLAKHNLGDPNSTLSGIVVVDRIEPI 660

Qy 661 PVDETYE 667  
 Db 661 PVDETYE 667

RESULT 13  
 AAU99260  
 ID AAU99260 standard; Protein; 673 AA.  
 XX AAU99260;  
 XX 07-OCT-2002 (first entry)  
 DT  
 DE  
 DE  
 KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;  
 KW Colorado potato beetle; western corn rootworm; southern corn rootworm;  
 KW insect target range; endotoxin; Cry1218; mutant; mutein.  
 XX  
 OS *Bacillus thuringiensis*.  
 OS Synthetic.  
 XX  
 PN WO200234774-A2.  
 XX  
 PD 02-MAY-2002.  
 XX  
 PF 24-OCT-2001; 2001WO-US45468.  
 XX  
 PR 24-OCT-2000; 2000US-242838P.  
 PR 23-OCT-2001; 2001US-0032717.  
 XX  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;  
 XX WPI; 2002-519178/55.  
 DR N-PSDB; ABK87239.  
 XX  
 PT New isolated pesticidal polypeptide useful for impacting insect pest  
 PT e.g. Colorado potato beetle -  
 XX  
 PS Claim 23; Page 121-122; 176pp; English.  
 CC The present invention relates to a new pesticidal polypeptide. The  
 CC invention is useful for impacting an insect pest by applying the  
 CC the molecules of the invention to the environment of the insect pest by  
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest  
 CC is selected from Colorado potato beetle, western corn rootworm or  
 CC southern corn rootworm. The invention is also useful for increasing  
 CC insect target range and for producing transgenic microorganisms and  
 CC plants that express the pesticidal polypeptide. The invention is also  
 CC useful for producing transformed plants and in transforming any organism  
 CC to produce the pesticidal polypeptide of the invention. The present  
 CC amino acid sequence represents a *Bacillus thuringiensis* mutant Cry1218  
 CC endotoxin protein.  
 XX  
 SQ Sequence 673 AA;  
 Query Match 55.3%; Score 3499; DB 23; Length 673;  
 Best Local Similarity 99.4%; Pred. No. 2.3e-226;  
 Matches 669; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNM DYKDYLMKMSAGNASYPPGSP 60  
 Db 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNM DYKDYLMKMSAGNASYPPGSP 60

Qy 61 EYLVSGQDAKAAIDIVGKLLSGLVPPGPIVSLYLTQIDILWPSEKSGOWEIFMEQVE 120  
 Db 61 EYLVSGQDAKAAIDIVGKLLSGLVPPGPIVSLYLTQIDILWPSEKSGOWEIFMEQVE 120

Qy 121 ELINOKIAEYARNKALSEGLEGNNGYQLYLTALBEEENPNSGRALDRVRNRFEL 176  
 Db 121 ELINOKIAEYARNKALSEGLEGNNGYQLYLTALBEEENPNSGRALDRVRNRFEL 180

QY 177 DLSFTQMPSPFRVTNFEVPLTVYMAANLHLLKLDASIFGEWGWSTTTINNYDROM 236  
DB 181 DLSFTQMPSPFRVTNFEVPLTVYMAANLHLLKLDASIFGEWGWSTTTINNYDROM 240  
QY 237 KLTAEYSDHCWKYETGLAKLKTSAKQWVDYQFREMFLAVLDDVALPPNYDRTYPM 296  
DB 241 KLTAEYSDHCWKYETGLAKLKTSAKQWVDYQFREMFLAVLDDVALPPNYDRTYPM 300  
QY 297 ETKAQLTREVTDPGAVNVSSIGSWYDKAPSGVIESSVIRPHVFDYITGLTVYTQSR 356  
DB 301 ETKAQLTREVTDPGAVNVSSIGSWYDKAPSGVIESSVIRPHVFDYITGLTVYTQSR 360  
QY 357 SISSARYIRHWAGHQISYHRVSRGSLQOMKYNQNLHSTSTDFNTYDIYKTLSDAVL 416  
DB 361 SISSARYIRHWAGHQISYHRVSRGSLQOMKYNQNLHSTSTDFNTYDIYKTLSDAVL 420  
QY 417 LDIVPGYTYIFFGMPVEFFVMVNLNNTKTLKYNPVSKDIIASTRDSLELPPTSQ 476  
DB 421 LDIVPGYTYIFFGMPVEFFVMVNLNNTKTLKYNPVSKDIIASTRDSLELPPTSQ 480  
QY 477 PNYESYSHRLCHITSPATGNTTGLVPSWTHRSADLNTIYSDKLTQIPAVKCDNLP 536  
DB 481 PNYESYSHRLCHITSPATGNTTGLVPSWTHRSADLNTIYSDKLTQIPAVKCDNLP 540  
QY 537 FVPVKGPGHTGDLQYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVN 596  
DB 541 FVPVKGPGHTGDLQYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVN 600  
QY 597 DAQIQMPKTMNPGEDLTSTKTFKVADAITTLNLTADSSALKHNLGDPNSTLSGIVVYDR 656  
DB 601 DAQIQMPKTMNPGEDLTSTKTFKVADAITTLNLTADSSALKHNLGDPNSTLSGIVVYDR 660  
QY 657 IEFIPVDETYEAE 669  
DB 661 IEFIPVDETYEAE 673

RESULT 14

AAU99265  
ID AAU99265 standard; Protein; 673 AA.  
XX  
AC AAU99265;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE Bacillus thuringiensis LKMS.N1218-1 mutant protein sequence.  
XX  
KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;  
KW Colorado potato beetle; western corn rootworm; southern corn rootworm;  
KW insect target range; endotoxin; Cry1218; mutant; mutein.  
XX  
OS Bacillus thuringiensis.  
OS Synthetic.  
XX  
PN WO200234774-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 24-OCT-2001; 2001WO-US45468.  
XX  
PR 24-OCT-2000; 2000US-242838P.  
PR 23-OCT-2001; 2001US-0032717.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Abad AR, Duck NB, Peng X, Flannagan RD, Kahn TW, Sims LE;  
XX  
DR WPI; 2002-519178/55.  
DR N-PSDB; ABR87244.  
XX  
PT New isolated pesticidal polypeptide useful for impacting insect pest  
e.g. Colorado potato beetle -

XX Claim 23; Page 138-139; 176pp; English.  
PS  
XX  
CC The present invention relates to a new pesticidal polypeptide. The  
invention is useful for impacting an insect pest by applying the  
the molecules of the invention to the environment of the insect pest by  
spraying, dusting, broadcasting, or seed coating, where the insect pest  
is selected from Colorado potato beetle, western corn rootworm or  
southern corn rootworm. The invention is also useful for increasing  
insect target range and for producing transgenic microorganisms and  
plants that express the pesticidal polypeptide. The invention is also  
useful for producing transformed plants and in transforming any organism  
to produce the pesticidal polypeptide of the invention. The present  
amino acid sequence represents a Bacillus thuringiensis mutant Cry1218  
endotoxin protein.  
XX  
SQ Sequence 673 AA;  
Query Match 55.3%; Score 3499; DB 23; Length 673;  
Best Local Similarity 99.4%; Pred. No. 2.3e-226;  
Matches 669; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
QY 1 MSPNNQNEYEIIDATPSTSVSNDNRYPPANPTNALQNMNDYKDKYKMSAGNASEYPGSP 60  
DB 1 MSPNNQNEYEIIDATPSTSVSNDNRYPPANPTNALQNMNDYKDKYKMSAGNASEYPGSP 60  
QY 61 EVLVSGQDAAKAIDIVGKLLSGLGVFPVPTVSLYLTQIDILWPSGKSWEIFMEQVE 120  
DB 61 EVLVSGQDAAKAIDIVGKLLSGLGVFPVPTVSLYLTQIDILWPSGKSWEIFMEQVE 120  
QY 121 ELINQKIAEYARNKALSEGLGNNTQVLTALTEEENP---NGSRALRDVNRNFEIL 176  
DB 121 ELINQKIAEYARNKALSEGLGNNTQVLTALTEEENP---NGSRALRDVNRNFEIL 180  
QY 177 DLSFTQMPSPFRVTNFEVPLTVYMAANLHLLKLDASIFGEWGWSTTTINNYDROM 236  
DB 181 DLSFTQMPSPFRVTNFEVPLTVYMAANLHLLKLDASIFGEWGWSTTTINNYDROM 240  
QY 237 KLTAEYSDHCWKYETGLAKLKTSAKQWVDYQFREMFLAVLDDVALPPNYDRTYPM 296  
DB 241 KLTAEYSDHCWKYETGLAKLKTSAKQWVDYQFREMFLAVLDDVALPPNYDRTYPM 300  
QY 297 ETKAQLTREVTDPGAVNVSSIGSWYDKAPSGVIESSVIRPHVFDYITGLTVYTQSR 356  
DB 301 ETKAQLTREVTDPGAVNVSSIGSWYDKAPSGVIESSVIRPHVFDYITGLTVYTQSR 360  
QY 357 SISSARYIRHWAGHQISYHRVSRGSLQOMKYNQNLHSTSTDFNTYDIYKTLSDAVL 416  
DB 361 SISSARYIRHWAGHQISYHRVSRGSLQOMKYNQNLHSTSTDFNTYDIYKTLSDAVL 420  
QY 417 LDIVPGYTYIFFGMPVEFFVMVNLNNTKTLKYNPVSKDIIASTRDSLELPPTSQ 476  
DB 421 LDIVPGYTYIFFGMPVEFFVMVNLNNTKTLKYNPVSKDIIASTRDSLELPPTSQ 480  
QY 477 PNYESYSHRLCHITSPATGNTTGLVPSWTHRSADLNTIYSDKLTQIPAVKCDNLP 536  
DB 481 PNYESYSHRLCHITSPATGNTTGLVPSWTHRSADLNTIYSDKLTQIPAVKCDNLP 540  
QY 537 FVPVKGPGHTGDLQYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVN 596  
DB 541 FVPVKGPGHTGDLQYNRSTGSGVTLFLARYGLALEKAGKYRRLRYATDADIVLHVN 600  
QY 597 DAQIQMPKTMNPGEDLTSTKTFKVADAITTLNLTADSSALKHNLGDPNSTLSGIVVYDR 656  
DB 601 DAQIQMPKTMNPGEDLTSTKTFKVADAITTLNLTADSSALKHNLGDPNSTLSGIVVYDR 660  
QY 657 IEFIPVDETYEAE 669  
DB 661 IEFIPVDETYEAE 673  
RESULT 15  
AAU99271

ID AAU99271 standard; Protein; 673 AA.  
AC AAU99271;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE Bacillus thuringiensis LRNS.N1218-1 mutant protein sequence.  
XX  
XX Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;  
KW Colorado potato beetle; western corn rootworm; southern corn rootworm;  
KW insect target range; endotoxin; Cry1218; mutant; mutein.  
XX  
OS Bacillus thuringiensis.  
OS Synthetic.  
XX  
XX WO200234774-A2.  
PN  
XX  
PD 02-MAY-2002.  
XX  
XX 24-OCT-2001; 2001WO-US45468.  
XX  
XX 24-OCT-2000; 2000US-242838P.  
PR 23-OCT-2001; 2001US-0032717.  
XX  
XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
XX Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;  
PI  
XX  
XX WPI; 2002-519178/55.  
DR N-PSDB; ABK87256.  
XX  
XX  
XX New isolated pesticidal polypeptide useful for impacting insect pest  
PT e.g. Colorado potato beetle  
PT  
PS Claim 23; Page 162-164; 176pp; English.  
XX  
XX The present invention relates to a new pesticidal polypeptide. The  
CC invention is useful for impacting an insect pest by applying the  
CC the molecules of the invention to the environment of the insect pest by  
CC spraying, dusting, broadcasting, or seed coating, where the insect pest  
CC is selected from Colorado potato beetle, western corn rootworm or  
CC southern corn rootworm. The invention is also useful for increasing  
CC insect target range and for producing transgenic microorganisms and  
CC plants that express the pesticidal polypeptide. The invention is also  
CC useful for producing transformed plants and in transforming any organism  
CC to produce the pesticidal polypeptide of the invention. the present  
CC amino acid sequence represents a Bacillus thuringiensis mutant Cry1218  
CC endotoxin protein.  
XX  
SQ Sequence 673 AA;

Query Match 55.3%; Score 3499; DB 23; Length 673;  
Best Local Similarity 99.4%; Pred. No. 2.3e-226;  
Matches 669; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 MSPNNQNEVEIIDATPSTSVNSDNRYPFANEPTNALQNDYKDYLMKSGAGNASEYPGSP 60  
DB 1 MSPNNQNEVEIIDATPSTSVNSDNRYPFANEPTNALQNDYKDYLMKSGAGNASEYPGSP 60  
QY 61 EVLVSGQDAAKAADIIVGKLLSGLVGPIVSLYTLQIDILWPSGKSWEIFMEQVE 120  
DB 61 EVLVSGQDAAKAADIIVGKLLSGLVGPIVSLYTLQIDILWPSGKSWEIFMEQVE 120  
QY 121 ELINOKIARYARNKALSELEGLGNNYQLYLTALKEEENP-----NGSRALRDVRNRFEL 176  
DB 121 ELINOKIARYARNKALSELEGLGNNYQLYLTALKEEENPRLMSNGSRALRDVRNRFEL 180  
QY 177 DSLFTQYMPSPRVTFEVPFLTVYMAANLHLLKLDASI FGEWGWSTTTINNYDROM 236  
DB 181 DSLFTQYMPSPRVTFEVPFLTVYMAANLHLLKLDASIFGEWGWSTTTINNYDROM 240  
QY 237 KLTAEYSDHCWKYETGLAKGTSAKQWVDYNOFPREMTLAVLDVVALFPNYDRTYPM 296  
DB 237 KLTAEYSDHCWKYETGLAKGTSAKQWVDYNOFPREMTLAVLDVVALFPNYDRTYPM 296

DB 241 KLTAEYSDHCWKYETGLAKGTSAKQWVDYNOFPREMTLAVLDVVALFPNYDRTYPM 300  
QY 297 ETKAQLTREVTDPGLGAVNVSSIGSWYDKAPSGFVIESVIRPPHVPDYITGLTVYTQSR 356  
DB 301 ETKAQLTREVTDPGLGAVNVSSIGSWYDKAPSGFVIESVIRPPHVPDYITGLTVYTQSR 360  
QY 357 SISSARYIRHWAGHQISYHRVSRGSLQOMYGTGNQNLHSTSTFTDFTNYDIYKTLSDAVL 416  
DB 361 SISSARYIRHWAGHQISYHRVSRGSLQOMYGTGNQNLHSTSTFTDFTNYDIYKTLSDAVL 420  
QY 417 LDIVYPGYTIYFFGMPVEYEFPMVNLNTRKTLKPNVSKDIIASTRSELELPPETSQ 476  
DB 421 LDIVYPGYTIYFFGMPVEYEFPMVNLNTRKTLKPNVSKDIIASTRSELELPPETSQ 480  
QY 477 PNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCDNLP 536  
DB 481 PNYESYSHRLCHITSIPATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCDNLP 540  
QY 537 FVPVVKPGHTGGDLLOYNRSTGSGVTFLFARYGLALEKAGKYRVLRYATDADIVLHVN 596  
DB 541 FVPVVKPGHTGGDLLOYNRSTGSGVTFLFARYGLALEKAGKYRVLRYATDADIVLHVN 600  
QY 597 DAQIOMPKTMNPGEDLTSKTPKVADAITTLNLTADSSALKHNLGDPNSTLSGIVYVDR 656  
DB 601 DAQIOMPKTMNPGEDLTSKTPKVADAITTLNLTADSSALKHNLGDPNSTLSGIVYVDR 660  
QY 657 IEFIPVDETYEAE 669  
DB 661 IEFIPVDETYEAE 673

Search completed: January 7, 2003, 05:13:49  
Job time : 75 secs





ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus thuringiensis  
STRAIN: kumamotoensis  
INDIVIDUAL ISOLATE: 50C  
IMMEDIATE SOURCE:  
LIBRARY: Lambdagem-11 library of L. Poncerra  
CLONE: 50C (b)  
US-08-315-468-4

Query Match 78.3%; Score 4959.5; DB 1; Length 1169;  
Best Local Similarity 79.8%; Pred. No. 0;  
Matches 967; Conservative 68; Mismatches 128; Indels 49; Gaps 8;

QY 1 MSPNNQNEVEIIDATPSTSVNSDNRYPANEPNALQNDYKDYDKMSAGNASVEYPGSP 60  
DB 1 MSPNNQNEVEIIDATPSTSVNSDNRYPANEPNALQNDYKDYDKMSAGNASVEYPGSP 60  
QY 61 EYLVSGQDAKAAIDIVGKLLSGLPVPGPIVSLYTLQIDILWPSEKQSEIEMEYVE 120  
DB 61 EYLVSEQDAKAAIDIVGKLLSGLPVPGPIVSLYTLQIDILWPSEKQSEIEMEYVE 120  
QY 121 ELINOKIABYARNKALSELEGNNYQLYLTALKEEHPNGSRALRDVNRFEILDSLF 180  
DB 121 ELINOKIABYARNKALSELEGNNYQLYLTALKEEHPNGSRALRDVNRFEILDSLF 180  
QY 181 TOYMPSEFRVNEFVPELTYVMAANLHLLLDKASIFGEWGWSTTTINNYDROMKLT 240  
DB 181 TOYMPSEFRVNEFVPELTYVMAANLHLLLDKASIFGEWGLSTTTINNYNRQMKLT 240  
QY 241 EYSDHCVKWYETGLAKLKGTSKQWVDYQFREMFLAVLDVVALLFPNDYTRTPMETKA 300  
DB 241 EYSDHCVKWYETGLAKLKGTSKQWVDYQFREMFLAVLDVVALLFPNDYTRTPMETKA 300  
QY 301 QUTREYVTDPLGANVSSIGSWYDKAPSGVIESSVIRPHVFDYITGLTVYQSRIS 360  
DB 301 QUTREYVTDPLGANVSSIGSWYDKAPSGVIESSVIRPHVFDYITGLTVYQSRIS 360  
QY 361 ARYIRHWAGHOISYHVRSGNSLQMGYGNONLHSTPDTFYNDYIKTISKDAVLLDIV 420  
DB 361 ARYIRHWAGHOISYHVRSGNSLQMGYGNONLHSTPDTFYNDYIKTISKDAVLLDIV 420  
QY 421 YPGYTYIFFGMEPEVEFMVNLNRTKLKYNPVSXIIASTRDSLELPPETSDQPNYE 480  
DB 421 YPGYTYIFFGMEPEVEFMVNLNRTKLKYNPVSXIIASTRDSLELPPETSDQPNYE 480  
QY 481 SYSHRLCHITSPATGNTGLVPVSWTHRSADLNNTIYSDKITQIPAVKWNLDLPVPV 540  
DB 481 SYSHRLCHITSPATGNTGLVPVSWTHRSADLNNTIYSDKITQIPAVKWNLDLPVPV 540  
QY 541 VKPGPHTGGDLQYNRSTGVTFLFARYGLALEKAGYVRVRYATDADIVLHV---N 596  
DB 541 VKPGPHTGGDLQYNRSTGVTFLFARYGLALEKAGYVRVRYATDADIVLHV---N 596  
QY 597 DAQIQMPT-MNPG-ELTSKTFKVDATITLMLATDSSLAKHNLGDPNSTLSGIVYV 654  
DB 597 DAQIQMPT-MNPG-ELTSKTFKVDATITLMLATDSSLAKHNLGDPNSTLSGIVYV 654  
QY 655 DRIEIPVDETEAEQDLBAKAVNALFTNFKDGLRPGVTDYEVNQANLVECLSDLY 714  
DB 655 DRIEIPVDETEAEQDLBAKAVNALFTNFKDGLRPGVTDYEVNQANLVECLSDLY 714  
QY 715 PNEKRLFDPAVEAKLSEARNLQDPDQOEINGENGWSTASTGIEVGDALPKGYRL 774  
DB 715 PNEKRLFDPAVEAKLSEARNLQDPDQOEINGENGWSTASTGIEVGDALPKGYRL 774  
QY 775 PGAREIDTETPTLYLQKVEEGLKPYTRYLRGFGVSSQGLEIFIRHQTNRIVKNVPD 834  
DB 775 PGAREIDTETPTLYLQKVEEGLKPYTRYLRGFGVSSQGLEIFIRHQTNRIVKNVPD 834  
QY 835 DLLPDVSPVNSDGSINRCSEQKYNVSRLEVNRSGBAHEFSIPIDTGEIDYENAGI 894  
DB 835 DLLPDVSPVNSDGSINRCSEQKYNVSRLEVNRSGBAHEFSIPIDTGEIDYENAGI 894

QY 895 FKITDEGYATLGNLELVEEGPLSGDALERLOREQQWKIOMTRREETDRYMASKQAV 954  
DB 895 FKITDEGYATLGNLELVEEGPLSGDALERLOREQQWKIOMTRREETDRYMASKQAV 949  
QY 955 DRLYADYQDQQLNPVDITDLTAAQDLIQSIPIYVYNMPPPEIPGMNYTKFTLTDLRLOA 1014  
DB 955 DRLYADYQDQQLNPVDITDLTAAQDLIQSIPIYVYNMPPPEIPGMNYTKFTLTDLRLOA 1009  
QY 1015 WSLYDORNAIENGDFRGLSNWNPATPGVEQOINHTSVLVIENWDEQVSOQFTVQPNQRY 1074  
DB 1015 WSLYDORNAIENGDFRGLSNWNPATPGVEQOINHTSVLVIENWDEQVSOQFTVQPNQRY 1069  
QY 1075 VLRVTRARKEGVNGVYVSRDGGNQTETITFSASDYDTNGMYNTQVSNNTGYNNTNAYNTQ 1134  
DB 1075 VLRVTRARKEGVNGVYVSRDGGNQTETITFSASDYDTNGMYNTQVSNNTGYNNTNAYNTQ 1108  
QY 1135 ASSTNGYNANNMYNTQASNTNGYNTNSVNDQGTYYTKTVPYPTDQMIEMSETEGTF 1194  
DB 1135 ASSTNGYNANNMYNTQASNTNGYNTNSVNDQGTYYTKTVPYPTDQMIEMSETEGTF 1157  
QY 1195 YIESVELIVDVE 1206  
DB 1195 YIESVELIVDVE 1169

## RESULT 2

US-07-876-280-30  
; Sequence 30, Application US/07876280  
; Patent No. 5262158  
; GENERAL INFORMATION:  
; APPLICANT: Payne, Jewel M.  
; APPLICANT: Cannon, Raymond J.C.  
; APPLICANT: Bagley, Angela L.  
; TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for  
; TITLE OF INVENTION: Controlling Acarides  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/876,280  
; FILING DATE: 19920430  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: M/S 104  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1157 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: YES  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
; STRAIN: kumamotoensis  
; INDIVIDUAL ISOLATE: PS50C

IMMEDIATE SOURCE:  
CLONE: E. coli NM522(pMYC2320) NRRL B-18769  
US-07-876-280-30

Query Match 62.4%; Score 3950.5; DB 1; Length 1157;  
Best Local Similarity 65.5%; Pred. No. 5.9e-284;  
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

QY 1 MSPNQNEYIIDATPSTSVNSDSNRYPFANEPTNALQNDYDYLKMSAGNASEYPCSP 60  
DB 1 MSPNQNEYIIDATPSTSVNSDSNRYPFANEPTDALQNNYKDYLYKMSGENFELFNP 60

QY 61 EVLVSGDAKAAIDIVKLLSGLVFVPGFIVSLYTLQIDILWPSGEKSQWEIFMQVE 120  
DB 61 ETPIS-SSTIQTGIGVIRILGALGVFASQIASFYFIVGQLWPSKVDIWMERVE 119

QY 121 ELINOKIABYARNKALSELGLGNNYQIYLTALFEWENPNSGALDRVRNRPILDSLP 180  
DB 120 ELVDQKIERKVKOKALAEKGLGNALDVYQOQSLDMLNDRDARTSVSVNQFALDLP 179

QY 181 TQWPSFRVTNFVFPFVTVYAMAANLHLLKASIFGEHMGWSTTTNNYDROMKLT 240  
DB 180 VSSIPFAVSGHEVLLAVYAQVNLHLLLRDASIFGEHMGFTPGELSRFYNQVQLTA 239

QY 241 EYSDHCVKYETGLAKLGTSAKQWVDYNQPRREMTLAVLDVVALFPNYDTRTYPMETKA 300  
DB 240 EYSDYCVKWKIGLDKLGTSKSWLTHQPRREMTLLVLDLVALFPNYDTHMPTIETTA 299

QY 301 QLRVYVTDPLGAVNVSIGSWDKARFQV----ISSVTRPHVFDYITGLTYTQSR 356  
DB 300 QLRDVTYDPIAFNIVTSTGFCNPMWTHSGILFYEVENNVRPPLFDILSSVEINT-SR 358

QY 357 ---SISARVIRHWAGHOISYHRSRSGNLQOMGTQNLHSTSTFDFTNYDIVKTLSD 413  
DB 359 GGIYTLNDAIVNWSGHTLKYRRTA-DSTVYTYANYGRITSEKSPALEDRDIFEINSTV 417

QY 414 AVLLDIYVPGTYTIFPGMEVPEFFMVNQANRKLKYNPVSKDIIASTR--DSELELPP 471  
DB 418 ANLANYOKAY----GVPGSFHVMKRGTSSTAYLYSKTHALQCTQVYESSDEPL 472

QY 472 ETSQDPNYESYSHRLCHITSIPATGNT---GLVPVSWTHRSADLNTIYSDKITQIPA 528  
DB 473 DRT-VPAVESYSHRLSHITSFSGKNGSAYGSPFVFWTHTSADLNTIYSDKITQIPA 531

QY 529 VKCWDNLPEV--PVVKGPHGTGDLLOYNRSTGVTGLFLARYGLALEKAGKYRVLRYA 586  
DB 532 VK--GDMILGGSVVQPGFTGGDLK--RTNPSILGTFAVTVNGSLSQ--RYRVRIRYA 585

QY 587 --TDADIVLVHND--QIQPKTNWPGEDLTSKTPKVADAITTLNL-ATDSSLAK--H 638  
DB 586 STTDFEFTLYLGDITKRNPNKMDNGASLTYTEFKFASFTDQFRETQDKILLSMGDF 645

QY 639 NLGSDPNSTLSGIVYVDRIEPIVDTEYAEODLEAKKANALFTNTKQGLRPGVTDYE 698  
DB 646 SSGOE-----VYIDRIEPIVDTEYAEQDLEAKKANALFTNTKQGLRPGVTDYE 697

QY 699 VNOANLVECLSDLLYNEKELLDAVREKRLSEARNLQDDPQFQINGENGWTAAGI 758  
DB 698 VNOANLVECLSDLLYNEKELLDAVREKRLSGARNLQDDPQFQINGENGWTAAGI 757

QY 759 EVIEGDALFKGRYLRLPGAREIDTETPTLYLYQKVEGVLPYTRYLRGFGVSSQGLEI 818  
DB 758 EIVGDAVFKGRYLRLPGAREIDTETPTLYLYQKVEGVLPYTRYLRGFGVSSQGLEI 817

QY 819 FTIRHQRNIRKVNVPDILLPVSPVNSDGSINRCSQKYVNSRLNVRNRSGEAHEFSLPI 878  
DB 818 YTIHQNRIRKVNVPDILLPVSPVNSDGSINRCSQKYVNSRLNVRNRSGEAHEFSLPI 877

QY 879 DTGEBIDNENAGIIVGPKITDPEGVATLGNLEVEEGLSGDALERLQRESQWKIOWTR 938  
DB 878 DIGELSDNENAGIIVGPKITDPEGVATLGNLEVEEGLSGDALERLQRESQWKIOWTR 937

QY 939 RREEDRRYMASQAVDRLYADYQDQQLNPVBEITDLTAAQDLIQSIPIVYVNMFPPEIPG 998

Query Match 62.4%; Score 3950.5; DB 1; Length 1157;

Best Local Similarity 65.5%; Pred. No. 5.9e-284;  
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

QY 1 MSNNQNEYELIADPTSTSVNSNRPPEANETNALONNDYKDYLMKSAGNASEYEGSP 60  
DB 1 MSNNQNEYELIADPTSTSVNSNRPPEANETNALONNDYKDYLMKSAGNASEYEGSP 60  
QY 61 EVLVSGDAAKAAADIIVGKLLSGLVGFVGVPIVSLYTLQIDILWPSGEKSEWEIFMEQVE 120  
DB 61 ETIS-SSTIQTGIGIVRGILGALGVFAQIASFYFIVQLWPSKSDVINGEMERVE 119  
QY 121 ELINQKIARYARKALSELGELGNNOYLYTALREWENPNPSSALRDVNRPIILDSLF 180  
DB 120 ELVDQKIEKVOKALAEALGKGNALDVYQOSLSDWLENRDARTSRVSVNQFALDLNF 179  
QY 181 TOYMSPSRVTFEVPFLTVVYAMANTHLLKLDASIFGEWGWSTTINNYDROMKLTA 240  
DB 180 VSSIPSAVSGHEVLLLAQAQVNLHLLLDASIFGEWGWSTTINNYDROMKLTA 239  
QY 241 EYSDHCVKVETGLAKIGTSKOWVDYNOFRREMTLAVLDVVALFPNYDTRTYPMETKA 300  
DB 240 EYSDYCVKWKIGLKGTSKSWYVHQFRREMTLLVLDLVALFPNYDTHYPIETTA 299  
QY 301 QLTREVTYDPLGAVNVSIGSWDKAPSGV-IBSSVIRPHVFDYITGLVYVYQSR 356  
DB 300 QLTREVTYDPLGAVNVSIGSWDKAPSGV-IBSSVIRPHVFDYITGLVYVYQSR 356  
QY 357 ---SISARIRHWAGHQSIVHRSRGSNLOQMYGTQNLHSTSTFPTNYDIYKTLSD 413  
DB 359 GGITLNDAYINWSGHTLYKRTA-DSTVTYNTANYGRITSEKNSPALEDRIFEINSTV 417  
QY 414 AVLLDIVYGVYTFEFGMEVEFPMVQNLNTRKTLKYNPVSKDIIAISTR--DSELELPP 471  
DB 418 ANLANYQKAY-----GVPGSWFWMVRGTSSTAYLYSKTHLTALOGCTQVYESDRIPL 472  
QY 472 ETSQPNYESYSHRLCHITSPATGNTT---GLVPVFSWTHRSADLNNITYSDKITQIPA 528  
DB 473 DRT-VPVAESYSHRLSHITSHSPKNGSAYYGFVFWTHTSADLNNITYSDKITQIPA 531  
QY 529 VKCWDNLFPV--PVVKGPGHTGDLLOYNRSTGSGVTLFLARYGLALEKAGKYRLRYA 586  
DB 532 VK--GDMLYLGGSVQVQPGFTGGDILK--RTNPSILGTFAVTVNGSLSQ--RYRVRIRYA 585  
QY 587 --TDADIVLHVND--OIQPKTNPCEDLTSKTFKVADAITLNL-ATDSSLALK--H 638  
DB 586 STTDFEFTLVGLDTIEKRNFKNTWNGASLYTFEYFKASFITDQFRETQDKILLSGWDP 645  
QY 639 NLGEDPNSTLSGIYVVDRIEPIVDETYEAEQDLEAAKAVNALFTNTKGLRPGVTDYE 698  
DB 646 SSGQE-----VYIDRIEPIVDETYEAEQDLEAAKAVNALFTNTKGLRPGVTDYE 697  
QY 699 VNOANLVECLSDDLYPNEKELLFDVAREAKRLSEARNLQDDPFOINGENGTASTGI 758  
DB 698 VNOANLVECLSDDLYPNEKELLFDVAREAKRLSGARNLQDDPFOINGENGTASTGI 757  
QY 759 EVLEGDALFKGYRLRLGAREIDTETPTLYQKVEGVLPKYTRYRLRGPVSGSQGLEI 818  
DB 758 EIVEGDVAFKGYRLRLGAREIDTETPTLYQKVEGVLPKYTRYRLRGPVSGSQGLEI 817  
QY 819 FTIRHOTNRIVKVPDILLPDVSPVNSDGSINRSEQKYNSRLEVENRSGEAHEFSIPI 878  
DB 818 YTIHOTNRIVKVPDILLPDVSPVNSDGSINRSEQKYNSRLEGENRSGDAHEFSIPI 877  
QY 879 DTGEIDNENAGIIVWPKITDPGEYATIGNLELVEBGPGLSGDALERLQREQQWKIOWTR 938  
DB 878 DIGELDYNENAGIIVWPKITDPGEYATIGNLELVEBGPGLSGDALERLQREQQWKIOWTR 937  
QY 939 RREEDRRYKASKAVDRLYADYQDQQLNPDEITDLTAAQDLIQSIPIVYNEMFPEIPG 998  
DB 938 RREEDRRYKASKAVDRLYADYQDQQLNPDEITDLTAAQDLIQSIPIVYNEMFPEIPG 997  
QY 999 MNYTKFTELTDLRQAAWLYDQRNAIPNGDFRNLGNLNNATPGVEVQOINHTSVLIPNW 1058  
DB 999 MNYTKFTELTDLRQAAWLYDQRNAIPNGDFRNLGNLNNATPGVEVQOINHTSVLIPNW 1058

DB 998 MNYTKFTELTDLRQAAWLYDQRNAIPNGDFRNLGNLNNATPGVEVQOINHTSVLIPNW 1057  
QY 1059 DEQVSOQFTVQPNQRYVLRVTAKEGVGNGYVIRDGNGQOTELTFSASDYDNGMYNTQ 1118  
DB 1058 DEQVSOQFTVQPNQRYVLRVTAKEGVGNGYVIRDGNGQOTELTFSASDYDNG 1112  
QY 1119 VSTNGYNTNNAYNTOASSTNGYNNANMYNTQASNTNGYNTNNSVYNDQTYIKTYTFFIP 1178  
DB 1113 -----VYNDQTYIKTYTFFIP 1129  
QY 1179 YTDQMIEMSETEGTFYIESVELIVDVE 1206  
DB 1130 YTDQMIEMSETEGTFYIESVELIVDVE 1157  
RESULT 4  
US-08-315-468-2  
; Sequence 2, Application US/08315468  
; Patent No. 5554534  
; GENERAL INFORMATION:  
; APPLICANT: Michaels, Tracy Ellis  
; APPLICANT: Foncerrada, Luis  
; APPLICANT: Narva, Kenneth E.  
; TITLE OF INVENTION: Process for Controlling Scarab Pests  
; TITLE OF INVENTION: with Bacillus thuringiensis Isolates  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/315,468  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/014,941  
; FILING DATE: 01 FEB 1993  
; APPLICATION NUMBER: 07/828,430  
; FILING DATE: 30-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/808,316  
; FILING DATE: 16-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: MA73.C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1157 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEetical: YES  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
; STRAIN: kumamotoensis  
; INDIVIDUAL ISOLATE: PS50C  
; IMMEDIATE SOURCE:  
; LIBRARY: Lambdagem (TM) - 11 LIBRARY OF LUIS FONCERRADA  
; CLONE: 50C(a)

US-08-315-468-2

Query Match 62.4%; Score 3950.5; DB 1; Length 1157;  
Best Local Similarity 65.5%; Pred. No. 5.9e-284;  
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

QY 1 MSPNNQNEVEIIDATSTSVNSDSNRYPPANEPNALONMDYKDYLOASAGNASEVPGSP 60  
DB 1 MSPNNQNEVEIIDATSTSVNSDSNRYPPANEPNALONMDYKDYLOASAGNASEVPGSP 60

QY 61 EVLVSGQDAKAADIDVGLKSLGLGVPPFVPIVSLYTLQDILILPSPCKSQWEIFMEOVE 120  
DB 61 ETPIIS-SSTIQTGIGVIRILGALGVFASQIASFYSFIVGLWPSPKSDVIGSEIMERVE 119

QY 121 ELINQIAEYARNKALSELGLGNVYQLYLTALREEMENPNRSGALRDVNRPEILDLSLF 180  
DB 120 ELVDQKIEKVVKALAEKGLGNALDVYQOSLEDMLENRDARTSRVSVNQFALDLP 179

QY 181 TQYMPFRVTNFEVFTVTVYAMAAHLHLLKODASIFGEBGWSTTTNNYDRQMKLTA 240  
DB 180 VSSIPSFANSGHEVLLAVTAQAANLHLLLRDASIFGEBGWSTPGEISRFYNRQVQLTA 239

QY 241 EYSDHCWKVETGLAKCTSAKQWVDYQFRREMTLAVLDVVALPNNYDTRTYPMETKA 300  
DB 240 EYSDYCVKWKYKIGLDKLGTTSKSWLNYHOFREMTLLLDLVALPNNYDTHMYPIETTA 299

QY 301 QLTREVTYDPLGANVWSSIGSYDKAPSGV-IESSVIRPPHVEDYITGLTVYQSR 356  
DB 300 QLTREVTYDPLGANVWSSIGSYDKAPSGV-IESSVIRPPHVEDYITGLTVYQSR 356

QY 357 ---SISARYIRHWAGHOISYHRVRSNLOQMVGTYNQNLHSTSTFPTNYDIYKTLSD 413  
DB 359 GGITLNDAYINWSGHTLYKRTA-DSTVITYANYGRITSEKNSPALEDRIPEINSTV 417

QY 414 AVLLDIVPGTYTIFPGMEVEPPWNLQNLNTRKLNPNVSKDIIASTR--DSELELPP 471  
DB 418 ANLANYQKAY-----GVPGSWFHWKRGTSSTAYLYSKTHALQCTQVYESSDRIPL 472

QY 472 ETSQDPNYSYSHLCHITSPATGNTT---GLVPFSWTHRSADLNTIYSDKITQIPA 528  
DB 473 DRT-VFVAESYSHLSHITSHSPKNGSAYGSPFVFWTHSTADLNTIYSDKITQIPA 531

QY 529 VKCWNLPFV--PVVKGFGHTGDLQYNSRSGVGLFLARYGLALEKAGKYRVLRYA 586  
DB 532 VK--GDMLYLGGSVVQPGFTGGDILK--RTNPSILGTFVAVNGSLSQ--RYRVRIRYA 585

QY 587 --TDADIVLVHND--QIQPKTNWPEDLTSTFKVADAITTNL-ATDSSLAK--H 638  
DB 586 STTDFEFTLYLGDTEKRNFKNTMDNGASLTFTFKPASFTDFQFRETQDKILLSMGDF 645

QY 639 NLGEDPNSTLSGIVVYDRIEPIVDETYEASQDLEAAKAVNALFTNTKGLRPGVTDYE 698  
DB 646 SSGQ8-----VYIURIPIVDETYEASQDLEAAKAVNALFTNTKGLRPGVTDYE 697

QY 699 VNQAANLVECLSDDLYPNEKELLFPAVREAKRLSEARNLLQDPDFQIEINGENGWASTGI 758  
DB 698 VNQAANLVECLSDDLYPNEKELLFPAVREAKRLSEARNLLQDPDFQIEINGENGWASTGI 757

QY 759 EVIEGDALFKGYRLRLPGAREIDTETPTLYLYQKVEGVLPKYTRYLRGLRFGVSSQGLEI 818  
DB 758 EIVEGDALFKGYRLRLPGAREIDTETPTLYLYQKVEGVLPKYTRYLRGLRFGVSSQGLEI 817

QY 819 FTIRHQTNRIVKNVPPDLLPVSVPNSDGSINRCSEQKYVNSRLEVENRSGEAHEFSPI 878  
DB 818 YTHHQTNRIVKNVPPDLLPVSVPNSDGSINRCSEQKYVNSRLEVENRSGEAHEFSPI 877

QY 879 DTGEIDYNENAGIWWGFKITDPEGVATLGNLELVEEGPLSGDALERLQREBQWKIOMTR 938  
DB 878 DIGELDYNENAGIWWGFKITDPEGVATLGNLELVEEGPLSGDALERLQREBQWKIOMTR 937

QY 939 RREETDRRYMAKQAVDRLYADYQDQQLNPVDEITDLTAAQDLIQSIPIVYVNMPEPIPG 998  
DB 938 RREETDRRYMAKQAVDRLYADYQDQQLNPVDEITDLTAAQDLIQSIPIVYVNMPEPIPG 997

## RESULT 5

US-07-941-650A-2  
; Sequence 2, Application US/07941650A  
; Patent No. 6294184  
; GENERAL INFORMATION:  
; APPLICANT: Uyeda, Kendrick A.  
; APPLICANT: Bradfisch, Gregory A.  
; TITLE OF INVENTION: Process for Controlling Lepidopteran Pests  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/941,650A  
; FILING DATE: 19920908  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/758,020  
; FILING DATE: 12-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/658,935  
; FILING DATE: 21-FEB-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/642,112  
; FILING DATE: 16-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1157 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
; STRAIN: kumamotoensis  
; INDIVIDUAL ISOLATE: PS50C  
; IMMEDIATE SOURCE:  
; CLONE: E. coli NM522(pMYC1638), NRRL B-18751

US-07-941-650A-2

Query Match 62.4%; Score 3950.5; DB 4; Length 1157;  
Best Local Similarity 65.5%; Pred. No. 5.9e-284;  
Matches 804; Conservative 120; Mismatches 211; Indels 93; Gaps 19;

QY 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNDYKYLKMSAGNASYPGSP 60  
DB 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTDALQNMNYKYLKMSGGENPELFGNP 60

QY 61 EVLVSGQDAAKAAIDIVCKLISGLGVPFVGIVSYLTQILDLWPSGKSOEIPMEQVE 120  
DB 61 ETVFIS-SSTIQTGIGVIRIIGLGLVPPASQIFASFSYFVIGQLWPSKSDVINGEIMERVE 119

QY 121 ELINOKIAEYARNKALSEGLGNNYQLYLTALBEWENPNPGRALDRVRNREFILDSLF 180  
DB 120 ELVDQKTEKYVKDKALAEKLGKGNALDVYQOSLEWLENRNDARTRSVVSNOQFALDINF 179

QY 181 TQYMPSFRVTNFPVFFLVYAMAANLHLLLLKDISIFGEEWGSTTTINNYDROMKILTA 240  
DB 180 VSSIPSPAVSGHEVLLAVYAQAQVNLHLLLRDASIFGEEWGSTTPEISRFVNRQVQLTA 239

QY 241 EYSDHCWKYETGLAKLGTSAKQWYDYNQFRREMTLAVLDVVALFPNYDTRTPMETKA 300  
DB 240 EYSDYCYKWKYIGLDKLGKGTTSKWLNYHQFRREMTLLVLDLVALFPNYDTHMYPETTA 299

QY 301 QLTREVYTDPLGAVNVSGISGWYDKAPSGV-IESSVIRPPHVRDYITGLTVYTOSR 356  
DB 300 QLTREVYTDPIAFNIVSTGFCNPNWTHSGILFYEVENNVIRPPLFDILSSVEINT-SR 358

QY 357-SSISARYIRHWAGHOISYHRSVRSNQQMYGTNQLNSTSTDFDNYDIYKTLASKD 413  
DB 359 GGITLNDAYINYSHTLKVRRTA-DSTVTVYANYGRITSEKNSFALEDREDIPEINSTV 417

QY 414 AVLLDIVYPGYTYLFFGMEPEVFPWVQNLNTRKTLKXNPVSKDIIASTR--DSELELPP 471  
DB 418 ANLANYQKAY-----GVPGSWFHWKRGTSSTAYLYSKTHTALQGTQVYESSDEIPL 472

QY 472 ETSQPNVESYSHRLCHITSIPATGNTT--GLVPVFSWTHRSADLNNIYSDKIKTOIPA 528  
DB 473 DRT-VPAESYSHRLSHITSHSPSKNGSAYYSGPFVFWTHTSADLNNIYSDKIKTOIPA 531

QY 529 VKWDLNLPFV--PVKPGHGTGDLLOVNRSTGVTGLFLARYGLALEKAGKYRVLRYA 586  
DB 532 VK--GDMLYLGGSVVQPGFGTGGDLK--RTNPSILGTFAVTVNGSLQ--RYRVRIRYA 585

QY 587--TDADIVLVHUNDA--QIQPKTNPGEDELTSKTFKVADATITNL-ATDSSLAK---H 638  
DB 586 STTDFEFTLYGDTIEKRNFKNTMDNGASLTYETFKTASFTIDFQFRETQDKILLSMGDF 645

QY 639 NLGEDPNSTLSGIVVDRIBFIPVDETVEABODLEAAKAVNALPTNTKGLRPGVTDYE 698  
DB 646 SSGQE-----VYIURIIFIPVDETVEABODLEAAKAVNALPTNTKGLRPGVTDYE 697

QY 699 VQAANLVECLSDLYPNEKRLFDVAREAKRLSEARNLLQDDPQFQINGENGWTAETGI 758  
DB 698 VQAANLVECLSDLYPNEKRLFDVAREAKRLSGARNLLQDDPQFQINGENGWTAETGI 757

QY 759 EVLEGDALFGRYLRLPGAREIDTETPTLYLYQKVEGVLKPYTRYRLRPGVSSQGLEI 818  
DB 758 EIVEGDAVFGRYLRLPGAREIDTETPTLYLYQKVEGVLKPYTRYRLRPGVSSQGLEI 817

QY 819 FTIRHOTNRIVKXNPVDDLDPVSPVNSDGSINRCSEOKYVNSRLEVRNRSCEAHSFPI 878  
DB 818 YTIHQTNRIKXNPVDDLDPVSPVNSDGSINRCSEOKYVNSRLEVRNRSCEAHSFPI 877

QY 879 DTGEIDYNENAGIUVGPKITDPEGYATLGNLVEEGLSGDALERLQREEQWQKIQWTR 938  
DB 878 DIGELDYNENAGIUVGPKITDPEGYATLGNLVEEGLSGDALERLQREEQWQKIQWTR 937

QY 939 RRETDYRYNASKQAVDRLYADYQDQQLNPDVEITDTLTAADLIQSIPTVYNEMFPPIPG 998  
DB 938 RRETDYRYNASKQAVDRLYADYQDQQLNPDVEITDTLTAADLIQSIPTVYNEMFPPIPG 997

QY 999 MNYTKFTLTDLQOAMSLYDORNALPNGDFRNLGNLNNATPGVEVQOINHTSVLVIPIPW 1058  
DB 998 MNYTKFTLTDLQOAMSLYDORNALPNGDFRNLGNLNNATPGVEVQOINHTSVLVIPIPW 1057

QY 1059 DEQVSQOFTVQPNORYLVLTARKEGVNGVYSIRDCGNQOTETLTFASDSDYDTNGMYNQ 1118  
DB 1058 DEQVSQOFTVQPNORYLVLTARKEGVNGVYSIRDCGNQOTETLTFASDSDYDTNGMYNQ 1112

QY 1119 VSTNGYNTNAYNTQASSTNGYNNANNMYNTQASNTNGYNTNSVYNDQOTGYITKVTTFIP 1178  
DB 1113 -----VYNDQOTGYITKVTTFIP 1129

QY 1179 YTDQMWIEMSETEGTFYIESVELIVDVE 1206  
DB 1130 YTDQMWIEISETEGTFYIESVELIVDVE 1157

## RESULT 6

US-07-915-203-2  
; Sequence 2, Application US/07915203  
; Patent No. 5359048  
; GENERAL INFORMATION:  
; APPLICANT: Ohba, Michio  
; APPLICANT: Iwabana, Hidenori  
; APPLICANT: Sato, Relichi  
; APPLICANT: Suzuki, No. 5359048ukazu  
; APPLICANT: Ogiwara, Katsutoshi  
; APPLICANT: Sakanaka, Kazunobu  
; APPLICANT: Hori, Hidetaki  
; APPLICANT: Asano, Shouji  
; APPLICANT: Kawasaki, Tadaaki  
; TITLE OF INVENTION: No. 5359048el Microorganism and Insecticide  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: US  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; APPLICATION NUMBER: US/07/915,203  
; FILING DATE: 19920723  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: M/K 301  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1149 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-915-203-2

Query Match 47.7%; Score 3021; DB 1; Length 1149;  
Best Local Similarity 50.2%; Pred. No. 4.3e-215;  
Matches 623; Conservative 177; Mismatches 295; Indels 146; Gaps 23;

QY 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNDYKYLKMSAGNASYPGSP 60  
DB 1 MSPNNQNEYIIDATPSTSVNSDNRYPFANEPTNALQNDYKYLKMSAGNASYPGSP 60



QY 181 TOYMPSEFRVTNEVEPFLTVYAMAANLHLLKDDASIFGEWGWSTTTINNYDQWMLTA 240  
DB 181 RTNMGFSFQTNVETPLPTTAAQASLHLVWMDVQVIGKRWGPQNDIDLKYEQVSYTA 240  
QY 241 EYSDHCWYETGLAKLKTSAQWVDYNOFRREMTLAVLDVVALPPNYDTRTYPMETKA 300  
DB 241 RYSDHCWYVWAGNKLKRGTKAQWVDYNRFRMNWVLDLVALPPNYDARIYPLETNA 300  
QY 301 QLTREYVTDPLGAV---NVSSGTSWD---KAPSEGVIESSVIRPHVDPVITGLTVVT 353  
DB 301 ELTREIFDTPVGSYVYGQSTLISWYDMPAALPSEFTLE-NLLRKPDPFTLLQEIEMVT 359  
QY 354 QSRSSISARYIRHWAGHOISYHVRSGSLQWYGNQNLHS-----TSTFDFTNYDIY 407  
DB 360 SFQNGTIEYNYWGGORUT-----LSYIGSFSFKVGLAGAEIDIPVQGNDDIY 410  
QY 408 KTLSDKAVLLDIVPG-YTYIFPGMEVEBFMVNQNLNTRKTLKYNPVSKDIIASTRDE 466  
DB 411 RVV-----WTYIGRYTNSLLGVNPVTFYF---SNNTQKTVS-KPKQFAGGKTIIDSG 458  
QY 467 LELPETSQPNYESYSHPLCHITS--IPATGNTT-GLVPVFSWTHRSADLNNIYSDKI 523  
DB 459 EELTYE-----NYQSYSHRVSIVTSFEIKSTGCTGLGVVPVIFGWTSSASRNNFIYATKI 513  
QY 524 TOIPAVKC-----WDNLPPV---PVVKGPHGTGDLLOVNRSTGSGVGLFLARYGL 571  
DB 514 SOIPINKASRTSGGAVNWPQELNGPVPWKLGS-SGSQVNLNLRVATDAKA----- 564  
QY 572 ALEKAGKYRVLRYATDADIVLHVN-----DAQIOMPKTMPNGBDLTSKTFKVAD 621  
DB 565 ---SORVIRIRYASDRAGKFTISSRSPENPATYSASIAYTNTWSTNASLTVSTPAYAE 620  
QY 622 AITTLNLTDS---LAKENLGEDPNSTLSGIYVVDRIEFPVDETYEAEQDLEAK 676  
DB 621 S-SPINLIGSGSRFTDISITKEAG-----AANLYIDRIEFIPVNTLFEAEEDLDVAK 672  
QY 677 KAVNALFTNTKDLRPGVTDYEVNOANLVECLSDLYENEXRLLFDVAREAKRLSEARN 736  
DB 673 KAVNGLFTNEKDALQTSVDYQVNOANLIECLSDLYENEXRMLMDVAREAKRLVQARN 732  
QY 737 LQDPDFQINGEWGTAETGIEVGEDALFKGRVRLFGAREIDTETPTTYLYQKVEG 796  
DB 733 LQDGTGFNRINGEWGTSVGTIEVGEVDLFDKDRSLRLTSAREIDTETPTTYLYQKIDBS 792  
QY 797 VLKPTRLRGFGVSSQGLEFTTRHOTNRIVKNVDPDLLPDPVSPVNSDGSINRCSEOK 856  
DB 793 LLKPYTRYKLGFGSSQDLEIKLIRHRANQIVKNVDPNLLPDRVPVNSCGGVDRCSQEQ 852  
QY 857 YVNSRLEVENR-----SGEAHEFSPTIDTGRIDYNNENAGIIVGPKITDPEGVATLGNLE 910  
DB 853 YDANLALENGENGMSSDSHAFSHIDTGEIDNENTGIWIFKPIPTNGATLGNLE 912  
QY 911 LVEGSLGDALERLQREEQWIKIOWTRREEDTDRRYMASKQAVDRLYADYQDQOLNPDV 970  
DB 913 FVEEGLSGTLEWAQOQOQOQWARKAASEKTYIAAKQIDRLFADYQDQKLSGV 972  
QY 971 EITDLTAQDLIOSIPYVYNEMFPEIPGMNYTKFTLDRLOQANSLYDQRNAIPNGDPR 1030  
DB 973 EMSDLLAAQNLVQSIPIVYVNDALPEIPGMNYTSFTLDRLOQANSLYDQNAIPNGDPR 1032  
QY 1031 NGLSNWNTAPGVEVOQINHTSVLVPNMDQVSOQFTVQPNORYLVRVTRKEGVNGVY 1090  
DB 1033 NGLSNWNTSDVNVQOQSDTSVLVLPNWNQVSOQFTVQPNORYLVRVTRKEGVNGVY 1092  
QY 1091 SIRDGNQTEITLTFGASVDYDNGMYNTQVSNNTNGYNTNAYNTQASSTNGYNNANMYNTQ 1150  
DB 1093 IIRDCANQTEITLTFNICDDDT-GVLST----- 1118  
QY 1151 ASNTNGYNTNSVNDQGTGIVTITVTFTPIVTDQWTEMSETE 1191  
DB 1119 -----DQTSYITKVTFTPEQWIDMSETE 1145

RESULT 8  
US-08-789-449-2  
; Sequence 2, Application US/08789449  
; Patent No. 5824878  
; GENERAL INFORMATION:  
; APPLICANT: Ohba, Michio  
; APPLICANT: Iwahana, Hidenori  
; APPLICANT: Sato, Reichi  
; APPLICANT: Suzuki, No. 5824878kukazu  
; APPLICANT: Ogiwara, Katsutoshi  
; APPLICANT: Sakanaka, Kazunobu  
; APPLICANT: Hori, Hidetaki  
; APPLICANT: Asano, Shouji  
; APPLICANT: Kawasugi, Tadaaki  
; TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: US  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/789,449  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,887  
; FILING DATE: 08-JUL-1994  
; APPLICATION NUMBER: US 07/915,203  
; FILING DATE: 23-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: M/K 301  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1149 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-789-449-2

Query Match 47.7%; Score 3021; DB 2; Length 1149;  
Best Local Similarity 50.2%; Pred. No. 4.3e-215;  
Matches 623; Conservative 177; Mismatches 295; Indels 146; Gaps 23;

QY 1 MSPNNQNEYIIDATPSTVSDNSNRYPFANEPTNALQNMDDYKDYLKMSAGNASEYPCGP 60  
DB 1 MSPNNQNEYIIDALSPTSVDNSIRYPLANDQNTLQNNYKDYLKWTESTNAELSRNP 60  
QY 61 EVLVSGDAAKAAADIYKLLSLGLGVPGVIVSLYQLIDILWPSGKSWEIFMEQVE 120  
DB 61 GTFISAQDAVGTGDIIVSTIISGLGIPVLGEVFSILGSLGLLWPSNNENYMQIFMNRVE 120  
QY 121 ELINQKTAEVARNKALSEGLGNQYLYLTALREWENPNRSGALRDVNRFEILDSLF 180  
DB 121 ELIDQKILDSVRSRAIDLANSRIAIFYQVNALEDWKNPHSTSAALVKERFGNAEL 180  
QY 181 TOYMPSEFRVTNEVEPFLTVYAMAANLHLLKDDASIFGEWGWSTTTINNYDQWMLTA 240  
DB 181 RTNMGFSFQTNVETPLPTTAAQASLHLVWMDVQVIGKRWGPQNDIDLKYEQVSYTA 240



QY 241 EYSDHCWVETGLAKLGTSAKQWVDYNOFRBMTLAVLDVVALPBNYDTRTPMETKA 300  
Db 241 RYSDHCWVQWVAGLNLKRGYGAQWVDYNOFRBMTLAVLDVVALPBNYDTRTPMETKA 300  
QY 301 QLTREVTDPGLAV---NVSGISGWYD---KAPSGVBISSVIRPPHVPDYITGLVYVT 353  
Db 301 ELTREIFTPVGSVTVQSTLSWYDMIPAALPSFTLE-NLLKDPDPFTLQIEIMYT 359  
QY 354 QSRSSISARYIRHWAGHQAISYHRVSRGSLNQMYGTGNTQNLHS-----TSTPFTNYDIY 407  
Db 360 SPQNGTIEYNYWGGQRLT-----LSYVGSFKNYSGLVAGAEIDIPVGQNDIY 410  
QY 408 KTLSDKAVLLDIYVPG-YTIFPGMPVEFPMVQNLNTRKTLKYNPVSKDIATSDSE 466  
Db 411 RVV-----WTYIGRYTNSLLGVNPTVTF---SNNOKTYS-KPKQFAGGKITDSG 458  
QY 467 LELPPTSDQPNYESYSHRLCHITS--IPATGNTT-GLVPFSTWTHESADLNNTIYSDKI 523  
Db 459 EELTYE-----NYQSYSHRYSYITSTFKSTGGTVLGVVPIFGWTHSSASRNNFIYATKI 513  
QY 524 TQIPAVKC-----WDNLPFV---PVVKGPGHGTGDLLOQYRSTGSGVTGLFLARYGL 571  
Db 514 SQIPINKASRTSGAVNPFQGLNGFPMKLSG-SGSQVNLNVAIDAKA-----564  
QY 572 ALEKAGYRVLRYATDADIVLHVN-----DAQIQPKTMNPGEDLTSKTFKVD 621  
Db 565 ---SQYRIRIRYASDRAGKFTISSRPNPATYSASIAVTNTMTNAGLTYSTPAYAE 620  
QY 622 AITLNLATDSS-----LALKHNLGEPDNPSTLSGIYVVDRIEFTPVDEYAEQDLBAK 676  
Db 621 S-SPINIGSGSRTPOISITKEAG-----AANLYDRIEFTPVNLTPEAEEDLDVAK 672  
QY 677 KAVNALFTNTKQGLRPGVTVYVNOANLVECLSDDLVPNEKRLLPDAVREAKLSBARN 736  
Db 673 KAVNGLETFNEKDALOTSVTDYQVNOANLVECLSDDLVPNEKRLLPDAVREAKLSBARN 732  
QY 737 LQDPDFQENGWGTASTGIEVIGDALPKGYRLPAGAREIDTPTLYLYQKVEEG 796  
Db 733 LQDTGPNRINENGWGTSTGIEVVEGDLVKDRSLRLTSAREIDTPTLYLYQKIDES 792  
QY 797 VLKPYTRYLRGFGVSSQGLEIFIRHQTRIVKGVNPDLLPDVSPVNSDGSINRCSEOK 856  
Db 793 LLKPYTRYLRKLGFTGSSQDLEIKLIRHRANQIVKXVNDLPPVPRVNSCGVGDRCSEOK 852  
QY 857 YVNSRLVEVNR-----SGRAHEPSIPTDGEIDYNNAGIUVGFKITDPEGYATLGNLE 910  
Db 853 YVDANLAEENNGENGNSSDSHAFSFHIDTGEIDNENTGIWIFKIPTTNGNATLGNLE 912  
QY 911 LVBEGLSGDALRLQREEQWKIQMTRRREBTDERRYMASKQAVDRLYADYQDQQLNPDV 970  
Db 913 FVEEGPLSGETLEWAQQEQEQWQDMKRAASEKTYAAQADRLFADYQDQQLNSGV 972  
QY 971 EITDLTAQDLIQSIPIVYNEMPEIPGMNVTKFTETLDRLOQAWSLYDQBNALPBGDFR 1030  
Db 973 EMSDLAQAQNLVQSIPIVYNEMPEIPGMNVTSTFELNRLQQAANLYDLQNALPBGDFR 1032  
QY 1031 NGLSNWATPEVVOQINHSVTVIPNWEQVSOQTPQPNQRYLRTARKEGVGVY 1090  
Db 1033 NGLSNWATSDVNVQQLSDTSVLVIPNWSQVSOQTPQPNRYLRTARKEGVGVY 1092  
QY 1091 SIRDGNQOTELTFASDYDNGMYNTQVSNNGYNTNNAVNTQASSTNGYNNANNMYNTQ 1150  
Db 1093 IIRDCANQOTELTFNICDDDT-GVLST-----1118  
QY 1151 ASNTNGYNTSNVNDQTYITKTTPFTPYDQMIEMSETE 1191  
Db 1119 -----DQSYIITKTEFTSTEQWIDMSETE 1145

## RESULT 9

US-08-532-547-5

; Sequence 5, Application US/08532547

; Patent No. 5861543

GENERAL INFORMATION:  
APPLICANT: LAMBERT, BART  
APPLICANT: JANSSENS, STEFAN  
APPLICANT: VAN AUDENHOVE, KATHRIEN  
APPLICANT: PEPEROEN, MARNIX  
APPLICANT: VAN RIE, JEROEN  
APPLICANT: VAN KARSSEN, ROEL  
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR  
INSECTICIDAL PROTEINS.  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,547  
FILING DATE: 06-DEC-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: SVENSSON, LEONARD R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 2121-109P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-532-547-5

Query Match 41.0%; Score 2595.5; DB 2; Length 1157;  
Best Local Similarity 44.1%; Pred. No. 1.5e-183;  
Matches 554; Conservative 197; Mismatches 348; Indels 157; Gaps 22;

QY 1 MSPNNQNEVEIIDATSTSVNSDNRYPFANBFTNALQNDYKDYKMSAGNASEYEGSP 60  
Db 1 MNRNNQNEVEIIDAPHCGCFSDDDVRYPLASDPNAAALQNNYKDYLOMTDEDYTSYINP 60  
QY 61 EVLVSGDAAKAALDIVGKLLSGLVPGVPGPIVSLYLTQILDLWPSEKQWEIFMEQVE 120  
Db 61 SLISGRDAVQTALTUVGRILGALGVFFSGQIVSFQFLNTLWPNVDTAWEAFMQVE 120  
QY 121 ELNQKIAEYARNKALSEGLNGNTQLYLTALEREENPNGRALDRVNRFEILDLSLF 180  
Db 121 ELVYNOQITEFARNQALRQLGDSFNVOQSLQNLADNRDNTLSVVRQAQFIALDLDF 180  
QY 181 TQYMPFRVTVFVPLTVTVYAMAANLHLLKQASIPGEWGWSTTTNNYIDROMKLT 240  
Db 181 VNAIPLFVNGVQVPLISVYAQAQVNLHLLKQASIPGEWGWSTTTNNYIDROMKLT 240  
QY 241 EYSDHCWVETGLAKLGTSAKQWVDYNOFRBMTLAVLDVVALPBNYDTRTPMETKA 300  
Db 241 KYTNYCETWNTGLDRGNTSRLRYHQFRREMTLVLDVVALPBNYDTRTPMETKA 300  
QY 301 QLTREVTDPGLAV---NVSGISGWYD---KAPSGVBISSVIRPPHVPDYITGLVYVT 353  
Db 301 QLTREVTDPGLAV---NVSGISGWYD---KAPSGVBISSVIRPPHVPDYITGLVYVT 356  
QY 354 QSRSSISARYIRHWAGHQAISYHRVSRGSLNQMYGTGNTQNLHS-----TSTPFTNYDIY 405  
Db 357 SNRPFVSSNFMWYSGHTLRRSYLNSDAVQSDSYGLITTTTTRATINPGVDGNTRIESTAVD 416

QY 406 IYKLSKDAVLLDIVPGYTYIFFGMEPEVEFFMNNLNTRKTKYNPVSKDIIASTRDS 465  
Db 417 FRSALIG-----IYGVNRFASFPVGLFNGT--TSPANGGCRDLY-----DT 455  
QY 466 ELEPPETSDQPNVESYHRLCHTISIPATN-----TTGLVPVFSWTHRSADLNNTIY 519  
Db 456 NDELFPEDEST-----GSSTHRLSHVTFQTNQAGSIANAGSVPTVYVTRDRVDLNNIT 511  
QY 520 SDKITQIPAVKCDNLPPVVPVKGPHGTGGLQYNRSTGSGVTLFLARYGALAEKAGKY 579  
Db 512 PNRITQPLVKAAPVSGTIVLKGFGTGGILR-RTNGTGFGL-RTVNSPLTQOY 567  
QY 580 RVLRYATDADIVLH-----VNDIAQIMPKTMNPGEDITSK-----TF 617  
Db 568 RLVRFASTGNFIRVLRGVSGIDVRLGSTMNRQELTYESFFTRFTTTGPNPPTF 627  
QY 618 KVADAILTNLATOSSALKENLGEDPNSTLSGIVYVDRIFIPVDEYIABQDLAAKK 677  
Db 628 TQAEIILTVNAEGYST-----GGEYIDRIEIVPNPAREAEEDLEAAK 672  
QY 678 AVNALFTNTKDLRPGVTDYEVNQAANLVECLSDOLYENKRLFLFDAVREAKRLSEARNL 737  
Db 673 AVASLFRTRDGLQVNYDYDQQAANLVSCLSDEQYGHDKMLLEAVRAAKRLSRERNL 732  
QY 738 LQDPDFQIEING--ENGWTAAGIEVIEGDALFKGRYLRLPGAREIDTETPTLYLYQKVEE 795  
Db 733 LQDPDFNTINSTENGWKAANGVTSIEGPPFKGALQASAR-----ENYFTIYQKVA 788  
QY 796 GVLKPYTRYRLRGVSGSQGLEIFTRHOTNRIVKNVPPDLLPDPVSPVNSDGS---INRC 852  
Db 789 SVLKPYTRYRLDGFVKSSQDLEIDLHKKVHLVKNVDPNL---VSDTYSBGSCSGINRC 845  
QY 853 SEOKYVNSRLVEN-----RSGEAHRESIDTGEIDYENAGIHWGFKITDEGYATL 906  
Db 846 DEHQVDMQDLAEHPMDCCAAQTHFSSYINTGDLNASVDQGIWVVLKVRTTDDGYATL 905  
QY 907 GNLEVEEGLSGDALRLOREEQOWKIOMTRREEDTDRRYMASKQAVDRLYADYDQOOL 966  
Db 906 GNLEVEEGLSGSLREQRDNKAKNAELGKRAEIDRVYLAQAQINHLFVYDQOOL 965  
QY 967 NPDVEITDLTAQDLIAGISPVVYNEMPEIPGMNFKPTLTDLRQQAWSLYDORNAIPN 1026  
Db 966 NPEIGLAEINAEASLVESISGVSDTLQIPGINVEIYITELSDRLQAASLYTSRNAVN 1025  
QY 1027 GDFRGLSNNAATPGVEVQQLNHTSVLVI PNWDEQVSQOFTVQNRXVLRVARTARKEGV 1086  
Db 1026 GDFNSGLSDSWNTTMDASVQODGNMHLVLHSHWDAQVSQQLRVNPNCKYVLRVARTARKEGV 1085  
QY 1087 NGVYSIRDDGNOTELTAFSADYDTNGMYNTQVNTNGYNTNNAINTQASSTNGYNANM 1146  
Db 1086 DGYVTRDGAHQHQTETFNACDYVNGTY-----1114  
QY 1147 YNTQASNTNGYNTSVNVDQGYTKVTFPIPYTDQMIEMSETEGYIESVELI 1202  
Db 1115 -----VNDNS-----YITEEVVFYFETKHMWVESESEGSFYIDSIEFI 1153

## RESULT 10

US-08-379-656B-5  
; Sequence 5, Application US/08379656B  
; Patent No. 5885571  
; GENERAL INFORMATION:  
; APPLICANT: Lambert Bart  
; APPLICANT: Jansens, Stefan  
; APPLICANT: Van Audenhove, Katrien  
; APPLICANT: Peteroen, Marnix  
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND  
; TITLE OF INVENTION: THEIR INSECTICIDAL PROTEINS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH  
; STREET: 8110 Gatehouse Road, Suite 500 East

; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22042  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/379,656B  
; FILING DATE: 23-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/01820  
; FILING DATE: 12-JULY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93400949.9  
; FILING DATE: 09-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92402358.8  
; FILING DATE: 27-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svensson, Leonard R.  
; REGISTRATION NUMBER: 30,330  
; REFERENCE/DOCKET NUMBER: 2121-104P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-379-656B-5

Query Match 41.0%; Score 2595.5; DB 2; Length 1157;  
Best Local Similarity 44.1%; Pred. No. 1.5e-183;  
Matches 554; Conservative 197; Mismatches 348; Indels 157; Gaps 22;

QY 1 MSPNNQNEYIIDIATSTSVNSNRYPPANETNALQNNKYDKYLKMSAGNASEYGPSP 60  
Db 1 MNRNNQNEYIIDIAPHCPCSDDDVRYPLASDPAALQNNKYDKYQMTDEDYDSVNP 60  
QY 61 EVLVSGODAAKAIDIVGKLLSGLVPPFVGVIVSLYQLIDILWPSEKSKQWIFMEQVE 120  
Db 61 SLSISGRDAVQTALTIVVGRILGALGVFPFSGQIVSFYQFLNTLWPNVNDTAEAFMRQVE 120  
QY 121 ELINOKIAEYARNKALSELEGLCNNYQLYLTALKEEENPNGSGRALDVRNRFILDSLF 180  
Db 121 ELVNNQITEFARNQALRQGLGDSFNVYQSRQLNWLADNRDTRNLVSVRAQIALDLDF 180  
QY 181 TOYMPFRVTNFEVPELVYVMAANLHLLKDKASIFGEGWGSTTTINNYYDROMKLT 240  
Db 181 VNAIPLFAVNGQVPLSVVAQAVNLHLLKDKASIFGEGWGSTTQGEISTYIDROELTA 240  
QY 241 EYSDCHVKVYETGLAKGTSKQWVDYQFREMVLAVLDVVVALFPNYDTRTPMETKA 300  
Db 241 KYTNYCETWYNTGLDRLGNTESMLRYHQFREMVLAVLDVVVALFPYDVRLYPTGSP 300  
QY 301 QLTREYVYDPL---GAVNVSSISGSW---YDKAPSGVIESSVIRPHVPDYITGLTVYT 353  
Db 301 QLTREYVYDPIVNPANVGLCRRWGTNPNY---TFSELENAFIRPPHPLFDRLNSLTI-S 356  
QY 354 QSRISISARYIRHWAGHQISYHRVSRGSLQQMYG-----TNQNLHSTSTFFDFTNYD 405  
Db 357 SNRFPVSSNFMWDYWSGHTLRSLVINDSAVQEDSYGLITTRATINPGVCGTNRISTAVD 416  
QY 406 IYKLSKDAVLLDIVPGYTYIFFGMEPEVEFFMNNLNTRKTKYNPVSKDIIASTRDS 465  
Db 417 FRSALIG-----IYGVNRFASFPVGLFNGT--TSPANGGCRDLY-----DT 455



Db 512 PNRITQLPLVKASAPVSGTTVLKPGFTGGILR-RTINGTFTL---RVTVNSLPTQY 567  
QY 580 RVLRYATDADIVLH-----VNDQIQMPKTMNCEDLTSK-----TF 617  
Db 568 RLRVFASTGNFSLRVKGGVSGIDVRLGSTMNGOELTYSFFTRFTTTPGPNPPTF 627  
QY 618 KVADAITTLNLTADSSALKHNLGEPDNPSTLSGIVVVDRIEPIFVDETYEAEQDLAAK 677  
Db 628 TQAEILLTVNAEGYST-----GGEYIIDRIILVFNVPAREAEEDLEAAK 672  
QY 678 AVNALFTNTKDLRPGVTDYEVNQAANLVECLSDLLYNEKRLFLFVAREAKRLSEARNL 737  
Db 673 AVASLFTRTDGLQVNTDYQVDAQANLVSCLSDEQYGHDKMLLEAVRAAKRLSRNL 732  
QY 738 LQDPDFQIEING--ENGWTAAGIEVIEDALFKGRLPLGAREIDTETPTLYLYKVEE 795  
Db 733 LQDPDFNTINSTENGWAKSANGVTISEGGPFKRALQASAR-----ENPTYIYQKVA 788  
QY 796 GVLKPYTRYRLRGFGVSGSQGLEIFTIRHOTNRIKVNQVPDDLPLDVPSPVNSDGS---INRC 852  
Db 789 SVLKPYTRYRLDGFVKSSQDLEIDLIIHHKVLKVNVPDNL---VSDTYSQSGSGINRC 845  
QY 853 SEQKYNSRLVEN-----RSGRAEFSIPIDTCEIDYNENAGIWWGVFKITDPEGYATL 906  
Db 846 DEQHOVMDQDAEHHPMDCCCEAAQTHEPSSYINTGDLNASVDQGLIWLVLKVRTTDDGYATL 905  
QY 907 GNLLEVEGPGSLGALRELQREEQWIKOMTRREEDTRRRYMAKQVADRLYADYQDQOL 966  
Db 906 GNLLEVEGPGSLGSESLREQRDNKAKNAELGRKRAEIDRVVLAQAKOINHLFVDYQDQOL 965  
QY 967 NPQVEITDLTAQDLIOISIPVYVNMPEPEIPGMVTKFTLTDLRLOQAWSLYDORNAIPN 1026  
Db 966 NPEIGLAEINEASNLVSIISGVSDTLQIPEINYEITELSDRLQASLYITSRNAVQN 1025  
QY 1027 GDFRNLGNMNAATPGVEVQOQINHTSVLVPNWDQVQSQOFTVQPNQRYVLRVARTARKEGVG 1086  
Db 1026 GDFNSGLDSWNNTDASVQDQGNMHFLVLSHWDQVQSQLRVNPENCKYVLRVARTARKEGVG 1085  
QY 1087 NGVYSIRDGNGQETLTFPSADYDNGMYNTQVNTNGYNTNAYNTQASSTNGYNANM 1146  
Db 1086 DGYVITRDGAHQHQLTFNACDYDNGFY----- 1114  
QY 1147 YNTQASNTNGYNTSVYNDQGYITKTFTVPIPTDQMIEMSETEGTFYIBSVELI 1202  
Db 1115 -----VNDNS-----YITEEVVFYPTKGMVVESESGFYIDSIEFI 1153

## RESULT 12

US-09-019-809-5

Sequence 5, Application US/09019809

Patent No. 6143550

## GENERAL INFORMATION:

APPLICANT: LAMBERT, BART

APPLICANT: JANSSENS, STEFAN

APPLICANT: VAN AUDENHOVE, KATRIEN

APPLICANT: PEPEROEN, MARNIX

APPLICANT: VAN RIE, JEROEN

APPLICANT: VAN AAKSEN, ROEL

TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR  
TITLE OF INVENTION: INSECTICIDAL PROTEINS.

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch &amp; Birch, LLP

STREET: P.O. Box 747

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,809

FILING DATE: 02-FEB-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: SVENSSON, LEONARD R.

REGISTRATION NUMBER: 30,330

REFERENCE/DOCKET NUMBER: 2121-135P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

TELEX: 248345

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1157 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-019-809-5

Query Match

Best Local Similarity 41.0%; Score 2595.5; DB 4; Length 1157;

Matches 554; Conservative 197; Mismatches 348; Indels 157; Gaps 22;

QY 1 MSPNNONEVEIITATSTSVSNDSNRYPPANEPTNALONMDYDYLKMSAGNASEYPCSP 60

Db 1 MNRNNOXEYIIDAPHGCGPSDDVDVPLASDPAALNNYKDYLTQMTDEDYDTSYINP 60

QY 61 EVLVSGDAAKAIDIVKLLSLGIVPFPVGVISLVLTQLIDILWPSEKSEKOWEIFMEQVE 120

Db 61 SLISIGEDAVQALTVVGRILGALGVFPFSGQIVSFQFLNTLWPNVDTAIWEAFMEQVE 120

QY 121 ELINQIAEYARNKALSEGLGNVQLYLTALAEWEENPNSGRALRDVNRFEILDSLF 180

Db 121 ELVNNQIQTEFARNQALRQGLGDSFNVYQSRQLONWLADRNDTNLSVVRQAFTALDLDF 180

QY 181 TQWPSFRVTNFPVPELVYVYMAANLHLKDAASIEGEWGHSTTTNNYIDROMKLLTA 240

Db 181 VNAIFPFAVNGQVPLSVYAQAANLHLKDAASLFGEGWGTQGEISTYIDRQELTA 240

QY 241 EYSDHCWKVZETGLAKLKGTSKQWVDYNQFREMILTALVDVVALFNYDTRVPMETKA 300

Db 241 KYTNYCETWNTGLDRLRGINTESMLRYHFREMILVLDVVALFPYDVRVLYPTGSPN 300

QY 301 QLTRFVYTDPL---GAVNVSSISGW---YDKAPSGVIESSVIRPPHVDYITGLFVYT 353

Db 301 QLTRFVYTDPIVENPPANVGLCRRWGTNPYN---TFSELENAFIRPHLFDRLNSLTI-S 356

QY 354 QSRSSISARVIRHWAGHOISYHRVSRGSLNQMYG-----TNQNLHSTSTDFDFTNYD 405

Db 357 SNRFPVSSNFMFWSGHTLRRSYLNDLSAQEDSYGLITTTTRATINPGVDGTRIESTAVD 416

QY 406 IYKTLKDAVLLDIVPGVYIIFPGMPEVEFFMVNQNLNTRKTLKYNPVSKDIIASTRDS 465

Db 417 FRSLALIG-----IYGNRASFPVPGGLFNGT--TSPANGGCCRDLY-----DT 455

QY 466 EELPETSQPNYESYSHRLCHITSIPATGN-----TTGLVPVFSWTHRSADLNTIY 519

Db 456 NDELPPDEST---GSSTHRLSHVTFPSFOTNQAGSIANAGSVPTVYVTRRDVDLNTIT 511

QY 520 SDKITQIPAKWCWDLNLPFPVVKVGRGHTGDDLQYNRSTGSGVGTFLFARYGLALEKAGKY 579

Db 512 PNRIITQLPLVKASAPVSGTTVLKPGFTGGILR-RTINGTFTL---RVTVNSLPTQY 567

QY 580 RVLRYATDADIVLH-----VNDQIQMPKTMNPGEDLTSK-----TF 617

Db 568 RLAVRFASTGNFSIRVLRGGVSGIDVRLGSTMNGOELTYSFFTRFTTTPGPNPPTF 627

QY 618 KVADAITTLNLTADSSALKHNLGEPDNPSTLSGIVVVDRIEPIFVDETYEAEQDLAAK 677

Db 628 TQAEILLTVNAEGVST-----GGEYIIDRIEIVFNVPAREAEEDLEAAK 672

Qy 678 AVNALFTNTKGLRPGVTDYEVNQANLVESLSDLLYPNEKRLLPDAVREAKRLSEARNL 737  
Db 673 AVASLFTRLTRDGLQVNTDYQVDAQANLVCSLDEQYGHDKMLLEAVRAAKRLSRNL 732  
Qy 738 LQDDPFOEING--ENGWTASTGIEVIEGDALFKGYLPLPGAREIDTETTYLYYKVEE 795  
Db 733 LQDDPFTNTTEENGWKAASGVITISEGGPFKRALQALASAR-----ENPTYTYQKVA 788  
Qy 796 GVLKPYTRYRLRGVSSQGLIEFTIRHTNRIVKNVPPDILLPVPVNSDGS---INRC 852  
Db 789 SVLKPTRYRLDGFVKSSQDLIEDLHKKHVLKVNVPDNL---VSDTYSOGSCGINRC 845  
Qy 853 SEQYVNSRLVEN-----RSGNAHEFSIPIDTGEIDYENAGIHWGFKITDPEGATL 906  
Db 846 DECHQVMDLDAEHPMDCCBAATHPESSVINTGDLNASVDQGIWVVLKVRTTIDGYATL 905  
Qy 907 GNLSLVEGPGSLGALRELQREEQWKLQMTREETDRRYWASKQAVDRLYADYQDQOL 966  
Db 906 GNLSLVEGPGSLGALRELQREEQWKLQMTREETDRRYWASKQAVDRLYADYQDQOL 965  
Qy 967 NPDEVEITDLTAAQDLIOSIPYVYVEMPEIPGMNYTKETELTDLRQQAWSLYDORNAIPN 1026  
Db 966 NPDEGLAEINASLVESISGVSYDQLQIFGINVEIITELSDRLQOASLYTSNVAQN 1025  
Qy 1027 GDFRGLSNMNPATGVEVQOQINHTSVLVPNWDQVSOQFTVQPNQRVYLVRTARKEGVG 1086  
Db 1026 GDFRGLSNMNPATGVEVQOQINHTSVLVPNWDQVSOQFTVQPNQRVYLVRTARKEGVG 1085  
Qy 1087 NGYVIRGGNQTETLFSASDYDNGMNTQVSNYNTGNTNNTNAYNTQASSTNGYNANM 1146  
Db 1086 DGYVIRGGNQTETLFSASDYDNGMNTQVSNYNTGNTNNTNAYNTQASSTNGYNANM 1145  
Qy 1147 YNTQASNTGNTNNTVNDQGYTKTTPYTDQMIEMSEGTFTVIESVELI 1202  
Db 1115 YNTQASNTGNTNNTVNDQGYTKTTPYTDQMIEMSEGTFTVIESVELI 1153

## RESULT 13

US-09-471-177-5  
; Sequence 5, Application US/09471177  
; Patent No. 6448226  
; GENERAL INFORMATION:  
; APPLICANT: LAMBERT, BART  
; APPLICANT: JANSSENS, STEFAN  
; APPLICANT: VAN AUDENHOVE, KATHIEN  
; APPLICANT: PEPEROEN, MARINX  
; APPLICANT: VAN RIE, JEROEN  
; APPLICANT: VAN AARSEN, ROEL  
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR  
; TITLE OF INVENTION: INSECTICIDAL PROTEINS.  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/471.177  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019.809  
; FILING DATE: 02-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SVENSSON, LEONARD R.  
; REGISTRATION NUMBER: 30,330

; REFERENCE/DOCKET NUMBER: 2121-135P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-471-177-5

Query Match 41.0%; Score 2595.5; DB 4; Length 1157;  
Best Local Similarity 44.1%; Pred. No. 1.5e-183;  
Matches 554; Conservative 197; Mismatches 348; Indels 157; Gaps 22;

Qy 1 MSPNQNEYHIIIDATPSTSVNSNRYPFANEPTNALQNMWDYKDYLOMSAGNASEYFGSP 60  
Db 1 MNRNQNEYHIIIDAPHCPCPDDDDRYPLASDPAALQNMNMYKDYLOMTDEDYTDYINP 60  
Qy 61 EVLVSGQDAKAAIDIVGKLLSGLVGPFVGPVLSLYTOLIDILWPSGKESOWEIFMEQVE 120  
Db 61 SLISGRDAVQTATVVRIGLALGVFPSCQIVSYQFLNLTLPVNDTALWEAFMEQVE 120  
Qy 121 ELINQKIARYARKALSEGLGNMYQLYLTALKEEENPNRSLDRDVRNRFELDSLF 180  
Db 121 ELVNOQITEFARNOALRQLGDSFNVOYQSLQNLADRNENTLSVRAQFIALDLDF 180  
Qy 181 TQYMPFRVNTFVFFITVYAMAANLHLLKQASIFGEGWGWSTTTNNYDRQMKLTA 240  
Db 181 VNAIFPAVNGQQVPLSVQAQVNLHLLKQASIFGEGWGWSTTTNNYDRQMKLTA 240  
Qy 241 EYSDHCYKWTETGLAKTKTSKOWVDYNOFRREMTLAVLDVVALFPNYDTRTYPMETKA 300  
Db 241 KYTNYCYTWTNTGLRLGTNTESWLRHYHQFRREMTLAVLDVVALFPNYDTRTYPMETKA 300  
Qy 301 QLREVTYTDPL---GAVNVSSIGSW---YDKAPSGVBISSVIRPPHVPFYITGLTVYT 353  
Db 301 QLREVTYTDPLVFNPPANVGLCRWGTNPYN---TFSELENAFIRPPHFDRLNSLII-S 356  
Qy 354 QSRSSISARYIRHWAGHOISYHRVSRGNSNQMYG-----TNQNLHSTSTFDFTNYD 405  
Db 357 SNRPVSNFMDYWSGHTLRRSYLNDSAVQEDSYGLITTTTTRATINPGVDGNTRIESTAVD 416  
Qy 406 IYKTLKDAVLLDIVPGYIYIFGMEPEVEFFVWVQNLNTRKTLKYNPVSXDIIASTRDS 465  
Db 417 FRSLIG-----IYGVNRASFPVGGLFNGT---TSPANGGCKDLY----DT 455  
Qy 466 ELELPPESTQPNYESYSHRLCHITSIIPATGN-----TTGLVPVFSWTHRSADLNNTIY 519  
Db 456 NDELPPDEST-----GSSTHRLSHVTFPSFQTNQAGSIANAGSVPTVYVTRDVLNNTIT 511  
Qy 520 SDKITQIPAVKWNLPFPVVKPGHTGGDLLQYNRESTSGVTLFLARYGLALEKAGKY 579  
Db 512 PNRITQLPLVKASAPVSGTTLKPGFTGGGILR-RITNGTFTGL---RVTVNSPLTQOY 567  
Qy 580 RVRLRYATDADIVLH-----VNDQAIQMPKTMNPDGDLTSK-----TF 617  
Db 568 RLVRFPASTGNFISRVLRGGVSGIDVRLGSTMNRQBELTVESFFTRFTTTTGPFPNPPFTF 627  
Qy 618 KVADAITTLNLTADSSLAKHNLGCEPNSTLSGIVVYVDRIEFIPVDETYEARQDLEAAKK 677  
Db 628 TQAEILTVNABGVST-----GGEYIYDRIEIVPNPAREADELEAAKK 672  
Qy 678 AVNALFTNTKGLRPGVTDYEVNQANLVESLSDLLYPNEKRLLPDAVREAKRLSEARNL 737  
Db 673 AVASLFTRLTRDGLQVNTDYQVDAQANLVCSLDEQYGHDKMLLEAVRAAKRLSRNL 732  
Qy 738 LQDDPFOEING--ENGWTASTGIEVIEGDALFKGYLPLPGAREIDTETTYLYYKVEE 795  
Db 733 LQDDPFTNTTEENGWKAASGVITISEGGPFKRALQALASAR-----ENPTYTYQKVA 788

|    |      |  |        |      |
|----|------|--|--------|------|
| Qy | 796  | GVLKPYTRYRLRGFGVSSQGLEIFTTRHQTNRIVKXVPDDLLPDPVSPVNSDGS---      | INRC   | 852  |
| Db | 789  | SVLKPYTRYRLDGFVKSSQDLEIDLHHHKHVLVKVNPDL---                     | VSDTYS | 845  |
| Qy | 853  | SEOKYNSRLEVEN-----RSGEAHEFSIPDITGEIDYNENAGIHWGFKITDPEGVATL     |        | 906  |
| Db | 846  | DEOHOVDMQJLADHHHPWDCCEAAQTHFESSYINTGDLNASVDQGIWVLKVRTTIDGVATL  |        | 905  |
| Qy | 907  | GNLELVEEGPLSGDALLERLQREBQOWKIOMTTRRRBEETDRYMAHQAVDRLYADYQDOOL  |        | 966  |
| Db | 906  | GNLELVEVGPLSGESLEREQORDNAKNWAGELGRKRAEIDRVYLAAQOAINHFLVDYQDOOL |        | 965  |
| Qy | 967  | NPDVEITDLTAAODLQSTPYVYNEMFPPIPGMNYTKFTFELTDRLQQAWSLYDORNAIPN   |        | 1026 |
| Db | 966  | NPEIGLAEINEASNLVESIGSVYSDTLLQIPGINVEIYETELSDRIQQAASYLTSRNAVON  |        | 1025 |
| Qy | 1027 | GDFRNLGSNNATPGVEVQOQIHNHTSVLVPNDNEQVSOQFTVPQPNORVVLVRLTARKEGVG |        | 1086 |
| Db | 1026 | GFNSGLDSWNITMDASVQDGNMHFLVLSHWDAAQVSQOLRVPNPCKYVLVRTARKVGGG    |        | 1085 |
| Qy | 1087 | NGVYSIRDGNGOTETITFSASDYDTNGMYNTQVSNNGYNTNNAVNTQASSTNGYNANNM    |        | 1146 |
| Db | 1086 | DGYVITRDGAHQETITFNACDYDNGTY-----                               |        | 1114 |
| Qy | 1147 | YNTQASNTNGYNTSVNBDQTGYITKVTFFIPYTDQMIEMSETGTFYIESVELI          |        | 1202 |
| Db | 1115 | -----VNDNS-----YITEVVYFYZETKHMWYVESGSGFVDSIRFI                 |        | 1153 |

RESULT 14

US-09-002-285-72  
; Sequence 72, Application US/09002285  
; Patent No. 6369213  
; GENERAL INFORMATION:  
; APPLICANT: Schnepf, H. Ernest  
; APPLICANT: Wicker, Carol  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Walz, Michelle  
; APPLICANT: Stockhoff, Brian  
; APPLICANT: Muller-Cohn, Judy  
; TITLE OF INVENTION: Toxins Active Against Pests  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/002,285  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/886,615  
; FILING DATE: 1-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/674,002  
; FILING DATE: 1-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanders, Jay M.  
; REGISTRATION NUMBER: 39,355  
; REFERENCE/DOCKET NUMBER: MA-701C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:

Db 861 MDCBAAQTHFSSYINTGDLNLSVDOQIIVWLVKRVITDGYATLGNLSELVEVGLSGESL 920  
Qy 923 ERLQEEQOWKIOMTRREEDRRYMASQKQAVDRLYADYQOQNLNPDVIEITDLTAOOLI 982  
Db 921 EREQDNKNAWELGRKEABIDRVYLAQALNHLFVYDQOQNLNPEIGLAEINEASNLV 980  
Qy 983 QSIPTVNEPPEIPGMNYPKFTLTLDRLOQMSLYDORNAIPNGDPFNGLSNWNATPGV 1042  
Db 981 ESIISGVSDTLQIPGINIEYITELSDRLQOASLYTSRNAVQNGDFNSGLDSNWTMDA 1040  
Qy 1043 EVQOINHTSVLIPNWDQVSOQFVQPNORVLRVARTARKEGNGVYISIRDGNOETEL 1102  
Db 1041 SVQDGNMHLFVSHWDAQVSOQLRVNPKVLRVARTARKEGNGVYITIRDGHHQETL 1100  
Qy 1103 TFSASDYDNGMYNTQVSNITNGYNTNAYNTQASSTNGYNANNMYNTQASNTNGYNTNSV 1162  
Db 1101 TFNACDYVNGY-----VNDNS- 1118  
Qy 1163 YNDOTGYITKTPTIPYTDQMIENSETGYIESVELI 1202  
Db 1119 -----YITEBWFVPETKHMWVEVSESGSYIDSIEFI 1152

RESULT 15  
US-08-542-921-2  
; Sequence 2, Application US/08542921  
; Patent No. 5736514  
; GENERAL INFORMATION:  
; APPLICANT: IIZUKA, TOSHIHIKO  
; APPLICANT: TAGAWA, MICHITO  
; APPLICANT: ARAI, SATOSHI  
; APPLICANT: NIIZEKI, MASATSUGU  
; APPLICANT: MIYAKE, TOSHIO  
; TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL  
; TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCELLELAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/542,921  
; FILING DATE: 13-OCT-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 276082/94  
; FILING DATE: 14-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN P  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 49-209-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1169 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-542-921-2

Query Match 40.4%; Score 2558.5; DB 1; Length 1169;  
Best Local Similarity 43.8%; Pred. No. 8.1e-181;

Matches 555; Conservative 188; Mismatches 356; Indels 169; Gaps 25;  
Qy 1 MSPNNOMEYELIDATPSTSVNSDSNRYPFANEPTNALQNNMDYKDYLKMSAGNASEYPCSP 60  
Db 1 MNRNNQMEYEVIDAPHCPCPADVVVKYPLDDPNAGLQNNMYKEYLQTYGGDYTDPLNP 60  
Qy 61 EVLVSGDAAKAAADIIVGKLLSGLVFPVGPVIVSLYLTOLIDILWPSGEKSQWEIPEOVE 120  
Db 61 NLSVSGKDVIVQGINIVGRLLSPFPFSSQWTVVYLLNSLWPDDESSVMDAFMERVE 120  
Qy 121 ELINOKIAEYARNKALSELGNGNYOLYLTALKEEENNGSALDRVRPEILDSLF 180  
Db 121 ELIDOKISEAVKGGALDDLTGLQYNYLYEALDEWLNRPNGARSL-VSQRFNLDLSLF 179  
Qy 181 TOYMPSE-----RVNFEVPEFLTVYMAANLHLLKLDASIFGEBWGSTTTNNYVDRQM 236  
Db 180 TOFMPFSGSGSQNYATILLPVYQAANLHLLKLDADIYGARWGLNQTQIDQFHSRQ 239  
Qy 237 KLTAEYSDHCYKMETGLAKLKGTSAKOWDYNOFREMTLAVLDVVALFPNYDRTYPM 296  
Db 240 SLTQTYNHCVTA YNDGLAELRGTTAESWPKYQVREMTLTAMDVALFPYVNLRYQPD 299  
Qy 297 ETKAQLTREVYT-----DPLGANNVSSIGSWYDAP-----SFGVIESSVTRPHVFDYI 346  
Db 300 GTNPQLTREVYTDPIAFDPLEQPTTQLCRSWYINPAFRNHLNFSVLENSLRPHLPERL 359  
Qy 347 TGLTVYTQSRSSISSARYIRHWAGHQISYHRSVRSNGSNLQOMY-----GTNQLHSTSTF 399  
Db 360 SNLOILVNYOTNGSA-----WRGSRVRYHYLHSSIIKEKSYGLLSDPVGANINQ----- 409  
Qy 400 DFTNYDIYKTLSDKADVLDDIYPCYT-----YIFPGMEVEFFFMVNO 441  
Db 410 ---NNDIYQIISQVSNFASPVGSSYSWDTNFWLSSGVSGISGYTQGIIPAV---CLQQ 463  
Qy 442 LNTRKTLKNPVSKDIIASTRDSELELPETSDQPNVESYSHRLCHITSI----- 492  
Db 464 RNSTDPLSLNP-EGDII-----RNYSRLSHITTYRFOATQSGS 502  
Qy 493 PATGNTTGLVPVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFPVPVKGPGHGGDL 552  
Db 503 PST--VSANLPTCVWTRHDVLDNTITANQITQPLKAYELSSGATVVGKPGFTGGDVI 560  
Qy 553 QYNRSTSGVGLFLARYGLALEKAGYRVRLYATDADIVLHVND-----QIQMPKTMN 607  
Db 561 R-RNTGGFGAIRVSVTGPLTQ---RYRIRFYASTIDDFVTRGGTTINFRFRTMN 616  
Qy 608 PGEILTSKTPKVAADAITLNLATSSALKNLGDNSTLSGIVYVDRIEPIPVDEIYE 667  
Db 617 RGESRYESYRTVEFTTFFNFPTQSDIIRTSIQGLSGN---GEVYLDRIEIIIPVNPARE 672  
Qy 668 AEQLEAAKAVNA-LPTNTKDLRPGVTDYEVNQAANLVECLSDDLVPNEKRLLFDAVR 726  
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Db 733 AAKLSRENNLLQDPDFNTINSTENGWKAANGVTISEGGPFFKGRALQLASAR---EN 788  
Qy 785 YPTLYYQKVEGVLPKYTRYRLRGVSSQGLEIFTIRHQTNRIVKNNVDPDLDLDPVSPN 844  
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Db 846 SDGSCGMNRCCEQOMVNAQLETHHHHPMDCCAAQTHFSSYINTGDLNLSVDOQIIVW 905  
Qy 895 FKITDPEGYATLGNLSELVEVGLSGESLEREQDNKNAWELGRKEABIDRVYLAQAL 954  
Db 906 LKVRTDGYATLGNLSELVEVGLSGESLEREQDNKNAWELGRKEABIDRVYLAQAL 965  
Qy 955 DRLVADYQDQQLNPDVEITDLTAQADLIQSIPTVYVNEPPEIPGMNYPKFTLDRLOQA 1014  
Db 966 NHLFVDYQDQQLNPEIGLAEINEASNLVESISGVYSDTLQIPGINIEYITELSDRLQOA 1025



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QY 1015 WSLYDQNAIPNGDFRNGLSNWNATPGVEVQOINHTSVLIPNWDQVSOQFTVQPNORY 1074
Db 1026 SYLTSRNVQNGDFNSGLDSWNITTDASVODGNGHFLVLSHWDQVSOQLRVNPNCKY 1085
QY 1075 VLRVTARKEGVNGYVSIRDGNGOTETLTFASDYDTNGMYNTQVSNNGYNTNNAINTQ 1134
Db 1086 VLRVTARKEGVNGYVSIRDGNGOTETLTFASDYDTNGMYNTQVSNNGYNTNNAINTQ 1134
QY 1135 ASSTNGYNANMYNTQASNTNGYNTNSVYNDOTGYITKTVTFIPYTDOMWEMSETEGTF 1194
Db 1127 -----VNDNS-----YITEEVVVFYFETKHMVVEVSESEGSF 1157
QY 1195 YIESVELI 1202
Db 1158 YIDSIEFI 1165
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Search completed: January 7, 2003, 05:18:17  
Job time : 32 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2003, 00:49:27 ; Search time 89 Seconds  
(without alignments)

12477.265 Million cell updates/sec

Title: US-10-032-717-1

Perfect score: 3621

Sequence: 1 atgagtcacaaataatcaaaa.....tgattgtagacgtagagtaa 3621

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.\*  
1: /cgm2\_6/ptodata/1/ina/5A.COMB.seq.\*  
2: /cgm2\_6/ptodata/1/ina/5B.COMB.seq.\*  
3: /cgm2\_6/ptodata/1/ina/6A.COMB.seq.\*  
4: /cgm2\_6/ptodata/1/ina/6B.COMB.seq.\*  
5: /cgm2\_6/ptodata/1/ina/PTUS.COMB.seq.\*  
6: /cgm2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description      |
|------------|--------|-------------|--------|----|------------------|
| 1          | 2565.2 | 70.8        | 3507   | 1  | US-08-315-468-3  |
| 2          | 1812.2 | 50.0        | 3471   | 1  | US-07-876-280-29 |
| 3          | 1812.2 | 50.0        | 3471   | 1  | US-07-812-180A-1 |
| 4          | 1812.2 | 50.0        | 3471   | 1  | US-08-315-468-1  |
| 5          | 1812.2 | 50.0        | 3471   | 4  | US-07-941-650A-1 |
| 6          | 1180   | 32.6        | 3797   | 1  | US-07-915-203-1  |
| 7          | 1180   | 32.6        | 3797   | 1  | US-08-272-887-1  |
| 8          | 1180   | 32.6        | 3797   | 1  | US-08-789-449-1  |
| 9          | 883.4  | 24.4        | 4344   | 2  | US-08-532-547-4  |
| 10         | 883.4  | 24.4        | 4344   | 2  | US-08-379-656B-4 |
| 11         | 883.4  | 24.4        | 4344   | 3  | US-08-455-838-4  |
| 12         | 883.4  | 24.4        | 4344   | 3  | US-09-019-809-4  |
| 13         | 883.4  | 24.4        | 4344   | 4  | US-09-471-177-4  |
| 14         | 882.8  | 24.4        | 3471   | 4  | US-09-002-285-73 |
| 15         | 848.6  | 23.4        | 3759   | 1  | US-08-542-921-1  |
| 16         | 848.6  | 23.4        | 3759   | 2  | US-08-880-685-1  |
| 17         | 848.6  | 23.4        | 3759   | 2  | US-08-880-684-1  |
| 18         | 822.2  | 22.7        | 3453   | 4  | US-09-002-285-75 |
| 19         | 734.2  | 20.3        | 3411   | 4  | US-09-002-285-77 |
| 20         | 733.6  | 20.3        | 3414   | 1  | US-07-973-320-3  |
| 21         | 731.4  | 20.2        | 3414   | 1  | US-07-973-320-1  |
| 22         | 678    | 18.7        | 3934   | 1  | US-08-100-709-3  |
| 23         | 678    | 18.7        | 3934   | 1  | US-08-176-865-3  |
| 24         | 678    | 18.7        | 3934   | 1  | US-08-474-038-3  |
| 25         | 678    | 18.7        | 3934   | 2  | US-08-779-046-3  |
| 26         | 678    | 18.7        | 3934   | 2  | US-08-881-340-3  |
| 27         | 673.6  | 18.6        | 4074   | 1  | US-08-377-690-1  |

|    |       |      |      |   |                  |                    |
|----|-------|------|------|---|------------------|--------------------|
| 28 | 659.2 | 18.2 | 3684 | 1 | US-08-448-170-7  | Sequence 7, Appli  |
| 29 | 659.2 | 18.2 | 3684 | 3 | US-08-961-803-5  | Sequence 5, Appli  |
| 30 | 618.6 | 17.1 | 3567 | 6 | 5188960-5        | Patent No. 5188960 |
| 31 | 615.4 | 17.0 | 3567 | 2 | US-08-980-071-58 | Sequence 5, Appli  |
| 32 | 615.4 | 17.0 | 3567 | 2 | US-08-980-071-58 | Sequence 58, Appli |
| 33 | 615.4 | 17.0 | 3567 | 2 | US-08-757-536-5  | Sequence 5, Appli  |
| 34 | 615.4 | 17.0 | 3567 | 3 | US-09-314-093-5  | Sequence 5, Appli  |
| 35 | 615.4 | 17.0 | 3567 | 3 | US-09-314-093-58 | Sequence 58, Appli |
| 36 | 615.4 | 17.0 | 3567 | 3 | US-09-250-848-5  | Sequence 5, Appli  |
| 37 | 615.4 | 17.0 | 3567 | 4 | US-09-251-885-5  | Sequence 5, Appli  |
| 38 | 615.4 | 17.0 | 3567 | 4 | US-09-337-635-5  | Sequence 5, Appli  |
| 39 | 615.4 | 17.0 | 3567 | 4 | US-09-337-635-58 | Sequence 58, Appli |
| 40 | 615.4 | 17.0 | 3567 | 4 | US-09-337-280-5  | Sequence 5, Appli  |
| 41 | 615.4 | 17.0 | 3567 | 1 | US-09-337-280-58 | Sequence 58, Appli |
| 42 | 613.8 | 17.0 | 3567 | 1 | US-08-602-737-1  | Sequence 1, Appli  |
| 43 | 613.8 | 17.0 | 3567 | 2 | US-08-980-071-1  | Sequence 1, Appli  |
| 44 | 613.8 | 17.0 | 3567 | 2 | US-08-980-071-9  | Sequence 9, Appli  |
| 45 | 613.8 | 17.0 | 3567 | 2 | US-08-980-071-11 | Sequence 11, Appli |

## ALIGNMENTS

RESULT 1  
US-08-315-468-3  
; Sequence 3, Application US/08315468  
; Patent No. 5554534  
; GENERAL INFORMATION:  
; APPLICANT: Michaels, Tracy Ellis  
; APPLICANT: Poncerrada, Luis  
; TITLE OF INVENTION: Process for Controlling Scarab Pests  
; TITLE OF INVENTION: with Bacillus thuringiensis Isolates  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/315,468  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/014,941  
; FILING DATE: 01 FEB 1993  
; APPLICATION NUMBER: 07/828,430  
; FILING DATE: 30-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/808,316  
; FILING DATE: 16-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: MA73.C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3507 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO

ANTI-SENSE: NO  
ORIGINAL SOURCE: Bacillus thuringiensis  
STRAIN: kunamotokoensis  
INDIVIDUAL ISOLATE: 50C  
IMMEDIATE SOURCE: LambdaGEM-11(tm) library of L. Poncerrada  
LIBRARY: 50C(b)  
CLONE: 50C(b)  
US-08-315-468-3

Query Match 70.8%; Score 2565.2; DB 1; Length 3507;  
Best Local Similarity 85.1%; Pred. No. 0;  
Matches 2906; Conservative 0; Mismatches 493; Indels 15; Gaps 3;  
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DB 1 ATGAGTCCAAATATCAAAATGAATGAATGAATATAGATCGACACCTCTTCTCTGTA 60  
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DB 181 GAGGTATTTCTAAGCGAGCAAGATGCAATTTAGCCCAATTTGATATAGTAGGTAAATTA 240  
QY 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTCTTTTATCTCAACTTTAT 300  
DB 241 CTAAACAGGTTTAGGGTCCCATTTGTTGGCCGATAGTCTTTTATCTCAACTTTAT 300  
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DB 361 GAACCTCAATTAATCAAAATATGACAGATATGCAAGGAATTAAGCGCTTTCGGAATTA 420  
QY 421 GGATAGGTAATTAATCAATATATCTAATCTGCGCTTGAAGAAATGGGAAGAAATCCA 480  
DB 421 GGCTTAGGGAATTAATCAATATATCTAATCTGCGCTTGAAGAAATGGGAAGAAATCCA 480  
QY 481 AATGGTTCAGAGCCTTACAGATGTCGGAATTCGATTTGAATCTCGGATAGTTATTT 540  
DB 481 AATGGTTCAGAGCCTTACAGATGTCGGAATTCGATTTGAATCTCGGATAGTTATTT 540  
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DB 541 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTCTTCTGTATAT 600  
QY 601 GCAATGGCAGCCAACTTCAATTTACTGTTATTAAGGACGCGTCAATTTTGGAGAGAA 660  
DB 601 ACAATGGCAGCCAACTTCAATTTACTGTTATTAAGGACGCGTCAATTTTGGAGAGAA 660  
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QY 721 GAATATTTCTGATCACTGTGTAAAGTGTATGAACTGTTTAGCAAAATTAAGGCAAG 780  
DB 721 GAATATTTCTGATCACTGTGTAAAGTGTATGAACTGTTTAGCAAAATTAAGGCAAG 780  
QY 781 AGCGCTAAACAATGGGTGATCTAATAACCAATTCGCTAGAGAAATGACACTGGCGTTTA 840  
DB 781 AGCGCTAAACAATGGGTGATCTAATAACCAATTCGCTAGAGAAATGACACTGGCGTTTA 840  
QY 841 GATGTTGTCGATTTTCCCAAAATTAATGACACAGCGAGTACCCAAATGGAAACGAAAGCA 900  
DB 841 GACGTTGTCGATTTTCCCAAAATTAATGACACAGCGAGTACCCAAATGGAAATTCATC 900

QY 901 CAACTAAACAGGGAAGTATATACAGATCCATCGGCGCGGTAAACGCTGCTTCAATTTGGT 960  
DB 901 CAGCTTACAGGGAAGTATATACAGATCCATCTTGCGCGGTAGATGCTCTAATATTGGC 960  
QY 961 TCTGTGTATGACAAAGACCTTCTTTCGGAGGTATAGATCATCCGTTATTCGACACCC 1020  
DB 961 TCTGTGTATGACAAAGACCTTCTTTCGAGAAATAGAAAAGCGCTATTCGTCACCT 1020  
QY 1021 CATGTATTTGATTATATAACGGGACTCACAGTGTATACAAATCAAGAAAGCATTTCTTCC 1080  
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QY 1081 GCTCGCTATATAAGCATTTGGGCTGCTCATCAATAAGCTACCATCGTGTAGTAGGGT 1140  
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QY 1141 AGTAATCTTCAACAAATGATGGAATCAATAATCAAAATCTACAGCACTAGTACTTTGAT 1200  
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DB 1321 CAATTGAATTAATACCAAGAAAGCTTTAAAGTATTAATCTTTCAGTTTCCAAAGATTTATAGAT 1380  
QY 1381 AGTACAGAGATTCGGAATTTAGAACTTCTCCAGAACTTCCAGGTCACCAAAATTTATGAG 1440  
DB 1381 CGGACAGAGATTCGGAATTTAGAACTTCTCCAGAACTTCCAGGTCACCAAAATTTATGAG 1440  
QY 1441 TCATATAGCCATAGATTTATGTCTATATCAAGTATTTCCGCGAGCGGTAACTTACCTACCGGA 1500  
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QY 1621 GTAAAAAGGACACAGGACATACAGGAGGGAATTTATACAGTATATAGAAAGTACTGGTTCT 1680  
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QY 1801 CAGATGCCAAAAACAAATGAACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCA 1860  
DB 1798 AACCAAGCATATTTCTAATAAATAAATGAATGATTTAAGCATATTAATGTTTCAATATATA 1857  
QY 1861 GATGCTTACCAACATTAATTTAGCAACAGATAGTTCGCTAGCATTTGAAACATAATTTA 1920  
DB 1858 GAATATC---CAAGAGTCTATTCAGTAAATGCTTCTTCAAAACATACAGAGGTTATCTATA 1914  
QY 1921 GGTGAGACCTTAATTTCAACATTTCTGTTATAGTTTTCGTTGACCGAATCGAATTCATC 1980  
DB 1915 GGTATACAAACGAATACAAATTTATTTATTTTAA-----GACCGAATCGAATTCATC 1965



US-07-876-280-29

| Query March           | 50.0%;          | Score 1912.2;   | DB 1;      | Length 3471; |
|-----------------------|-----------------|---|------------|--------------|
| Best Local Similarity | 72.2%;          | Fred. No. 0;  |            |              |
| Matches 2504;         | Conservative 0; | Mismatches 908;   | Indels 57; | Gaps         |
| Qy                    | 1               | ATGAGTCACAAATAATCAAAATGAATATGAAATATATAGATGCGACACACCTTCTACTCTCTGTA | 60         |              |
| Db                    | 1               | ATGAGTCACAAATAATCAAAATGAATATGAAATATATAGATGCGACACCTTCTACTCTGTA     | 60         |              |
| Qy                    | 61              | TCCAAATGATTTCTAAACAGATACCCCTTTTGGGAATGAGCCCAAAATGCGGTCTACAAATATG  | 120        |              |
| Db                    | 61              | TCCAGTGAATCTTAAACAGATACCCCTTTTGGGAATGAGCCCAACAGATGCGTTACAAATATG   | 120        |              |
| Qy                    | 121             | GATTATAAGATTTATTTAAAAATGTCGCGGAAATGCTAGTGAATPACCCCTGTTCCACCT      | 180        |              |
| Db                    | 121             | AATTTATAAGATTTATCTGAAATGTCGCGGAGAGATCTCGAATATTTTGGAAATCCG         | 180        |              |
| Qy                    | 181             | GAACTACTTTGTAGCGGACAGATGACGCTAAGCGCGCAATATGATATAGTATAGTAAATTA     | 240        |              |
| Db                    | 181             | GAGACGTTTATTA---GTTTACTCCAGATTCAAATCGGAATGGCATCTGTGTCGAATA        | 237        |              |
| Qy                    | 241             | CTATCAGGTTTAGGGGTCCCATTTGTTGGCGCGATGAGTGAGTCTTTATACTCAACTATT      | 300        |              |
| Db                    | 238             | CTAGAGGCTTTAGGGGTTCCATTTGCTAGTACAGATGCTAGTCTTATAGTTTCAITGTT       | 297        |              |
| Qy                    | 301             | GATATCTGTGCGCTTTGAGCGGAAAGAGTCAATGCGGAAATTTTATGGAACAAGTAGAA       | 360        |              |
| Db                    | 298             | GGTCAATATGSCCGCTCAAGAGCGTAGATATATGGGAGAAATATGGAACGAGTGAA          | 357        |              |
| Qy                    | 361             | GAACTCATTAATCAAAAAATGACAGATATGCAAGGAATAAAGCGCTTTGCGNAATTAGAA      | 420        |              |
| Db                    | 358             | GAACTCGTTGATCAAAAAATAGAAAAATATGTAAGAGATAGGCTCTTCTGTAATTTAAAA      | 417        |              |
| Qy                    | 421             | GGATTAGGTAAATTTACCAATTTATATCTAACTGCGCTTTGAAGAAATGGGAAGAAATCCA     | 480        |              |
| Db                    | 418             | GGGCTAGGAATGCTTTGGATGTATATCAGCAGTCACTTGAAGATTTGGTGGNAATCGC        | 477        |              |
| Qy                    | 481             | AATGTTTCAAGAGCCTTACGAGATGTCGAAATCGAATTTGAAATCTCGATAGTTTATTT       | 540        |              |
| Db                    | 478             | AATGATGCAAGAACTAGAACTGTTGTTCTTAATCAATTTATAGCTTTAGATCTTAACTTT      | 537        |              |
| Qy                    | 541             | ACGCAATATATGCCATCTTTTAGAGTGACAATAATTTTGAAGTACCATTCTTACTGTATAT     | 600        |              |
| Db                    | 538             | GTTAGTTCAAATTTCCATCTTTTTCGAGTATCCGACACGAAGTACTATTTATAGCAGTATAT    | 597        |              |
| Qy                    | 601             | GCAATGGCAGCCAACTCTCATTTTACTGTTTATTAAGGACGCGTCAATTTTGGAGAGAA       | 660        |              |
| Db                    | 598             | GCACAGGCTGTGAACCTACATTTATGTTTATTAAGAGATGCTTCTATTTTGGAGAGAG        | 657        |              |
| Qy                    | 661             | TGGGAGTGGTCAACAACTACTATTAATACTATTAATGATCGTCAAAATGAAACTTACTGCA     | 720        |              |
| Db                    | 658             | TGGGGATTTTACACCGAGGTGAAATTTCTAGATTTTATAATCGTCAAGTGCACCTTACC       | 717        |              |
| Qy                    | 721             | GAAATATCTGATCACTGTCTGAAGTGTATGAACTGGTTTACCAAAATTTAAAGGCACG        | 780        |              |
| Db                    | 718             | GNAATTTGACACTTTTGTGAAGTGTATTAATCGGCTTAGATTAATTTGAAGGTACC          | 777        |              |
| Qy                    | 781             | AGCGTAAACAATGGGTTGACTATATAACCAATTCGCTAGAGAAATGACACTGGCGGTTTTA     | 840        |              |
| Db                    | 778             | ACTTCTAAAAGTTGGCTGAAATTTATCATCTAGTTCCGTTAGAGAGATGACATTTACTG       | 837        |              |
| Qy                    | 841             | GATGTTGTTGCAATATTTCCCAAAATATGACACAGCAGCTGACCCCAATGGAACGAAAGCA     | 900        |              |
| Db                    | 838             | GATTTGGTGGCGTTATTTCCAACTAATGACACATATGTATCTCAATCGAAACACAGCT        | 897        |              |
| Qy                    | 901             | CAACTAAACAAGGGAAGTATATACAGATCCACTGGGCGCGGTAAACGCTGCTTCTCAAT       | 960        |              |
| Db                    | 898             | CAACTTACACGGGATGTGTATACAGATCCGATAGCATTTAAACATAGTGAACAAGTACTGGA    | 957        |              |
| Qy                    | 961             | TCCTGATG------ACAAAGCACCTTCTTTTGGAGTGTATAGAAATCATCCGTT            | 1008       |              |
| Db                    | 958             | TTCTCGAAACCTTTGGTCAACCCACAGCTGGTATTTCTTTTTATGAAGTTGAAACCAACGTA    | 1017       |              |

QY 2074 CCAGCGGTAAACGGAATATGAAAGTGAATCAAGCGGCAAACTTAGTGGAAATGCTATCGGAT 2133  
DB 2071 CCAGGTGTAAACGGAATATGAAAGTGAATCAAGCGGCAAACTTAGTGGAAATGCTATCGGAT 2130  
QY 2134 GATTGTATCAAAATGAAGAACGATTTGTTATGATGACAGTGAAGAGGCGAAAACGGCTC 2193  
DB 2131 GATTGTATCAAAATGAAGAACGATTTGTTATGATGCGGTGAGAGAGCGAAAACGGCTC 2190  
QY 2194 AGTGAAGCAGTAAATTTGCTTCAAGATCCAGATTTCCAGAGAGATAAATGGAGAAAATGGC 2253  
DB 2191 AGTGGGCGACGTAACTTACTACAGATCCAGATTTCCAGAGAGATAAATGGAGAAAATGGC 2250  
QY 2254 TGGAGCGCAAGTACGGGAATTTAGGTTATAGAGGGGATGCTTTATCAAAAGGCGTTAT 2313  
DB 2251 TGGGCGGCAAGTACGGGAATTTAGGTTATAGAGGGGATGCTTTATTAAGGACGTTAT 2310  
QY 2314 CTAGCGCTTACCAGGTGCGAGAGAAATAGATACGGAAAGTATCCAAAGTATCTGTATCAA 2373  
DB 2311 CTAGCGCTTACCAGGTGCGAGAGAAATGATACGGAAAGTATCCAAAGTATCTGTATCAA 2370  
QY 2374 AAAGTAGAGGAAGTGTATTAAGAACCATACACAAAGATATAGATTGAGAGGGTTTGTGCGA 2433  
DB 2371 AAAGTAGAGGAAGTGTATTAAGAACCATACACAAAGATATAGATTGAGAGGGTTTGTGCGA 2430  
QY 2434 AGCAGTCAAGATTTGGAATTTTCAAAATTCGTATCAAAACCGAATCGGAATTTGTAAGAAAT 2493  
DB 2431 AGTAGTCAAGATTTGGAATTTTATACGATACGTACCAAAACCGAATCGGAATTTGTAAGAAAT 2490  
QY 2494 GTACCGGATGATTTGCTGCCAGATGATCTCTGTTAACTCGGATGGTAGTATCAATCGA 2553  
DB 2491 GTACCGGATGATTTGCTGCCAGATGATCTCTGTTAACTCGGATGGTAGTATCAATCGA 2550  
QY 2554 TGCAGCGCAACAAAGTATGTAATAGCGTTTGAAGTAGAAGAACCGTTCTGTTGGAAGCG 2613  
DB 2551 TGCAGCGCAACAAAGTATGTAATAGCGTTTGAAGTAGAAGAACCGTTCTGTTGGAAGCG 2610  
QY 2614 CATGAGTCTCTATTCCTATTGATACAGGTGAAATCGATTAATGAAATGCAAGGAATA 2673  
DB 2611 CATGAGTCTCTATTCCTATTGATACAGGTGAAATCGATTAATGAAATGCAAGGAATA 2670  
QY 2674 TGGTTCGATTTAAGATTCAGGCCAGCGGATATGCAACACTCGGAACCTAGAAATG 2733  
DB 2671 TGGTTCGATTTAAGATTCAGGCCAGCGGATATGCAACACTCGGAACCTAGAAATG 2730  
QY 2734 GTCGAAGAGGACCTTTATCAGGAGAGCGATTAGAACGCTTGCAAGAGAGAAACAACAG 2793  
DB 2731 GTCGAAGAGGACCTTTATCAGGAGAGCGATTAGAACGCTTGCAAGAGAGAAACAACAG 2790  
QY 2794 TGGAAAGTTCAATGACAAGAGACGTGAAGAAAACAGATAGAGGTATATGGCATCGAAA 2853  
DB 2791 TGGAAAGTTCAATGACAAGAGACGTGAAGAAAACAGATAGAGGTATATGGCATCGAAA 2850  
QY 2854 CAAGCGGTAGATCGTTTATATGCGGATATCAGATCAGCACTGAATCTGTATGATAG 2913  
DB 2851 CAAGCGGTAGATCGTTTATATGCGGATATCAGATCAGCACTGAATCTGTATGATAG 2910  
QY 2914 ATTACAGATCTTACTCGGCGCCAGATCTGATACAGTCCATCTCTACGTATATAAGAA 2973  
DB 2911 ATTACAGATCTTACTCGGCGCCAGATCTGATACAGTCCATCTCTACGTATATAAGAA 2970  
QY 2974 ATGTTCCAGAAATACAGGGATGAATCTATACGAAGTTTACAGAAATTAACAGATCGACTC 3033  
DB 2971 ATGTTCCAGAAATACAGGGATGAATCTATACGAAGTTTACAGAAATTAACAGATCGACTC 3030  
QY 3034 CAACAGCGTGGATTTGTTATGATCAGGAAATGCCATACCAATGTTGATTTTCGAAAT 3093  
DB 3031 CAACAGCGTGGATTTGTTATGATCAGGAAATGCCATACCAATGTTGATTTTCGAAAT 3090  
QY 3094 GGGTTAGTAATTTGGAATGCAACGCTGGGTGAGAGTACAAACCAATCAATCATCT 3153  
DB 3091 GGGTTAGTAATTTGGAATGCAACGCTGGGTGAGAGTACAAACCAATCAATCATCT 3150  
QY 3154 GTCCTTTGATTTCCAACTGGGATGAGCAAGTTTTCGCAACAGTTTACAGTTTCAACCGAAT 3213

DB 3151 GTCCTTTGATTTCCAACTGGGATGAGCAAGTTTTCACACAGTTTACAGTTTCAACCGAAT 3210  
QY 3214 CAAAGATATGTTTACAGATTACTGCGAGAAAAGAGGGGTAGAAAATGATATGTAAGT 3273  
DB 3211 CAAAGATATGTTTACAGATTACTGCGAGAAAAGAGGGGTAGAAAATGATATGTAAGT 3270  
QY 3274 ATCCGTGATGTTGGAATCAACAGAAAACGCTTACTTTTAGTGCAGCGAATATGATACA 3333  
DB 3271 ATTGCGTATGTTGGAATCAATCAGAAAACGCTTACTTTTAGTGCAGCGAATATGATACA 3330  
QY 3334 AATGGAATGTTAATACGCAAGTGTCCAATCAAAATGGAATATAACACAAATATGCGTAT 3393  
DB 3331 AATGTTGTTGTTAATACGCAAAACCGGCTATATCAGAAAACAGTGACATTCATCCCGTAT 3390  
QY 3394 AATACACAGCATCGAGTACAAAGCGGATATAACGCAAAATATATATGATATA 3442  
DB 3391 ACAGATCAATGTGGATTGGAATTAAGTGAAACAGAGGTACGTTCTATA 3439

## RESULT 3

US-07-812-180A-1  
; Sequence 1, Application US/07812180A  
; Patent No. 5366892  
; GENERAL INFORMATION:  
; APPLICANT: Foncerrada, Luis R  
; APPLICANT: Payne, Jewel M  
; APPLICANT: Sick, August J  
; TITLE OF INVENTION: No. 5366892el Coleopteran-Active Bacillus  
; TITLE OF INVENTION: thuringiensis Isolate and a No. 5366892el Gene Encoding a  
; TITLE OF INVENTION: Coleopteran-Active Toxin  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Roman Saliwanchik  
; STREET: 2421 N.W. 41st Street, Ste A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/812,180A  
; FILING DATE: 19920102  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, Roman  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3471 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
; STRAIN: kumamotoensis  
; INDIVIDUAL ISOLATE: PS50C  
; IMMEDIATE SOURCE:  
; LIBRARY: LAMBDAEM (TM) - 11 LIBRARY OF LUIS  
; LIBRARY: FONCERRADA  
; CLONE: 50C

US-07-812-180A-1

Query Match 50.0%; Score 1812.2; DB 1; Length 3471;

| Best Local Similarity 72.28; Pred. No. 0; Matches 2504; Conservative 0; Mismatches 908; Indels 57; Gaps 9; |      |   |      |  |  |  |  |  |  |
|--|------|---|------|--|--|--|--|--|--|
| Qy   | 1    | ATGAGTCCAAATATCAAAATGAATATGAATATAGATGCGACACCTTCTACTCTGTGA     | 60   |  |  |  |  |  |  |
| Db   | 1    | ATGAGTCCAAATATCAAAATGAATATGAATATAGATGCGACACCTTCTACTCTGTGA     | 60   |  |  |  |  |  |  |
| Qy   | 61   | TCCAAATGATTTACAGATACCTTTTGGCAATGAGTACCAATGCGCTACCAAAATATG     | 120  |  |  |  |  |  |  |
| Db   | 61   | TCCAGTGAATTTAAACAGATACCTTTTGGCAATGAGTACCAATGCGCTACCAAAATATG   | 120  |  |  |  |  |  |  |
| Qy   | 121  | GATTTATAAGATATTTAAATATGCTCGCGGAAATGCTAGTGAATACCTTGGTTCACCT    | 180  |  |  |  |  |  |  |
| Db   | 121  | AATTTATAAGATATTTAAATATGCTCGCGGAGAGATCTGGAATTTTGGAAATCCG       | 180  |  |  |  |  |  |  |
| Qy   | 181  | GAAGTACTTGTAGCGGACAGATGAGCTAAGCGCGCAATGATATAGTAGGTAAATTA      | 240  |  |  |  |  |  |  |
| Db   | 181  | GAGACGTTTATTA---GTTTCATCCAGATTCAAATCGGAATGGCAATTTGGTTCGAATA   | 237  |  |  |  |  |  |  |
| Qy   | 241  | CTATCAGTCTTAGGGTCCCAATTTTGGCGCGATAGTGTCTTTTACTCAACTTATT       | 300  |  |  |  |  |  |  |
| Db   | 238  | CTAGAGCTTTTAGGGTTCCTAATTTGCTAGTCAGATAGCTAGTTCTATAGTTTCATGTT   | 297  |  |  |  |  |  |  |
| Qy   | 301  | GATATTTCTGTGCGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAACAAAGTAGAA  | 360  |  |  |  |  |  |  |
| Db   | 298  | GGTCAATTTAGCGCGTCAAGAGCGTAGATATATGGGAGAGAAATTTATGGAACGAGTGAA  | 357  |  |  |  |  |  |  |
| Qy   | 361  | GAATCTAATTAATAAATAAGCAGATATGCAAGGAATTAAGCGCTTTCGGAATTAGAA     | 420  |  |  |  |  |  |  |
| Db   | 358  | GAATCTGTTGATCAAAAATAGAAAAATATGTAAAGATAAGGCTCTTGTGGAATTTAAA    | 417  |  |  |  |  |  |  |
| Qy   | 421  | GGATAGTGAATATACCAATATATCTACTGCGCTTGAAGATGGAAGAAATCCA          | 480  |  |  |  |  |  |  |
| Db   | 418  | GGGCTAGGAATGCTTTGGATGTATATCAGCAGTCACTTGAAGATTTGGCTGGAAATCGC   | 477  |  |  |  |  |  |  |
| Qy   | 481  | AATGGTTCAAGAGCTTACGAGATGTGCGAAATCGAATTTGAAATCCTCGATAGTTTATT   | 540  |  |  |  |  |  |  |
| Db   | 478  | AATGATGCAAGAACTAGAGTGTGTTCTAATCAATTTATAGCTTTAGATCTTAACCTT     | 537  |  |  |  |  |  |  |
| Qy   | 541  | ACGCAATATATGCAATCTTTTAGAGTGAACAAATTTTGAAGTACCAATCCTTACTGTATAT | 600  |  |  |  |  |  |  |
| Db   | 538  | GTTAGTTCAATTCATCTTTTGCAGTATCCGAGACACGAACTACTATTATTAGCAGTATAT  | 597  |  |  |  |  |  |  |
| Qy   | 601  | GCAATGCGAGCAACCTTCATTTACTGTTTATTAAGGAGCGGTCAATTTTGGAGAGAA     | 660  |  |  |  |  |  |  |
| Db   | 598  | GCAAGGCTGTGAACCTACATTTATTTGTTTATTAAGAGATGCTTCTATTTTTGGAGAGAG  | 657  |  |  |  |  |  |  |
| Qy   | 661  | TGGGGATGGTCAACAACTACTATTAACTATTATGATCGTCAAAATGAAATCTTACTGCA   | 720  |  |  |  |  |  |  |
| Db   | 658  | TGGGGATTTACACCAAGTGAAATTTCTAGATTTTATATCGTCAAGTCAACTTACCGCT    | 717  |  |  |  |  |  |  |
| Qy   | 721  | GAATATCTGATCACTGTGTAAGTGGTATGAACTGGTTTGTAGCAAAATTAAGGCGACG    | 780  |  |  |  |  |  |  |
| Db   | 718  | GAATATCTCAGACTATTGTGTAAGTGGTATAAATTCGGCTTAGATAAAATGGAAGGTACC  | 777  |  |  |  |  |  |  |
| Qy   | 781  | AGCGTAAACAAATGGTTGACTATACCAATTTCCGTAGAGAAATCACACTGCGCGTTTAA   | 840  |  |  |  |  |  |  |
| Db   | 778  | ACTTCTAAAGTTGCTGGAATTAATCACTGTTCCGTAGAGATGACATTAATCTGGTATTA   | 837  |  |  |  |  |  |  |
| Qy   | 841  | GATGTTGTTGATTTATCCCAATTTATGACACACGACGTCACCCCAATGGAACGAAAGCA   | 900  |  |  |  |  |  |  |
| Db   | 838  | GATTTGGTGGCTTATTTCCAAACTATGACACACATATGATATCCCAATCGAAACACAGCT  | 897  |  |  |  |  |  |  |
| Qy   | 901  | CAACTAACAGGGAAGTATATACAGATCCATGCGCGCGGTAAAGCTGCTTCAATTTGGT    | 960  |  |  |  |  |  |  |
| Db   | 898  | CAACTTACCGGGATGTGTATACAGATCCGATAGCAATTTAAACATAGTGACAGTACTGGA  | 957  |  |  |  |  |  |  |
| Qy   | 961  | TCCTGGTATG-----ACAAAGCACTTCTTTCGGAGTGAATGATCATCCGTT           | 1008 |  |  |  |  |  |  |
| Db   | 958  | TTCTGCAACCTTGGTCAACCCACAGTGGTATTTCTTTTATGAAGTTGAAACCAACGTA    | 1017 |  |  |  |  |  |  |
| Qy   | 1009 | ATTCGACCAACCCATGTTATTTGATTTATTAACGGGACTCACAGTGTATACAAATCAAGA  | 1068 |  |  |  |  |  |  |

|    |      |   |      |  |  |  |  |  |  |
|----|------|---|------|--|--|--|--|--|--|
| Db | 1018 | ATTCTGTCGCCACACACTTTGTTTGATATATACTCAGCTCAGTAGAAAATTAATACAGTAGAGGG | 1077 |  |  |  |  |  |  |
| Qy | 1069 | AGCATTTCTTCCCTCGCTATATA-AGACATTTGGGCTGGTCAATCAATAGCTTACCATCG      | 1127 |  |  |  |  |  |  |
| Db | 1078 | GGTATTACGTTAAATTAATGATGATATATAAACTACTGGTCAGGACATACCCCTAAATAT      | 1137 |  |  |  |  |  |  |
| Qy | 1128 | TGTCAGTAGGGGTAGTAATCTTCAACAAATGATGGAACCTAAATCAAAATCTACACAGCAC     | 1187 |  |  |  |  |  |  |
| Db | 1138 | CGTAGAACAGCTGATTCGACCGTAAACATACAGCTACTTACGGTCCAATCACTTTCAGAA      | 1197 |  |  |  |  |  |  |
| Qy | 1188 | TAGTA--CCTTTGATTTTACGAATATGATTTTACAAGCTCTATCAAAAGGATGCAAGTA       | 1245 |  |  |  |  |  |  |
| Db | 1198 | AAGAAATTCATTTGCACTTGAGGATAGGATATTTTGAATTAATTTCAACTGTGGCAAC        | 1257 |  |  |  |  |  |  |
| Qy | 1246 | CTCCTTGATATTTTACCTCGTGTATACGTATATATTTTTCGAAATGCCAGAGTCCGAG        | 1305 |  |  |  |  |  |  |
| Db | 1258 | CTAGCTAA-----TTACTACAAAGGCATATGGTGTGCGGGGATCTTGG                  | 1302 |  |  |  |  |  |  |
| Qy | 1306 | TTTTTTCATGTTAAACCAATTTGAATTAATACAGAAAGACGTTAAAGTATAATCCAGTTTCC    | 1365 |  |  |  |  |  |  |
| Db | 1303 | TTCCATATGTTAAAGGGGAACCTCATCAACACAGCGTATTATATTCAAAAACACAT          | 1362 |  |  |  |  |  |  |
| Qy | 1366 | AAGATATATAGCGAGTACAAGAGATTCGGAATTA---GAATACCTCCAGAAACTTCA         | 1422 |  |  |  |  |  |  |
| Db | 1363 | ACAGCTCTCAAGGGGTGTACACAGGTTTATGAATCAAGTGTGAATGAAATACCTCTAGATA     | 1422 |  |  |  |  |  |  |
| Qy | 1423 | GATCAACCAAAATATGATCATATAGCATAGATTTATGTCATATCAAGTATTTCCCGCG        | 1482 |  |  |  |  |  |  |
| Db | 1423 | ACTGTACCGGTAGCTGAAGCTAGTCAAGATTTATCTCATATTAACCTCCCATTTCTTTC       | 1482 |  |  |  |  |  |  |
| Qy | 1483 | ACGGGTAACTACTACCGGAT-----TAGTACCTGTATTTTCTTGGAACACATCGAAGT        | 1533 |  |  |  |  |  |  |
| Db | 1483 | TCATAAATGGGAGTGCATACTACTGGGATTTCCCTGTATTTGTTGGACACATACTAGT        | 1542 |  |  |  |  |  |  |
| Qy | 1534 | GCAGTTTAAACAAATCAATATATTCAGATAAATCACTCAAAATCCGCGCTTAAATGT         | 1593 |  |  |  |  |  |  |
| Db | 1543 | GCGGATTTAAATAATACAATATATTCAGATAAATCACTCAAAATCCAGCGGTAAGGGA        | 1602 |  |  |  |  |  |  |
| Qy | 1594 | TGGGATTAATTTACGTTTGTTCAGTGTAAAGGACGAGACATACAGAGGGGATTTA           | 1653 |  |  |  |  |  |  |
| Db | 1603 | GACATGTTATCTTAGGGGTTCGTTAGTAGTACAGGTCCTGGATTTACAGGAGGAGTATA       | 1662 |  |  |  |  |  |  |
| Qy | 1654 | TTACAGTATTAATAGAGTACTGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCCTA       | 1713 |  |  |  |  |  |  |
| Db | 1663 | TTA---AAAGAACCAATCTTAGCATATTAGGACCTTTGGGTTACAGTAATGGGTG           | 1719 |  |  |  |  |  |  |
| Qy | 1714 | GCATTAGAAAAGCAGGAAATATCGTGTAGACTGAGATATGCTACTGATGCAAGATTT         | 1773 |  |  |  |  |  |  |
| Db | 1720 | TTATCACAAAG-----ATATCGTGTAAAGAAATTCGCTATGCTCTACAAACAGATTTT        | 1770 |  |  |  |  |  |  |
| Qy | 1774 | GTATTGCAATGAACGATGCTCAGATTCAGTGCCTAAACAAACATGACCCAGGTGAGAT        | 1833 |  |  |  |  |  |  |
| Db | 1771 | GAATTTACTCTATACCTTGGCGCACAAATAGAAAAAATAGATTTAAACAAACTATGGAT       | 1830 |  |  |  |  |  |  |
| Qy | 1834 | CTGACATCTAAAACCTTTTAAAGTTGACAGTGTCTATCAACACATTTAAATTTAGCAACAGAT   | 1893 |  |  |  |  |  |  |
| Db | 1831 | AATGGGCACTTTTAAAGTATGAACATTTAAATTTCCGAGTTTCACTACTGATTTCCAA        | 1890 |  |  |  |  |  |  |
| Qy | 1894 | AGTTCCGTAGCAATGAAACATAATTTAGGTGGAAGACCCCTAATTCACAACTATCTGGTATA    | 1953 |  |  |  |  |  |  |
| Db | 1891 | TTACAGAGAAACACAAAGATAAAATACTCCTATCCATGGGTGATTTTAGCTCCGGTCAAGAA    | 1950 |  |  |  |  |  |  |
| Qy | 1954 | GTTTACGTTGCAAGATCGAATTCATCCAGTAGATGAGACATATGAGCGGGAACAGAT         | 2013 |  |  |  |  |  |  |
| Db | 1951 | GTTTATATAGACCGAATTCGAATTCATCCAGTAGATGAGACATATGAGCGGGAACAGAT       | 2010 |  |  |  |  |  |  |
| Qy | 2014 | TTAGAGCAGCGAAGAAAGCAGTGAATGCTTGTTTACGAATAACAAAGATGGCTTACGA        | 2073 |  |  |  |  |  |  |
| Db | 2011 | TTAGAGCGGCGAAGAAAGCAGTGAATGCTTGTTTTACGAATAACAAAGATGGCTTACGA       | 2070 |  |  |  |  |  |  |
| Qy | 2074 | CCAGCGGTAAACGGAATTATGAGTGAATCAAGCGGCAAACTTTAGTGGAAATGCTTACGGAT    | 2133 |  |  |  |  |  |  |
| Db | 2071 | CCAGGTGTAACGGATTTAGTGAATTAATCAAGCGGCAAACTTTAGTGGAAATGCTTACGGAT    | 2130 |  |  |  |  |  |  |



QY 2134 GATTGTATCCAAATGAAATCGAATGTTATTTGATGACGTGAGAGCGGAAACGGCTC 2193  
DB 2131 GATTATATCCAAATGAAATCGAATGTTATTTGATGCGGTGAGAGCGGAAACGGCTC 2190  
QY 2194 AGTGGGCGAGTAAATGCTTCAAGATCCAGATTTCCAGAGATAAATGAGAAATGGC 2253  
DB 2191 AGTGGGCGAGTAAATGCTTCAAGATCCAGATTTCCAGAGATAAATGAGAAATGGC 2250  
QY 2254 TGGACGGCAAGTACGGGAATTTGAGGTTTATAGAGGGGATGCTTTATTTCAAGGGCGTTAT 2313  
DB 2251 TGGGCGGCAAGTACGGGAATTTGAGGTTTATAGAGGGGATGCTTTATTTAAAGGACGTTAT 2310  
QY 2314 CTACGCTTACCGGTGCGAGAGAAATAGATACGGAACGATCCAAAGTATCTGTATCAA 2373  
DB 2311 CTACGCTTACCGGTGCGAGAGAAATAGATACGGAACGATCCAAAGTATCTGTATCAA 2370  
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QY 2434 AGCAGTCAAGGATTTGAAATTTTCAAAATTCCTCATCAACGACCGAATTTGTAATAAT 2493  
DB 2431 AGTAGTCAGGATTTGAAATTTTCAAAATTCCTCATCAACGACCGAATTTGTAATAAT 2490  
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DB 2491 GTACCGGATGATTTGCTGCCAGATGATCTCTGTTAACTCGGATGCTAGTATCAATCGA 2550  
QY 2554 TGCAGGCAACAAAGTATGTAATAGCGTTTGAAGTAGAAGAAACCGTTCTGTTGAAGCG 2613  
DB 2551 TGCAGGCAACAAAGTATGTAATAGCGTTTGAAGTAGAAGAAACCGTTCTGTTGAAGCG 2610  
QY 2614 CATGAGTCTCTATCTTCTATGATACAGGTGAATCGATTACAAATGAAATGACGAGTA 2673  
DB 2611 CATGAGTCTCTATCTTCTATGATACAGGTGAATGAAATGAAATGACGAGTA 2670  
QY 2674 TGGGTTGGAATTTAAGATTAACGACCCAGAGGGATATGCAACACTCGGAAACCTAGAAATG 2733  
DB 2671 TGGGTTGGAATTTAAGATTAACGACCCAGAGGGATATGCAACACTCGGAAATCTTGAATTA 2730  
QY 2734 GTCCAGAGGAGCTTTATCAGAGAGCGATAGAGCGTTGCAAGAGAGAAACACAG 2793  
DB 2731 GTCCAGAGGAGCTTTATGTCAGAGAGCGATAGAGCGTTGCAAGAGAGAAACACAG 2790  
QY 2794 TGGAGATTTCAATGACAGAGACGCTGAGAGACAGATAGAGGTATATGCGCATCGAA 2853  
DB 2791 TGGAGATTTCAATGACAGAGACGCTGAGAGACAGATAGAGGTATATGCGCATCGAA 2850  
QY 2854 CAAGCGGTAGATCGTTTATATGTCGGATTTATCAGGATCAGCAACTGATCTGTATGAG 2913  
DB 2851 CAAGCGGTAGATCGTTTATATGTCGGATTTATCAGGATCAGCAACTGATCTGTATGAG 2910  
QY 2914 ATTAAGATTTCTCTGCGGCCCAAGATCTGATACAGTCCATCTTACGATATAACGAA 2973  
DB 2911 ATTAAGATTTCTCTGCGGCCCAAGATCTGATACAGTCCATCTTACGATATAACGAA 2970  
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DB 2971 ATGTTCCCAAGAAATACAGGATGAACTATACGAGTTTACAGATTTACAGATCGACTC 3030  
QY 3034 CAACAGCGGTGGAATTTGATGATCAGCGAAATGCCATACCAATGCTGATTTTCAAAAT 3093  
DB 3031 CAACAGCGGTGGAATTTGATGATCAGCGAAATGCCATACCAATGCTGATTTTCAAAAT 3090  
QY 3094 GGGTTAAGTAAATTTGGAATGCAACCGCTTGGCTGAGAGTACAAATCAATCATCATCT 3153  
DB 3091 GGGTTAAGTAAATTTGGAATGCAACCGCTTGGCTGAGAGTACAAATCAATCATCATCT 3150  
QY 3154 GTCTTGTGATTTCCAACTGGGATGAGCAGTTTTCGCAACAGTTTACAGTTCAACCGAAT 3213  
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DB 3271 ATCCGTGATGTTGGAATCAACAGAAACGCTTACTTTTAGTGCAGGCGATTTATGATACA 3330  
QY 3334 AATGGAATGTATAATACGCAAGTGTCCATACAAATGGAATATAACACAAATATGCGTAT 3393  
DB 3331 AATGGAATGTATAATACGCAAGTGTCCATACAAATGGAATATAACACAAATATGCGTAT 3390  
QY 3394 AATACACAGCAATCGAGTACAAACCGGATATAACGCAAAATAATATGATATA 3442  
DB 3391 ACAGATCAATGTGATTCGAATAGTGAACAGAGGTACGTTCTATA 3439

## RESULT 4

US-08-315-468-1  
Sequence 1, Application US/08315468  
Patent No. 5554534  
GENERAL INFORMATION:  
APPLICANT: Michaels, Tracy Ellis  
APPLICANT: Poncerrada, Luis  
APPLICANT: Narva, Kenneth E.  
TITLE OF INVENTION: Process for Controlling Scarab Pests  
with *Bacillus thuringiensis* Isolates  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25.  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/315,468  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/014,941  
FILING DATE: 01 FEB 1993  
APPLICATION NUMBER: 07/828,430  
FILING DATE: 30-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/808,316  
FILING DATE: 16-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: MA73.C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3471 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: *Bacillus thuringiensis*  
STRAIN: kumamotoensis  
INDIVIDUAL ISOLATE: PS50C  
IMMEDIATE SOURCE:

LIBRARY: LAMBDAGEN (TM) - 11 LIBRARY OF LUIS  
LIBRARY: FONCERRADA  
CLONE: 50C(a)  
US\_08-315-468-1

Query Match 50.0%; Score 1812.2; DB 1; Length 3471;  
Best Local Similarity 72.2%; Pred. No. 0;  
Matches 2504; Conservative 0; Mismatches 908; Indels 57; Gaps 9;

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DB 61 TCCAAATGATCTCAACAGATACCTTTTCGGAATGAGCAACAAATGCGCTACAAATATG 120
QY 121 GATTATAAGATATTTTAAATGTCGCGGAAATGCTAGTGAATACCGTGGTTCACT 180
DB 121 AATTATAAGATTTATCTGAAATGTCGCGGAGAGAAATCTGGAATTTATTTGGAATCCG 180
QY 181 GAAGTACTTTAGCGGACAGATGACGTAAGCGCGCAATGATATAGTAGGTAAATTA 240
DB 181 GAGACGTTTATTA---GTTCTACACGATTCAAACTGGAATTTGGCATTTGTTGGTCAATA 237
QY 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCGGATAGTGAGTCTTTTACTCAACTTAT 300
DB 238 CTAGAGCTTTTAGGGTTCCTATTTGCTAGTCAGATAGCTAGTTCTCTAGTTTCAATGTT 297
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DB 298 GGTCAATTTATGCGCTCAAGAGCGTAGATATATGCGGAGAAATTTATGGAACGAGTGAA 357
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DB 358 GAATCTCGTTGATCAAAAATAGAAAATATGTAAGAGATAAGGCTCTTGTCTGAATTAATA 417
QY 421 GGATTTAGTGAATATTAACCAATTTATCTAACTGCGCTTGAAGATGGAAGAAATCCA 480
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DB 478 AATGATCAAGAACTAGAAAGTGTCTTTCTAATCAATTTATAGCTTTAGCTTTAACTTT 537
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QY 601 GCAATGGCAGCCCAACTTCATTTACTGTATTATTAAGGAGCGCTCAATTTTGGAGAGAA 660
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1534 GCAGTTTAAACAATATCAATATATTCAGATAAATATCTCAAAATTCGCGGCGTTAAATGT 1593
1543 CGCGATTTAAATAATACAAATATATTCAGATAAATCACTCAAAATCCAGCGGTAAAGGA 1602
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1954 GTTTACGTTGACCGAATCGAATTTCCCTAGTATGATGAGATATGAGCGGAAACAGAT 2013
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2014 TTAGAAGCAGCGAAGAAAGCAGTGAATGCTTGTGTTTACGAATACAAAAAGATGGCTTACGA 2073
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Db 2011 TTAGAAGCGCGAAGAAAGCAGTGAATGCTTGTGTTACGAATACAAAGATGGCTTACGA 2070  
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Db 2911 ATTACAGATCTTACTGCGGCTCAAGATCTGATACAGTCCATTTCTTACGTTATTAACGAA 2970  
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Db 3091 GGGTTAAGTAATTTGGAATGCAACGCTGCGGTAGAGTACACAAATCAATCATATCT 3150  
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Db 3211 CAAAGATATGTTGTACAGTTACTGCGAGAAAGAGGAGGTTAGGAATGGATATGTAAGT 3270  
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Db 3271 ATTCGATGTTGGGAAATCAATCAGAAACGCTTACTTTTAGTGCAAGCGATTTATGATACA 3330  
Qy 3334 AATGGAATGTTAATACGCAAGTGTCCATCAATATGGAATATAACCAATATGCGTAT 3393  
Db 3331 AATGGTGTATTAATGACCAACCGGCTATATCAAAAAACAGTGACATTCATCCCGTAT 3390  
Qy 3394 AATACACAGCATCCAGTACAAACCGATATAACGCAAAATAATATATGTTATA 3442  
Db 3391 ACAGATCAATGTTGATGGAATGAAATAGTGAACAGAGGTACGTTCTATA 3439

RESULT 5  
US-07-941-650A-1  
; Sequence 1, Application US/07941650A  
; Patent No. 6294184  
; GENERAL INFORMATION:  
; APPLICANT: Oyeda, Kendrick A.  
; APPLICANT: Bradfisch, Gregory A.  
; TITLE OF INVENTION: Process for Controlling Lepidopteran Pests  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/941,650A  
; FILING DATE: 19920908  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/758,020  
; FILING DATE: 12-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/658,935  
; FILING DATE: 21-FEB-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/642,112  
; FILING DATE: 16-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3471 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:

ORGANISM: Bacillus thuringiensis  
STRAIN: kumamotoensis  
INDIVIDUAL ISOLATE: P950C  
IMMEDIATE SOURCE:  
CLONE: E. coli NM522(pMYC1638), NRRL B-18751  
US-07-941-650A-1

Query Match 50.0%; Score 1812.2; DB 4; Length 3471;  
Best Local Similarity 72.2%; Pred. No. 0;  
Matches 2504; Conservative 0; Mismatches 908; Indels 57; Gaps 9;

QY 1 ATGAGTCCAAATATCAAAATGAATATGAATATAGATGCGACACCTTCTACTCTGTGA 60  
DB 1 ATGAGTCCAAATATCAAAATGAATATGAATATAGATGCGACACCTTCTACTCTGTGA 60

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QY 121 GATTATAAAGATATTTAAATATGTCGCGGAATGCTAGTGAATACCTCGGTTCACTT 180  
DB 121 AATTATAAAGATATCTGAAATATGTCGCGGAGAGATCTCTGAATATTTTGGAAATCCG 180

QY 181 GAAGTACTGTTAGCGGACAAAGATGCAAGCTAAGCGCGCAATGATATAGTAGGTAATTA 240  
DB 181 GAGACGTTTATTA--GTTTCATCACGATTCAAACTGGAATGGCAATGTTGGTCTGAATA 237

QY 241 CTATCAGGTTTAGGGTCCCAATTTGTTGGCGGATAGTAGTCTTTATCTACTCACTTATT 300  
DB 238 CTAGGAGCTTTTAGGGGTTCCATTTGCTAGTCAGATAGTAGTCTTCTATGATTTTCAATGTT 297

QY 301 GATATTTCTGTGGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAACAAAGTAGAA 360  
DB 298 GGTCAATTTAGCGCGTCAAAGAGCGTAGATATATGGGAGAAATATGGAACGAGTGAA 357

QY 361 GAATCAATTAATCAAAAATAGCAGAAATATGCAAGGAATAAGCGCTTTTCGGAATTAAGAA 420  
DB 358 GAATCGTTGATCAAAAATAGAAAATATGTAAGAGATAAGGCTCTTGTCTGAATTAATAA 417

QY 421 GGATAGTGAATATTAACCAATATATCTACTCGCTTGAAGATGGGAAGAAATCCA 480  
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QY 481 AATGGTTCAAGAGCTTACAGAGATGTGCAAAATCGAATTTGAAATCCTCGATAGTTTATTT 540  
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QY 721 GAATATTCTGATCATCTGTGTAAGGTGATGAACCTGTTTAGCAAAATTTAAGGACGACG 780  
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QY 901 CAACCTAACAGGGAAGTATATACAGATCCACTGGCGCGGTTAAACGTCGTTCAATTCGT 960  
DB 901 CAACCTAACAGGGAAGTATATACAGATCCACTGGCGCGGTTAAACGTCGTTCAATTCGT 960

DB 898 CAACCTAACAGGGAAGTATATACAGATCCGATAGCATTTTAAACATAGTGACACAGTACTGGA 957  
QY 961 TCTCGGTATG-----ACAAAGCACCTTCTTTTGGAGTGTAGTAATCATCCGTT 1008  
DB 958 TTTGCGAACCTTTGGTCAACCCACAGTGGTATTTCTTTTATGAAGTTGAAACACAGTA 1017

QY 1009 ATTGCAACCCCACTGATTTTGAATATATAACGGGACTCTACAGTGTATACACAAATCAAGA 1068  
DB 1018 ATTGCTCGGCAACACTGTTTGTATATACTCAGCTCAGTAGAATTAATAACAGTAGAGGG 1077

QY 1069 AGCATTTCTTCCGCTCGTATATA-AGACATTTGGGCTGGTGCATCAATAAGCTACCAATCG 1127  
DB 1078 GGTATTTACGTTAAATAATGATGCATATATAAATCTACTGGTCAGGACATACCTTAAATAT 1137

QY 1128 TGTCACTAGGGGTAGTAATCTTCAACAAATGATGGAATTAATCAAAATCTACACAGCAC 1187  
DB 1138 CGTAGAACACTGATTCGACCGTAACATACACAGCTAATTTACGTCGATCATCTTCAAGAA 1197

QY 1188 TAGTA--CCTTTGATTTTACGAATATGATATTTTACAAGACTCTCTATCAAAAGGATGCA 1245  
DB 1198 AAGAAATTCATTTGCACCTTGAGGATAGGATATTTTGAATTAATTTCAACTGTGGCAAAAC 1257

QY 1246 CTCCTGATATTTGTTTACCTCGGTTATACGTATATATTTTGGAAATGCGCAGAGTGCAG 1305  
DB 1258 CTAGCTAA-----TTACTACAAAGGACATATGTTGTGCGCGGATCTTGG 1302

QY 1306 TTTTTCATGTTAAACCAATTTGAATATACCAAGAAAGCGTTAAAGTATATATCCAGTTTTC 1365  
DB 1303 TTTCCATATGTTAAAGGGGAACCTCATCAACACACAGCGTATTTATATTTCAAAACACAT 1362

QY 1366 AAAGATATTTATAGCAGTACAAAGAGATTCGGAATTA---GAATTTACCTCCAGAAACTTCA 1422  
DB 1363 ACAGCTCTCAAGGGGTACACAGGTTTATGAATCAAGTGAATGATGAAATACCTCTAGATAGA 1422

QY 1423 GATCAACCAATTTATGATCATATAGCCATAGATTTATGTCATATCAAGATTTTCCGCG 1482  
DB 1423 ACTGTACCGGTAGCTGAAGCTATAGTCATAGATTTATCTCATATTTACTCTCCCATTTCTTC 1482

QY 1483 ACGGGTAACTACACCGGAT-----TAGTACCTGTATTTTCTGGACACATCGAAGT 1533  
DB 1483 TCTAAATATGGAGTGCATACTATGGAGTTTCCCTGTATTTTGTGGACACATACTAGT 1542

QY 1534 GCAGATTTAAACAAATACAAATATATTTCAAGATAAATCACTCAAAATTCGCGCGTTAAATGT 1593  
DB 1543 GCGGATTTAAATTAATACAAATATATTTCAAGATAAATCACTCAAAATTCAGCGGTAAAGGGA 1602

QY 1594 TGGATTAATTTACGTTTGTTCAGTGTAAAGGACAGACATACAGAGGGGATTTA 1653  
DB 1603 GACATGTTATATCTTAGGGGGTTCGTTAGTAGTACAGGGTCTCGGATTTTACAGGAGGATATA 1662

QY 1654 TTACAGTATATAGAGTACTGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCCTA 1713  
DB 1663 TTA---AAAAGAACCAATCTTAGCATATTAGGGACCTTTGCGGTTACAGTAAATGGGTGCG 1719

QY 1714 GCATTAAGAAAAGCAGGGAATATCTGTGAAGACTCGAGATATGCTATGTCAGATATTT 1773  
DB 1720 TTAATCAACAAG-----ATATGTTGTAAGAAATTCGCTATGCTCTACACAGATTTT 1770

QY 1774 GTATTGATGTAACGATGCTCAGATTCAGATGCGCAAAAACAAATGAACCCAGGTTGAGAT 1833  
DB 1771 GAATTTACTCTATACCTTGGCGACAAATAGAAAAAATAGATTTTAAACAAACTATGGAT 1830

QY 1834 CTGACATCTAAAACTTTTAAAGTTGCGAGATGCTATCAACCAATTTAAATTTAGCAACAGAT 1893  
DB 1831 AATGGGCGATCTTTACGATATGAACCAATTTAAATTTCCAGAGTTTCATTTACTGATTTCCAA 1890

QY 1894 AGTTCCGTAGCATTTGAACCAATAATTTTAGTGAAGACCCCTAATTTCAACAATTTATCTGGTATA 1953  
DB 1891 TTCAGAGAAACACAAAGATAAAATACTCTCTATCCATGGGTGATTTTAGCTCCGGTCAAGAA 1950

QY 1954 GTTTTACGTTGACCGAATCGAATTTTCAATCCAGTAGATGAGACATATGAAGCGGAAACAGAT 2013  
DB 1951 GTTTTATATAGACCGAATCGAATTTCAATCCAGTAGATGAGACATATGAGCGGAAACAGAT 2010

QY 2014 TTAAAGCAGCGAAGAAAGCAGTGAATGCTTGTGTTACGAATACAAAAGATGGCTTACGA 2073  
DB 2011 TTAAAGCGCGAAGAAAGCAGTGAATGCTTGTGTTACGAATACAAAAGATGGCTTACGA 2070  
QY 2074 CAGGCGTAACGGAATATGAAGTGAATCAAGCGGCAAACTTAGTGGAAATCGCTATCGGAT 2133  
DB 2071 CAGGCGTAACGGAATATGAAGTGAATCAAGCGGCAAACTTAGTGGAAATCGCTATCGGAT 2130  
QY 2134 GATTGTATCAAAATGAAATGCTTATTTGATGCGAGTGAAGGCAAAACGCTC 2193  
DB 2131 GATTGTATCAAAATGAAATGCTTATTTGATGCGGAGAGGCAAAACGCTC 2190  
QY 2194 AGTGAGCAGTAATTTGCTTCAAGATCCAGATTTCAAGAGATAAATGGAGAAATGGC 2253  
DB 2191 AGTGAGCAGTAATTTGCTTCAAGATCCAGATTTCAAGAGATAAATGGAGAAATGGC 2250  
QY 2254 TGAACGCAAGTACGGAATATGAGTTATAGAGGGGATGCTTATTTCAAGAGCGGTAT 2313  
DB 2251 TGGCGCGCAAGTACGGAATATGAGTTATGAGAGGGGATGCTTATTTAAAGGACGTTAT 2310  
QY 2314 CTACGCTACACGCTGCGAGAGAAATAGTACCGGAAACGTTATCAACGTTATCTGTATCAA 2373  
DB 2311 CTACGCTACACGCTGCGAGAGAAATGATACCGGAAACGTTATCAACGTTATCTGTATCAA 2370  
QY 2374 AAAGTAGAGGAAGTGTATTAACCAATACACAGATATAGATTGAGAGGTTTGTCCGA 2433  
DB 2371 AAAGTAGAGGAAGTGTATTAACCAATACACAGATATAGATTGAGAGGTTTGTCCGA 2430  
QY 2434 AGCAGTACAGGATGGAAATTTTCAAAATTCGTCATCAAAACGAAACCGAATTTGTAAGAAAT 2493  
DB 2431 AGTAGTCAAGGATAGAAATTTTATACGATACGTCACCAACGAAATGTTGTAAGAAAT 2490  
QY 2494 GTACCGGATGATTTGCTGCGAGATGATCTCTGTGTTAACTCGGATGATGATCAATCGA 2553  
DB 2491 GTACCGGATGATTTGCTGCGAGATGATCTCTGTGTTAACTCGGATGATGATCAATCGA 2550  
QY 2554 TGCAGCGAAACAAAGTATGTAATAGCGGTTTGAAGTACGAAACCGTTCTGTTGAGCG 2613  
DB 2551 TGCAGCGAAACAAAGTATGTAATAGCGGTTTGAAGTACGAAACCGTTCTGTTGAGCG 2610  
QY 2614 CATGATCTCTATCTTATGATACAGGTGAATGAAATGATGATGAAATGACAGGAATA 2673  
DB 2611 CATGATCTCTGCTCTCTATCGATATAGGAGAGCTGGAATGAAATGACAGGAATA 2670  
QY 2674 TGGTTGGATTTAAGATTACGACCGGAGGATGATGCAACCTCGAAACCTGATGTTG 2733  
DB 2671 TGGTTGGATTTAAGATTACGACCGGAGGATGATGCAACCTCGAAACCTGATGTTG 2730  
QY 2734 GTCGAAGAGGACCTTTATCAGGAGAGCGATTAGAACGTTGCAAGAGAGAACACACAG 2793  
DB 2731 GTCGAAGAGGACCTTTGTCAGGAGAGCGATTAGAGCGCTTGCNAAGAGAGAACACACAG 2790  
QY 2794 TGAAGATTCAAATGACAGAGACGTTGAAGAACACAGATAGAGGTTATGGCATCGAAA 2853  
DB 2791 TGAAGATTCAAATGACAGAGACGTTGAAGAACACAGATAGAGGTTATGGCATCGAAA 2850  
QY 2854 CAGCGGTAGATCGTTTATATGCGGATTCAGATCAGATCAGCACTGAATCTGATGTAGAG 2913  
DB 2851 CAGCGGTAGATCGTTTATATGCGGATTCAGATCAGATCAGCACTGAATCTGATGTAGAG 2910  
QY 2914 ATTACAGATCTTACTGCGGCGCAAGATCTGATACAGTCCATTCCTTACGTTATACGAA 2973  
DB 2911 ATTACAGATCTTACTGCGGCGCAAGATCTGATACAGTCCATTCCTTACGTTATACGAA 2970  
QY 2974 ATGTTCCCAAGAAATACAGGAGTGAATATACGAAGTTTACAGAAATTAACAGATCGACTC 3033  
DB 2971 ATGTTCCCAAGAAATACAGGAGTGAATATACGAAGTTTACAGAAATTAACAGATCGACTC 3030  
QY 3034 CAAACAGCGTGGATTTGATGATCAGCGAAATGCCATACAAATGGTGTATTTTGGAAAT 3093  
DB 3031 CAAACAGCGTGGATTTGATGATCAGCGAAATGCCATACAAATGGTGTATTTTGGAAAT 3090

QY 3094 GGGTTAAGTAATTTGGAATGCAACGCTGGCTAGAGTACAAACAAATCAATCATCATCT 3153  
DB 3091 GGGTTAAGTAATTTGGAATGCAACGCTGGCTAGAGTACAAACAAATCAATCATCATCT 3150  
QY 3154 GTCCTTGTGATTTCCAAACTGGGATGAGCAAGTTTCCCAACAGTTTACAGTTCAACCGAAT 3213  
DB 3151 GTCCTTGTGATTTCCAAACTGGGATGAGCAAGTTTCCCAACAGTTTACAGTTCAACCGAAT 3210  
QY 3214 CAAAGATATGTTGTACGAGTTACTGCGAGAAAGAGAGGGGTAGGAATGATATGAAGT 3273  
DB 3211 CAAAGATATGTTGTACGAGTTACTGCGAGAAAGAGAGGGGTAGGAATGATATGAAGT 3270  
QY 3274 ATCCGTGATGGTGGAAATCAAAACAGAAACGCTTACTTTTAGTCCAAAGCGATTATGATACA 3333  
DB 3271 ATCCGTGATGGTGGAAATCAATCAGAAACGCTTACTTTTAGTCCAAAGCGATTATGATACA 3330  
QY 3334 AATGGAATGATTAATACGCAAGTGTCCAATACAAATGGATATTAACAACAATATGGGTAT 3393  
DB 3331 AATGAGTGTGTAATTAATGCAACCAACCGCTATATCACAACCAACAGTGACATTCATCCCGTAT 3390  
QY 3394 AATACACAGGATCGAGTACCAACGATATTAACGCAAAATATATGTATA 3442  
DB 3391 ACAGATCAAAATGTGGATTGAAATAGTGAACAGAAAGGACGTTCTATA 3439

## RESULT 6

US-07-915-203-1

; Sequence 1, Application US/07915203

; Patent No. 5359048

; GENERAL INFORMATION:

; APPLICANT: Obba, Michio

; APPLICANT: Iwahana, Hidenori

; APPLICANT: Sato, Reichi

; APPLICANT: Suzuki, No. 5359048ukazu

; APPLICANT: Ogiwara, Katsutoshi

; APPLICANT: Sakana, Kazunobu

; APPLICANT: Hori, Hidetaki

; APPLICANT: Asano, Shouji

; APPLICANT: Kawasugi, Tadaaki

; TITLE OF INVENTION: No. 5359048el Microorganism and Insecticide

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESS: David R. Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: US

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/915,203

; FILING DATE: 19920723

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Saliwanchik, David R.

; REGISTRATION NUMBER: 31,794

; REFERENCE/DOCKET NUMBER: M/K 301

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 904-375-8100

; TELEFAX: 904-372-5800

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3797 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; ORGANISM: Bacillus thuringiensis

STRAIN: japonensis  
INDIVIDUAL ISOLATE: Buibu1  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 187..3636  
US-07-915-203-1

Query Match 32.6%; Score 1180; DB 1; Length 3797;  
Best Local Similarity 61.4%; Pred. No. 3.9e-248;  
Matches 2094; Conservative 0; Mismatches 1230; Indels 86; Gaps 9;

|    |      |  |      |
|----|------|--|------|
| Qy | 1    | ATGAGTCCAAATATCAAAATGAATATGAATATAGATGACACCTTCTACTTCTGTA          | 60   |
| Db | 187  | ATGAGTCCAAATATCAAAATGAATATGAATATAGATGACACCTTCTACTTCTGTA          | 246  |
| Qy | 61   | TCCATGATTTCAACAGATACCTTTTGGATGAGCAACAAATGCGCTCAAAATATG           | 120  |
| Db | 247  | TCCGATAATTTCTATTAGATATCTTTAGCAACGATCAACAAATGACATTAACAAACATG      | 306  |
| Qy | 121  | GATTATAAGATTTATTAATAATGCTCGGGAAATGCTAGTGAATACCCCTGGTTCACT        | 180  |
| Db | 307  | AATTATAAGATTTATCTGAATGACCGAATCAACAAATGCTGAATTTGCTCGAATCC         | 366  |
| Qy | 181  | GAACTACTTTAGCGGCAAGATGAGCTAAGCGCGCAATTTGATATAGTAAATTA            | 240  |
| Db | 367  | GGGACATTTATTAGTGGCAGGATCGGTTGGAACTGGAAATGATATTTAGTACTATA         | 426  |
| Qy | 241  | CTATCAGTTTAGGGTCCCATTTCTGGCCGATGATGAGTCTTTTATCTCAACTATT          | 300  |
| Db | 427  | ATAAGTGGTTTAGGGATTTCCAGTGTCTGGGGAAGTCTTCTCAATTTCTGGTTTCATTAAT    | 486  |
| Qy | 301  | GATATTTCTGGCCCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAGTAGAA       | 360  |
| Db | 487  | GGCTTATTGTGGCCGTCAAATTAATGAATGTATGGCAATATTTATGAATCGAGTGGAA       | 546  |
| Qy | 361  | GAACTCATTAATCAAAATATGACAGATATGCAAGGAATAAAGCGCTTTTCGGAAATAGAA     | 420  |
| Db | 547  | GAGCTAAATTGATCAAAATATTTAGATTCTGTAAGATCAAGAGCCATTGCGAGTTAGCT      | 606  |
| Qy | 421  | GGATTAGTAAATTAATCAAAATATATCTAACTGCTGCTGAGATGAGTCTTTTATCTCAACTATT | 480  |
| Db | 607  | AATTTCTAGAATAGCTGTAGAGTACTATCAAAATGACATTTGAAGACTGGAGAAACCCCA     | 666  |
| Qy | 481  | AATGGTTCAAGAGCTTTACGATGATGCGAAATCGATTTGAAATCTCGATAGTTTATT        | 540  |
| Db | 667  | CACAGTACAGAGCGCAGCATCTGTAAAGAAAGATTTGGAAATGCCAAGCAATTTTA         | 726  |
| Qy | 541  | ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTCTTTACTGTATAT     | 600  |
| Db | 727  | CGTACTAAATGGGTTCAATTTCTCAAAAGCAATTAATGAGACTCCACTCTTACCCACATAT    | 786  |
| Qy | 601  | GCAATGGCAGCCCAACTTCAATTTACTGTTTATTAAGGAGCGCTCAATTTTTCGGAGAGAA    | 660  |
| Db | 787  | GCACAGGCGGCTCTCTGCAATTTGCTGTAATGAGGATGTTCAAAATTTACGGGAGAGAA      | 846  |
| Qy | 661  | TGGGATGGTCAACAACTACTATTAATACTATTATGATCGTCAAAATGAACTTACTGCA       | 720  |
| Db | 847  | TGGGATATCTTCAAAATGATATGACCTATTTTATAAGAACAGTATCTTTATACGGCT        | 906  |
| Qy | 721  | GAATATTCATGATCTGTGTAAGTGGTATGAAATCTGGTTTACGAAATTAAGAGCAG         | 780  |
| Db | 907  | AGATATTCGATCAATTCGCTCAATGGTCAATGGTCAATGGTCTGGTTTAAATTAAGAGGAGCG  | 966  |
| Qy | 781  | ACCGCTAAACATGGGTTGACTATTAACCAATTTCCGTAGAGNAATGACATGGCGGTTTAA     | 840  |
| Db | 967  | GGTGTAAAGCAATGGGTTGATATATAATCGTTTCCGAGAGAAATGAATGTGATGGTATTG     | 1026 |
| Qy | 841  | GATGTTGTTGCTATTTCCTCAATATGACACAGCAGCTACCCATGGAAACGAAAGCA         | 900  |
| Db | 1027 | GATCTAGTTGCAATTTTCCAAACTACAGTGGCGGTATATATCCATCTGGAAACAAATGCA     | 1086 |
| Qy | 901  | CAACTAACAGGAGATATATACAGATCCACTGGGCGGCTAAACGTTGCTTCAATTTGTT       | 960  |
| Db |      |  |      |
| Db | 1087 | GAATTACAAGAGAAATTTTTCACAGATCCCTGTTGGAAGT-----TACGTAACTGGA        | 1137 |
| Qy | 961  | TCCTGGTATGACAAAGCAGCACTTCTTCGGAGTGTAGAAATCATCGTTATTTCGACCAACC    | 1020 |
| Db | 1138 | CAATCGAGTACCTTATATCTTGTGATGATGATTCAGCAGCTCTTCTCTCATTTTCA         | 1197 |
| Qy | 1021 | CATGTAATTTGATATATAAAGCGGACTCACAGTGTATACAAATCAAGAGCAATTTCTTCC     | 1080 |
| Db | 1198 | ACGCTCGAAGAACCTTACTTAGAAAACCTGATTTCTTTACTTGTGCAAGAAATTAGAATG     | 1257 |
| Qy | 1081 | GCTCGCTATATAGACATTTGGCTGGTCAATCAATAGCTACCATCGTGTGAGTGGGT         | 1140 |
| Db | 1258 | TATCAAGTTTATAGCAAAACGGTACGATGGAATATTATTAATTTGGGGAGGACAAAGG       | 1317 |
| Qy | 1141 | AGTAATCTTCAACAAATGATGGAACCTAAATCAAAATCTACACAGCACTAGTACCTTTGAT    | 1200 |
| Db | 1318 | TTAACCTTTCTTATATCTATGTTCTCTCATTAATAATAG-----TGGGGTCTTGCC         | 1374 |
| Qy | 1201 | TTTACGAATTAATGATATTTTCAAGACTCTATCAAAAGGATGAGTACTCTCTTGAATTTGT    | 1260 |
| Db | 1375 | GGTCTGAGGATATTAATTCCTGTGGTCAAAATGATATTTACAGAGTTGTATGACTTAT       | 1434 |
| Qy | 1261 | TACCTCGTTATAGTATATTTTGGATGCGCAGAGTGGAGTTTTCATGAGTAAAC            | 1320 |
| Db | 1435 | ATAGGAAGGTACACGAATAGTCTGCTAGGAGTAAATCCAGTTACTTTT-----            | 1483 |
| Qy | 1321 | CAATTGAATATACAGAAAGACGTAAAGTATTAATCAGTTTCCAAAGATATTATAGCG        | 1380 |
| Db | 1484 | -ACTTCAGTAAATATACAAATAAATTTTTCGAAGCCAAACAAATTCGCGGTGGATTA        | 1542 |
| Qy | 1381 | AGTACAAGAGATTCGGAATTAAGATTAACCTCCAGAACTTCAGATCAACCAAAATTTATGAG   | 1440 |
| Db | 1543 | AAACAAATTTGATTCGGCGAAGATTTAACTTACGAAATTAATCAATCTTATAGTCACAGG     | 1602 |
| Qy | 1441 | TCATATAGCCATAGATTTATGTCATATCAAGATTTCCGCGACGGGTAAACACTACCCGA      | 1500 |
| Db | 1603 | GTAAGTTACATTTACATCTTTTGAATAAAGTA-----CCGGTGGTACAGTATTAGGA        | 1656 |
| Qy | 1501 | TTAGTACCTGTATTCTTTCGGACACATCGAAGTGCAGATTTTAAACAAATCAATATATTCA    | 1560 |
| Db | 1657 | GTAGTTCTTATTTTGGTTGGACGATAGTAGTGCAGTCCGCAATTAATTTTATTACGCA       | 1716 |
| Qy | 1561 | GATAAATCACTCAAAATTCGGCCCGTTAA---ATGTTGGGATAATTTTACCGTTTGTCCA     | 1617 |
| Db | 1717 | ACAAAAATCTCACAAATCCCAATCAATAAAGCAAGTAACTAGCGGTGGAGCGGTTGG        | 1776 |
| Qy | 1618 | GTGGTAAAGACCCAGGACATACAGAGGGGATTTTATACAGTATATAGAGTACTGTT         | 1677 |
| Db | 1777 | AATTTCCAGAGGCTCTATATTAATGAGGAGCTGTGAATGNAATTAATCTGGGCTCGGTTCC    | 1836 |
| Qy | 1678 | TCTGTAGGAACCTTATTTCTAGCTCGATAT-----GGGCT                         | 1712 |
| Db | 1837 | CAAGTAAATACTTAAGGTCGCAACAGATGCAAGGGAGCAAGTCAAGATATCGTATT         | 1896 |
| Qy | 1713 | AGCATTAGAAAAAGCAGGGAATATCGTGAAGACTGAGATATGCTACTGATGCAATAT        | 1772 |
| Db | 1897 | AGAAATCAGATATGCTCTGATAGAGCGGTAAATTTACGATATCTTCCAGATCTCCAGAG      | 1956 |
| Qy | 1773 | TGATTTGATGTAAACGATGCTCAGATTCAGATGCCAAAAACAAATGAACCCAGGTGAGGA     | 1832 |
| Db | 1957 | AATCTCGAACCTATTCAGCTTCTATTGCTTTATA-CAAAATACTGTCTACAAATGCTTC      | 2015 |
| Qy | 1833 | TCTGACATCTAAAACCTTTTAAAGTTGAGATGCTATCAACATTTAAATTTAGCAACAGA      | 1892 |
| Db | 2016 | TCTAACGTATAGTACTTTTGCATATGCAATCTGGCCCTATAAATCTTAGGATTTCCGG       | 2075 |
| Qy | 1893 | TAGTTTCGCTAGCATTGAAACATAATTTTAGTGAAGCCCTTAATTCACATTTATCTGGTAT    | 1952 |
| Db | 2076 | AAAGTTCAAGGACTTTTGTATATATCTATTACAAAGCA-----AGCAGGTGCTGCTAA       | 2126 |
| Qy | 1953 | AGTTTACGTTGACCAATCGAATTTCCAGTAGATGAGACATATGAAGCGGAACAGA          | 2012 |
| Db | 2127 | CCTTTTATATGATAGAAATGGAATTTTATTTCCAGTTAATAGCTTTTATTTGAAGCAGAAAGGA | 2186 |

QY 2013 TTATAGACGACGAGAAAGAGTGAATGCTTGTGTTTAAAGAAATACAAAGATGGCTTACG 2072  
Db 2187 CCTAGATGGGCANAGAAAGCTGTGAATGGCTTGTGTTTACGAATGAAAGATGGCTTACA 2246  
QY 2073 ACCAGCGGTAAACGGATTTATGAAGTGAATCAAGCGGCAAACTTAGTGAATGCTTATCGA 2132  
Db 2247 GCAAGTGTAAACGGATTTATGAAGTGAATCAAGCGGCAAACTTAGTGAATGCTTATCGA 2306  
QY 2133 TGATTTGATCAAAATGAAAGAAACGATTTGTTATGATGAGAGAGGCAAAAGCGCT 2192  
Db 2307 TGAGTTATACCAATGAAAGAAACGATTTGTTATGAGAGAGGCAAAAGCGCT 2366  
QY 2193 CAGTGAAGCACTAATTTGCTTCAAGATCCAGATTTTCAAGAGATTAATGAGAAATGCG 2252  
Db 2367 TGTTCCAGGCACGTAATTTACTTCCAGATACAGCTTTTAATAGATTAATGAGAAATGCG 2426  
QY 2253 CTGAGCGCAAGTACGGGAATTTAGGTTATAGAGGGATGCTTTATTCAAAGGGGTTA 2312  
Db 2427 ATGGACGGGAAGTACGGGAATTCGAGTTGTGAAGGAGATGTTCTGTTTAAAGATCGTTT 2486  
QY 2313 TCTACGCCCTACAGGTGCGAGAGAAATAGATACGGAAGAGTATCCAACTATCTGTATCA 2372  
Db 2487 GCTTGGTTTGACAGTGGCAGAGAGATTTGATACAGAAACATATCCAACTATCTGTATCA 2546  
QY 2373 AAAAGTAGAGGAGTGTATTTAAACCAATACACATACAGATATAAACTAAAAGTTTATAGG 2432  
Db 2547 ACAATAGATGAATCGCTTTTAAACCAATACATACAGATATAAACTAAAAGTTTATAGG 2606  
QY 2433 AAGCAGTCAAGGATTTGGAATTTTCAATTTGATGATGATGATGATGATGATGATGATGATG 2492  
Db 2607 AAGTAGTCAAGATTTAGAGATTAATTAATACGTCATCGGGCAATCAATCGTCAAAA 2666  
QY 2493 TGACCGGATGATTTGCTGCGAGATGATCTCTGTTTAACTCGGATGATGATGATGATGATGATG 2552  
Db 2667 TGACCGATTAATCTTGGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2726  
QY 2553 ATGACGCAACAAAGTATGTAATGCGGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2601  
Db 2727 CTGAGTGAACAAAGTATGTAAGCGGAATTTAGCACTCGAAGAAACATGGAAGAAATGG 2786  
QY 2602 -----TCTGGTGAAGCGCATGATCTCTATTTTAAATTCGACAAACAAATGGAAGAAATGG 2846  
Db 2787 AATATGCTTCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTGATTCCTG 2846  
QY 2655 CAATGAAATGCGAGATATGCTGTTGATTTAAAGATTTAGGATTTAGGATTTAGGATTTAGGAT 2714  
Db 2847 GATGAAATGCGAGATTTGATGCTGATTTAAATTCGACAAACAAATGGAAGAAATGG 2906  
QY 2715 ACTCGGAACTTGAATTTGTCGAGAGAGGACCTTTATCAGGAGAGCGATTTAGAACGCTT 2774  
Db 2907 ACTAGGAACTTGAATTTGTCGAGAGAGGACCTTTATCAGGAGAGCGATTTAGAACGCTT 2966  
QY 2775 GCAAGAGAGAAACAAAGTGAAGATTTCAATGACAGAGAGCTGTAAGAAACAGATAG 2834  
Db 2967 CCAACAAACAGAGAAACAAATGTCGAGAGAGGACCTTTATCAGGAGAGCGATTTAGAAC 3026  
QY 2835 AAGTATATGTCGAGAGAGGACCTTTATCAGGAGAGCGATTTAGAACGCTTATCAGGATCAG 2894  
Db 3027 -AACATATTTATGAGCAAGAGCGGATGATGCTTTATGATGATGATGATGATGATGATGATG 3086  
QY 2895 ACTGAATCCTGATGATGAGATTTACAGATCTTACTGCGGCCCAAGATCTGATACAGTCCAT 2954  
Db 3087 ACTTAAATCTGTTGATGAAATCTCAGATTTGTTGCGAGCCCAAACTTGTATACATCCAT 3146  
QY 2955 TCCTTACGTATATACGAATTTTCCCGAAGAAATACAGGATGAACTATACGAATTTTAC 3014  
Db 3147 TCCTTACGTATATATGATGCTTACCGGAAATCCCTGGAATGAATATACGATTTTAC 3206  
QY 3015 AGAATTAACAGATCAGTCCACAGCGTGGAGTTTGTATGATCAGGAAATGCCATACC 3074  
Db 3207 AGAGTTAAACAAATAGATCCCAACAGCATGGAATTTGTATGATCTTCAAAAGCGCTATACC 3266

QY 3075 AAATGGTGAATTTTGAATGGTTAAATTAATTTGGAATCAACGCTGCGGTAGAAATGACA 3134  
Db 3267 AAATGGATTTTGAATGGTTAAATTAATTTGGAATCAACATCAGATGTAATGTTGCA 3326  
QY 3135 ACAATCAATCATATCATCTGCTTGTGATTTCCAACTGGGATGAGCAATTTTCCCAACA 3194  
Db 3327 ACAATCAAGCATATCATCTGCTTGTGATTTCCAACTGGGATTTTCCAACTGTTCAACA 3386  
QY 3195 GTTATCAGTTTCAACGGAATCAAGATATGTTTACAGTTTACTGCGAGAAAGAGGGGT 3254  
Db 3387 ATTATCAGTTTCAACGGAATTTATGATTTGTTAGTTGTTGTTGTTGTTGTTGTTGTTG 3446  
QY 3255 AGGAATCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3314  
Db 3447 AGGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3506  
QY 3315 TGCAAGCGATTTATGATCAAAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 3364  
Db 3507 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3556

## RESULT 7

US-08-272-887-1  
; Sequence 1, Application US/08272887  
; Patent No. 5747450  
; GENERAL INFORMATION:  
; APPLICANT: Ohba, Michio  
; APPLICANT: Iwahana, Hidenori  
; APPLICANT: Sato, Reilchi  
; APPLICANT: Suzuki, No. 5747450kazu  
; APPLICANT: Ogiwara, Katsutoshi  
; APPLICANT: Sakanaka, Kazunobu  
; APPLICANT: Hori, Hidetaki  
; APPLICANT: Asano, Shouji  
; APPLICANT: Kawasugi, Tadaaki  
; TITLE OF INVENTION: No. 5747450el Microorganism and Insecticide  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: US  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/272,887  
; FILING DATE: 08-JUL-1994  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/915,203  
; FILING DATE: 23-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: M/K 301  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3797 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
; STRAIN: japonensis



INDIVIDUAL ISOLATE: Buibui

**FEATURE:**

NAME/KEY: CDS

LOCATION: 187..3636

US-08-272-887-1

Query Match 32.6%; Score 1180; DB 1; Length 3797;

Best Local Similarity 61.4%; Pred. No. 3.9e-248;

| Matches | Conservative | Mismatches | Indels | Gaps |
|---------|--------------|------------|--------|------|
| 2094    | 0            | 1230       | 86     | 9    |

[illegible]

QY 2013 TTTAGACGAGGAAAGAAAGCAATGCAATGCTTGTGTTTACGAATACAAAAGATGGCTTACG 2072  
Db 2187 CCTAGATGGCAAGAAAGCTGTGAATGGCTTGTGTACGAATGAAGAAAGATGCTTACA 2246  
QY 2073 ACCAGGCGTAACGGAATTAAGTGAATCAACGCGCAAACTTAGTGGATGCTTATCGGA 2132  
Db 2247 GACAAGTGAACGGAATTAACGATCAATCAACGCGCAAACTTAATAGATGCTTATCGGA 2306  
QY 2133 TGATTTGTATCAAAATGAAACAGATTTGATTTGATGCAATGAGAGGCAAAACGCT 2192  
Db 2307 TGATTTATACCAATGAAACAGATTTGATTTGATGCAATGAGAGGCAAAACGCT 2366  
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QY 2253 CTGACGCGCAAGTACGGAATTTGAGTTATAGAGGGGATGCTTTATCAAGGGCGTTA 2312  
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QY 2313 TCTACGCTACACGCTGCGAGAGAAATAGATACGGAACGATTCACCACTATCTGTATCA 2372  
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QY 2373 AAAAGTAGAGGAGGTGATTAATAACCATACACAGATATAGATTTGAGAGGTTTGTGCG 2432  
Db 2547 ACAATAGATGAATCGCTTTTAAACCATATACAGATATTAACCTAAAGGTTTATAGG 2606  
QY 2433 AAGCAGTCAGGATTTGGAATTTTCAACATTCGTCATCAACAGCAACCAATTTGAAAAA 2492  
Db 2607 AAGTAGTCAGATTTAGAGATTAATTAATATAGTCATCGGCAAAATCAAAATCGTCAAAA 2666  
QY 2493 TGTAACGCGATGATTTGCTGCGAGATGATCTCTGTTAACTCGGATGTTAGTATCAATCG 2552  
Db 2667 TGTAACAGATATCTTGTGCGAGATGACGCTGTCATTTCTGTTGTTGAGTGCATCG 2726  
QY 2553 ATGACGCGAAACAAAGTATGGAATAGCGGTTTGAAGTAGAAGTAAACCGT----- 2601  
Db 2727 CTGAGTGAACCAACAGTATGAGACGGAATTTAGCACTCGAATAATGAGAAATGG 2786  
QY 2602 -----TCTGTTAGCGGATGAGTCTCTATTCCTATTTGATACAGTGAATCGATTA 2654  
Db 2787 AAATATGCTTCTGATTTCCCATGCAATTTCTTCCATATTTGATACGGGTGAATAGATTT 2846  
QY 2655 CAATGAAATGACGAAATATCGGTTGGAATTAAGATTAAGCAACCCAGAGGGATGCAAC 2714  
Db 2847 GAATGAAATACAGAAATTTGATGCTGATTTAAATTCGCAACAAATGGAACGCAAC 2906  
QY 2715 ACTCGGAACTAGAAATTTGTTGCGAAGGGGACCTTTATCAGGAGACGATTAGAACGCTT 2774  
Db 2907 ACTAGGAAATCTTGAATTTGTAGAAGAGGGGCCATTTGTACGGGAAACATTAGAATGGC 2966  
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Db 2967 CCAACAAAGAGAACCAAGTGGCAAGCAAAATGCGCAAGAAACGTCAGCATCAGAAA 3026  
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Db 3027 AACATATATGCAAGCAAGCAATGATGCTTTATTCGAGATTAACAGACCAAAA 3086  
QY 2895 ACTGAATCCTGATGATGAGATTAAGATCTTTACTGCGGCCCAAGATCTGATACAGTCCAT 2954  
Db 3087 ACTTAAATCTGCTGATGAAATGTCAGATTTGTGCGACGCCCAAAACCTTTGATAGTCCAT 3146  
QY 2955 TCCTTAGCTATATACGAATTTCCCGAAATACCGAGGATGAACTATAGCAAGTTTAC 3014  
Db 3147 TCCTTAGCTATATAGTATGCTGTTTACCGGAAATCCCTGGAATGAATATACAGGTTTAC 3206  
QY 3015 AGAATTAACAGATCGATCCCAACAGGCTGAGTTTGTATGATCAGCGAAATGCCATACC 3074  
Db 3207 AGAGTTAACAAATAGATCCCAACAGGATGGAATTTGTATGATCTTCAAAACGCTATACC 3266  
QY 3075 AAATGGTGAATTTTTCGAATGGTTTAAAGTAAATGGAATGCAACGCTGCGGTAGAAGTACA 3134

Db 3267 AAATGGAGATTTTCGAATGGAATTAAGTAAATGGAATGCAACATCAGATGTAATGTGCA 3326  
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Db 3327 ACAATAGCGATACATCTGCTTGTGATTCGAACTGGGATTTCTCAAGTGTCAACA 3386  
QY 3195 GTTTACAGTTCCAAACGCAATCAAGATATGTTTACGAGTTACTGCGAGAAAGAGGGGT 3254  
Db 3387 ATTTACAGTTCCAAACGCAATTAAGATATGTTTACGTTTACGTTTACGAGAAAGAGGGAGT 3446  
QY 3255 AGGAAATGGAATATTAAGTATTCCTGATGTTGGAATCAAAACAGAAACGCTTTACTTTTAG 3314  
Db 3447 AGGAGCGGATATGATGATCATCCGTTGATGTTGCAATCAGACAGAAACACTCACATTTAA 3506  
QY 3315 TGCAGCGATTAATGATCAAAATGGAATGTAATACGCAAGTATGCTCCCAATA 3364  
Db 3507 TATATGATGATGATACAGGTGTTTATCTACTGATCAAACTAGCTATA 3556

## RESULT 8

US-08-789-449-1  
; Sequence 1, Application US/08789449  
; Patent No. 5824878  
; GENERAL INFORMATION:  
; APPLICANT: Ohba, Michio  
; APPLICANT: Iwahana, Hidenori  
; APPLICANT: Sato, Reiichi  
; APPLICANT: Suzuki, No. 5824878ukazu  
; APPLICANT: Ogiwara, Katsutoshi  
; APPLICANT: Sakanaka, Kazunobu  
; APPLICANT: Hori, Hidetaki  
; APPLICANT: Asano, Shouji  
; APPLICANT: Kawasaki, Tadaaki  
; TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: US  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/789,449  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,887  
; FILING DATE: 08-JUL-1994  
; APPLICATION NUMBER: US 07/915,203  
; FILING DATE: 23-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: M/K 301  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3797 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis

STRAIN: japonensis  
INDIVIDUAL ISOLATE: Buibui  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 187..3636  
US-08-789-449-1

Query Match 32.6%; Score 1180; DB 1; Length 3797;  
Best Local Similarity 61.4%; Pred. No 3 9e-248; Indels 86; Gaps 9;  
Matches 2094; Conservative 0; Mismatches 1230;

QY 1 ATGAGTCCAAATATCAAAATGAATATGAATATAGATCGACACTTCTACTTCTGTA 60  
DB 187 ATGAGTCCAAATATCAAAATGAATATGAATATAGATCGACACTTCTACTTCTGTA 246  
QY 61 TCCAAATGATCTCAACGATACCTTTTCCGAATGAGCCCAAAATGCGCTCACAATATG 120  
DB 247 TCCGATAATCTATAGATATCTTTAGCAACGATCAAAACGACATTAACAACATG 306  
QY 121 GATTATAAAGATTATTAATAATGCTGCGGAAATGCTAGTAGTAATACCTGGTTCACT 180  
DB 307 AATTATAAAGATTATCTGAATAATGACCGAATCAAAATGCTGAATGCTCGAATCCC 366  
QY 181 GAAGTACTCTTTAGCGGACAGATGCGAGCTAAGCCCGCAATGATATAGTAGGTAAATTA 240  
DB 367 GGCACATTATATAGTGGCAGGATGCGTTGGAACCTGGAATGATATGTTAGTACTATA 426  
QY 241 CTATCAGTTTATAGGGTCCCATTTGTTGGCCGATAGTAGTCTTTATATCTCACTTATT 300  
DB 427 ATAAAGTGGTTAGGATTCAGAGTCTGTTGGGAACTCTCTCAATTTCTGGGTTCATTAAT 486  
QY 301 GATTATCTGGCTTCAGGGGAAAGAGTCAATGGGAATTTTATGGAAACAGTAGAA 360  
DB 487 GGCTTATTTGGCCGCTCAAAATAATGAATAATGTAATGGCAATAATTTATGAATCGAGTGGAA 546  
QY 361 GAATCTAATTAATCAAAATAATAGCAGAAATATGCAAGGAATTAAGAGCTTTCCGAATTAAGAA 420  
DB 547 GAGCTAATTCGATCAAAATAATATAGATTCTGTAAGATCAAGAGCCATTCGAGATTTAGCT 606  
QY 421 GGATTAGGTAAATTAATACCAATATATCTAATCTGCTGCTGAGAAATGGGAAGAAATCCA 480  
DB 607 AATTCTAGAATAGCTGTAGAGTACTATCAAAATGCATCTGAAGACTGGAGAAAACCCCA 666  
QY 481 AATGGTTCAAGAGCTTACAGAGTGTGCAAAATCGATTTGAAATCCTGGATAGTTTATT 540  
DB 667 CACAGTACAGAGCGCAGCACTTGTAAAGAAAGATTTGGAATGCAAGAGCAATTTTA 726  
QY 541 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTCTCTTACTGTATAT 600  
DB 727 CGTACTAACATGGGTTCATTTCTCAACGAAATATAGACTCCACTTTACCCACATAT 786  
QY 601 GCAATGGCAGCCAACTTCTACTTTACTGTTATTAAGAGCGGTCAATTTTGGAGAGAA 660  
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QY 661 TGGGATGGTCAACACTACTATTAATAACTATTTATGATCTGCAATGAACTTACTTGCA 720  
DB 847 TGGGGATATCCTCAAAATGATATTTGACCTATTTTATAAAGAACAAAGTATCTTTATACGGCT 906  
QY 721 GAATATTTCTGATCACTGTATAAGTGGTATGAAACTGGTTTATGCAAAATTAAGAGGCAAG 780  
DB 907 AGATATTTCCGATCATTTGGTCCAAATGGTACATGCTGGTTTAAATTAATTAAGAGGAACG 966  
QY 781 AGCGCTAAACAAATGGGTGATATAACCAATTCGCTAGAGAAATGACACTGGCGGTTTAA 840  
DB 967 GGTCTTAAGCAATGGGTGATTAATAATCGTTTCCGAAGAGAAATGAATGTGATGTTATG 1026  
QY 841 GATGTTGTTGCAATTTTCCCAAAATTTGACACGACGCTACCCCAATGGAAACGGAAGCA 900  
DB 1027 GATCTAGTTGCAATTTTCCCAAACTACGATGCGGTATATATCCACTGGAAACCAATGCA 1086  
QY 901 CAACATAACGGGAGATATATACAGATCCACTGGCGCGGTAAACGCTGCTTCAATTTGGT 960

DB 1087 GAACTTACAAGAGAAAATTTTTCAGATCCTGTGTGAAGT-----TACGTAACTGA 1137  
QY 961 TCCTGCTATGACAAAGCACCTTCTTTCGGAGTGATAGAAATCATCCGTTATTTCGACACACC 1020  
DB 1138 CAATCGAGTACCTTATATCTTGGTACGATATGATTCAGAGCTCTTCCCTCAITTTCA 1197  
QY 1021 CATGTATTTGATTAATTAACGGGACTCAAGTGATATACAAATCAAGAAAGCAATTTCTCC 1080  
DB 1198 ACGCTCGAGAACCTACTTAGAAAACCTGATTTCTTTACTTGTCTGCAGAAATTAAGATG 1257  
QY 1081 GCTCGCTATATAAGACATTTGGCTGGTCAATCAATAAGCTACCATCGTCTAGTAGGGT 1140  
DB 1258 TATACAAGTTTATAGCAAAACGGTACGATGAATTAATTAATTAATTTGGGGAGGACAAAG 1317  
QY 1141 AGTAATCTTCAAAATGATGGAACCTAATCAAAATCTACACAGCACTAGTACCTTTGAT 1200  
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DB 1375 GGTGCTGAGGATATTTCTCTGGGTCAAAATGATATTTTACAGAGTTGTATGAGACTTAT 1434  
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DB 1435 ATAGGAAGGTACACGAATAGTCTGCTAGGATTAATCCAGTTTACTTTTT----- 1483  
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QY 1381 AGTACAAGAGATTCCGAATTTAGAAATTTACCTCCAGAAACTTTCAGATCAACCAATTTATGAG 1440  
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QY 1441 TCATATAGCCATAGATTTATGTCATATCAAGATATTCGCGCAGCGGTAACTACCGGA 1500  
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DB 1657 GTAGTTCTTATATTTGGTTGGACGATATAGTGTCCAGTGCAGATTAATCTTTATTTAGCA 1716  
QY 1561 GATPAAATCACTCAAAATTCGCGCGTTAA---ATGTTGGGATAATTTTACCGTTTGTTC 1617  
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QY 1713 AGCATTTAGAAAAGAGCGGAAATATCTGTAGACTGAGATATGCTACTGATCGAGATAT 1772  
DB 1897 AGAATCAGATATGCTCTGATAGAGCGGTAAATTTACGATATCTTCCAGATCTCCAGAG 1956  
QY 1773 TGTATTTGCATGTAAACGATGCTCAGATTCAGATGCCAAAACAAATGAACCCAGGTGAGGA 1832  
DB 1957 AATCTGCAACCTTATTCAGCTTCTATTTGCTTATA-CAAAATCTATGCTACAAATGCTTC 2015  
QY 1833 TCTGACATCTAAACCTTTTAAAGTTGCAGATGCTATCACAACATTAATTAATTTAGCAACGA 1892  
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QY 1893 TAGTTGCTAGCATTCGAAACATAAATTTAGGTGAAGCCCTTAATTTCAACATTTATCTGGTAT 1952  
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QY 1953 AGTTTACGTTGACCGAATCGAATTTCAATCCAGTAGATGACATATGAACGGAACGAAGA 2012  
DB 2127 CTTTATATTGATGAAATTTGAAATTTTATTCAGTTAATACGTTATTTGAACGAGAGAAGA 2186

QY 2013 TTTAGAGCAGCGAAGAAAGCAGTGAATGCTTTGTTTACGAATACAAAGAGTGGCTTACG 2072  
DB 2187 CCTAGATGTGCGCAAGAAAGCTGTGANTGCTTTGTTACGATGAAGAAAGAGTCCCTTACA 2246  
QY 2073 ACAGGCGTAAACGGATTTAGAGTGAATCAAGGCGCAAACTTAGTGAATGCCCTATCGGA 2132  
DB 2247 GACAGGTGAACGGATTTATCAAGTCAATCAAGGCGCAAACTTAATAGAAATGCCCTATCCGA 2306  
QY 2133 TGATTTGTATCCAAATGAAAGAAAGATTTGTTATTTGATGCGAGTGAAGAGCGCAAGCGCT 2192  
DB 2307 TGAGTTATACCCAAATGAAAGAAAGATTTGTTATGCGAGTGAAGAGCGCAAGCGCT 2366  
QY 2193 CAGTGAAGCGATTAATTTGCTTCAAGATCCAGATTTTCCAGAGATTAATGGAGAAATGG 2252  
DB 2367 TGTTCAAGGACGTAACCTTCTCAAGATACAGGCTTTAATAGGATTAATGGAGAAACGG 2426  
QY 2253 CTGAGCGGCAAGTACGGGAATGAGGTTATAGAGGGGATGCTTTATTTCAAGGGCGTTA 2312  
DB 2427 ATGACGGGGAAGTACGGGAATCGAGGTTGTGAGGAGATGTTCTGTTTAAAGATCGTTC 2486  
QY 2313 TCTACCGCTTACAGGTGCGAGAGAAATAGATACGGAACGATCCCAAGTATCTGTATCA 2372  
DB 2487 GCTTCTGTTTGAAGTTCGAGAGAGATTTGATACAGAAACATATCCCAAGTATCTGTATCA 2546  
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DB 2667 TGTACAGAGATAATCTCTTGGCAGATGATGACCGCTGTCATTTCTTGTGTGAGTTCGATCG 2726  
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DB 2787 AAATATGCTCTCTGATCCCATGCAATTTCTTCCATATTGATAGGGTCAATAGATTT 2846  
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QY 2715 ACTCGGAAACCTAGAAATTTGTCGAAGAGGAGCCTTTATCAGGAGAGCGATTAGAACGCTT 2774  
DB 2907 ACTAGGAATCTTGATTTGTAGAGGCGGCCATTTGTCAGGGGAACATTAGATGGGC 2966  
QY 2775 GCAAGAGAGAAACACAGTGGAGAGATTTCAATGCAAGAGAGCGTGAAGAAACAGATAG 2834  
DB 2967 CCAACCAAGAAACAAATGCGAGAGCAAAATTTGCGCAAGAAACGTCAGCATCAGAAAA 3026  
QY 2835 AAGGTATAGCATCGAACAAGCGGTAGATCGTTTATATGCGGATTTATCAGGATCAGCA 2894  
DB 3027 ACATATTTATGCGAAGCAAGCAAGCCATTTGATCGTTTATTCGAGATTTATCAGACCAAAA 3086  
QY 2895 ACTGAATCTGATGTAGAGATTTACAGATCTTACTGCGGCGCAAGATCTGTATACAGTCCAT 2954  
DB 3087 ACTTAATTTGTTGTTAGAAATGTGATTTGTTGGGAGCGCAAACTTGTATAGTCCAT 3146  
QY 2955 TCTTACGTATATACGAAATTTTCCAGAAATACCAAGGATGAATATATACGAGTTTAC 3014  
DB 3147 TCTTACGTATATATGATCGTTTACCGGAAATCCCTGGATGAACTATACGAGTTTAC 3206  
QY 3015 AGAATTAACAGATCGACTCCAAAGCGGTGAGTTTGTATGATCAGCGAAATGCCATACC 3074  
DB 3207 AGAGTTTAAACAAATAGACTCCAAAGCATGGAATTTGTATGATCTTCAAAACGCTATACC 3266

QY 3075 AAATGGTGAATTTTCGAAATGGGTTAAGTAAATGGAATGCAACGCCCTGGCTAGAGTACA 3134  
DB 3267 AAATGGAGATTTTCGAAATGGATTAAGTAAATGGAATGCAACATCAGATGTAATGTTGCA 3326  
QY 3135 ACAATCAATCATACATCTGTCTTGTGATTTCCAACTGGGATGAGCAAGTTTTCGCAACA 3194  
DB 3327 ACAATCAAGCGATACATCTGTCTTGTCAATCCAACTGGAATTTCTCAAGTGTCAACA 3386  
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DB 3387 ATTACAGTTCACCGAATTTATAGATATGTTTACGTCACACAGCGAGAAAGAGGAGT 3446  
QY 3255 AGGAATGATATGTAAGTATCGTATCGTGAATCGGAAATCAACAGAAACGCTTACTTTTAG 3314  
DB 3447 AGGAGCGGATGATGATCATCGTATCGTGAATGTCGAATCAGACAGAAACACTCATTTAA 3506  
QY 3315 TCGAAGGATTTAGATACAAATGGAATGATTAATACGCAAGTGTCCAATA 3364  
DB 3507 TATATGATGATGATACAGGTTGTTTATCTACTGATCAAACTAGCTATA 3556

## RESULT 9

US-08-532-547-4  
; Sequence 4, Application US/08532547  
; Patent No. 5861543  
; GENERAL INFORMATION:  
; APPLICANT: LAMBERT, BART  
; APPLICANT: JANSSENS, STEFAN  
; APPLICANT: VAN AUDENHOVE, KATHRIEN  
; APPLICANT: PEPEROEN, MARINX  
; APPLICANT: VAN RIE, JEROEN  
; APPLICANT: VAN RARSEN, ROEL  
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR  
; TITLE OF INVENTION: INSECTICIDAL PROTEINS.  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/532,547  
; FILING DATE: 06-DEC-1996  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SVENSSON, LEONARD R.  
; REGISTRATION NUMBER: 30,330  
; REFERENCE/DOCKET NUMBER: 2121-109P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4344 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 668..4141  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1..4344  
; OTHER INFORMATION: /note= "encompasses entire sequence"

OTHER INFORMATION: of SEQ ID NO (SID) 2: from nt position 474 to 2034  
OTHER INFORMATION: in SID 4"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..4344  
OTHER INFORMATION: /note= "also encompasses part of  
OTHER INFORMATION: the sequence of SID 3: from nt position 2994 to  
OTHER INFORMATION: 4344 in SID 4"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..4344  
OTHER INFORMATION: /note= "SID 3 shows additional  
OTHER INFORMATION: nucleotides, located 3' from the sequence shown in  
OTHER INFORMATION: SID 4 (1352-1554 in SID 4)"  
US-08-532-547-4

Query Match 24.4%; Score 883.4; DB 2; Length 4344;  
Best Local Similarity 56.6%; Pred. No. 1.5e-183;  
Matches 1936; Conservative 0; Mismatches 1386; Indels 101; Gaps 12;  
QY 1 ATGAGTCCAAATATCAAAATGAATGAAATATAGATGCGACACCTTCTACTCTGTA 60  
DB 668 ATGAATCGAAATATCAAAATGAATGAAATATAGATGCGACACCTTCTACTCTGTA 727  
QY 61 TCCAAATGATTTCAACAGATACCTTTTTCGGAATGAGCCAAACAAATGCGCTACAAATATG 120  
DB 728 TCAGATGACGATGAGATATCTTTTGGCAATGAGCCAAATGCGCTTACAAATATG 787  
QY 121 GATTATAAAGATATTTAAATATGTCGCGGAAATGCTAGTGAATACCTTGGTTCACCT 180  
DB 788 AACTATAAAGATATTTCAAAATGACAGATGAGGACTACACTGATTTCTATATAAATCCT 847  
QY 181 GAAGTACTTTAGCGGACAGATGCGCTAGGCGCAATGATATAGTATAGTAAATTA 240  
DB 848 AGTTATCTATTTAGTGGTAGAGTACAGTTCAGACTGCGCTTACCTGTTGGGAGAATA 907  
QY 241 CTATCAGGTTTATGAGGTCCTTATTTTGGCGGATGATGAGTCTTTTATCTCAACTTAT 300  
DB 908 CTCGGGCTTTAGTGTTCGGTTCTGCGACAAATGATGAGTCTTTTATCAATTCCTTTTA 967  
QY 301 GATATTTCTGCGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360  
DB 968 AATACACTGTGCGGCTTAATGATACAGCTATATGGGAAGCTTTTCATCGCAGGTGGAG 1027  
QY 361 GAATCTAATTAACAAATAGCAGAAATATGCAAGGATTAAGCGCTTTCGGAATTAGAA 420  
DB 1028 GAATCTGCAATCAACAAATTAACAGAAATTTGCAAGAAATCGGCACTTGCAGATTTGCA 1087  
QY 421 GGATTAGTAAATTAACCAATTTATCTAATCTGCTGCTTGAAGATGGAAGAAATCCA 480  
DB 1088 GGATTAGGAGACTCTTTTAAATGATATCAACGTTCCCTTCAAAATTTGGTGGCTGATCGA 1147  
QY 481 AATGGTTCAAGAGCTTACGAGATGTGCGAAATCGATTGGAATCCTGGATGTTTATTT 540  
DB 1148 AATGATACACGAAATTTAAGTGTGCTGCTCAATTTATAGCTTTAGACCTTGATTTT 1207  
QY 541 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATCTCTACTGTATAT 600  
DB 1208 GTTAATGCTATTCCTATTTGCGATTAATGGACAGCAGGTTTCCATTAATCTGTCAATAT 1267  
QY 601 GCAATGGCAGCAACCTTCAATTTACTGTTTAAAGGAGCGCTCAATTTTGGAGAGAA 660  
DB 1268 GCACAGCTGTGAATTTACATTTGTTATTTTAAAGATGATCTCTTTTGGAGAGAA 1327  
QY 661 TGGGGATGGTCAACAACTACTATTAAATCACTATTATGATCGTCAATGAACTTACTGCA 720  
DB 1328 TGGGGATTCACACAGGGGGAATTTCCACATATTATGACCGTCAATTTGGAACCTAACCGCT 1387  
QY 721 GAATATTCGATCACTGATGTAAGTGGTATGAACCTGGTTAGCAAAATTAAGAGGACG 780  
DB 1388 AAGTACACATAATTAAGTGAACCTGGTATTAATACAGGTTTATAGATCGTTTAAAGAGAA 1447  
QY 781 AGCGCTAAACAAATGGGTTGACTATTAACCAATTTCCGTAGAGAAATGACACTGCGGCTTTTA 840

DB 1448 AATACTGAAAGTTGGTTAAGATATCATCAATTCGTAGAGAAATGACTTTAGTGGTATTA 1507  
QY 841 GATGTTGTTGCAATTTATCCCAATTTATGACACAGCAGTACCAATGGAAACGAAGCA 900  
DB 1508 GATGTTGTTGCGCTTTATTTCCATATTTATGATGATGATGATGATGATGATGATGATG 1567  
QY 901 CAACAAAGGGAAGTATATACAGATCCACTGGCGCGGTAAACGTTCTTCAATTTG-- 958  
DB 1568 CAGCTTACAGTGAAGTATATACAGATCCGATTTGTTATTAATCCACAGCTAATGTTGGA 1627  
QY 959 -----GTTCTCTGATGACAAAGCACCTTTCTTTTCGAGGTGATAGATCAATCCGTT 1008  
DB 1628 CTTTTCGCGAGTTGGGGTACTTAATCCCTATAATATCTTTTCTGAGCTCGAAATGCTTTC 1687  
QY 1009 ATTGACACACCCATGATTTTGAATATATAACGGGACTCAGGTGATATACAAATCAAGA 1068  
DB 1688 ATTGCGCCACACATCTTTTGTAGCTGAATAGCTTAAATCAGCAGTAATCGATTT 1747  
QY 1069 AGCATTTTCTCCGCTCGCTATATAAGACATTTGGGCTGTCATCAAAATAGCTACCATCGT 1128  
DB 1748 CCAGTTTCACTAAT-----TTTATGATTTTGGTTCAGACATAGCTTACGCCGCTAGTTAT 1804  
QY 1129 GTCAGTAGGGGTAGTAACTCTTCAACAAATGATGGAACCTAATCAAAATCTACACAGCACT 1188  
DB 1805 CTGAACGATTCAGCAGTACAAAGAGATGTTATGG-----CCTAATTAACACCAAGA 1858  
QY 1189 AGTACCTTTGATTTTTCGAATATGATATTTCAAGACTCTATCAAAAGGATGAG-TACT 1247  
DB 1859 GCACAAATTAATCCCGGAGTTTGTAGTGAACAAACCCGATAGAGTCAACGGCAGTAGATTTT 1918  
QY 1248 CTTTGAATTTGTTTACCCTGTTATACGTATATATTTTGGATGTCAGAGTCCAGAGTTCGAGTT 1307  
DB 1919 CGTTCTCGATTTGATGATATATATGCGGTGAATAGACTTCTTTTTCAGGAGGCTTG 1978  
QY 1308 TTTTCATGTTAAACCAATTTGAATATATACAGAAAGACCTTTAAAGTATATATCCAGTTTCCAA 1367  
DB 1979 TTTAATGCT-----ACGACTTCTCTCTAATGGAGGATGAG 2016  
QY 1368 AGATATTTATAGCGAGTCAAGAGATTCGGAATTTAGAAATTCCTCCAGAACTTCAGATCA 1427  
DB 2017 AGATCTCTATGATACAAATGATGAATTTACCACAGATGAAAGTACCAGAGTTTCAACCCA 2076  
QY 1428 ACCAAATTTAGTGCATATAGCCATAGATTTATGTCATATCACAGTATTTCCCGGACGGG 1487  
DB 2077 TAGACTATCTAGTTTACCTTTTTCAGCTT-----TCAAACCTAATCAGGCTGATCTAT 2130  
QY 1488 TAACACTACCGGATTTAGTACTCTGTTATTTTCTTGGACACATCGAAGTGCAGATTTAAACAA 1547  
DB 2131 AGCTAATGCGAGGAGTGTACTCTTATGTTTGGACCCGCTCGTGAATGAGACCTTAATA 2190  
QY 1548 TACAATATATTCAGATAAATCACTCAAAATTCGCGCGCTTAAATTTTGGGATATTTTACC 1607  
DB 2191 TACGATTTACCCCAATTAAGATTTACAAATTTACCAATTTGTAAGGCACTCTGCACTGTTTC 2250  
QY 1608 GTTTGTTCCAGTGTGTAAGGACGAGCAGATACAGAGGGGATTTATACAGTATATATAG 1667  
DB 2251 GGGTACTACGGTCTTAAAGGTTCCAGGATTTACAGGAGGGGTATATCTCC---GAAGAAC 2307  
QY 1668 AAGTACTGTTCTGTAGGAACCTTTATTTCTAGCTCGATATGGCTAGCATTTAGAAAAAGC 1727  
DB 2308 AACTAATGGCACATTTGGAACGTTAAGATTAACGTTAATTTCCATTACACCAACATA 2367  
QY 1728 AGGGAATATCGTGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1787  
DB 2368 TCGCTTAAGAGTTCTGTTTTCCTCAACAGGAAATTTTCAAGTATAGGGTACTCTCCGTGGAG 2427  
QY 1788 CGATGC-----TCAGATTCAGATGCGCAAAACAAATGAAACCCAGGTGAGGATCTGACATC 1841  
DB 2428 GGTTCCTATCGGTGATGTTAGATTTAGGAGCAATGAGAGGAGGAGGAGGAGGAGGAGGAGG 2487  
QY 1842 TAAACCTTTTAAAGTTGTCAGATGCTATCAACA-----TTAAATTTAGCAACAGATAG 1895

|    |      |  |      |
|----|------|--|------|
| Db | 2488 | CGAATCCCTTTTTCACAAGAGAGTTTACTACTACTGCTCGTTTCAATCCGCCTTTTACATT    | 2544 |
| Qy | 1896 | TTCCGCTAGCATNTGAACATAAATTTAGTGAAGACCCCTAAATTCAAATTTATCTCGGTATAGT | 1955 |
| Db | 2548 | TACAACAGCTCAAGAGATTCTAACAGCTGAATGCAGAAAGGTGTAGCACCGTGGTGAATA     | 2607 |
| Qy | 1956 | TTACGTTGACCGAATCGAATTTCAATCCAGTAGTAGTAGACATATGAAGCGGAAACAGATTTT  | 2015 |
| Db | 2608 | TTATATAGTAGAATTTGAATTTGTCCTCTGTGAATCCGGCAAGAGAGCGGAGAGAGATTT     | 2667 |
| Qy | 2016 | AGAACGACGGAAGAAAGCAGTGAATGCCCTTTGTTTACGAATACAAAGAGTGCCTTACGACC   | 2075 |
| Db | 2668 | AGAACGCGCGAAGAAAGCGTGGCGAGCTTTGTTACACGTACAGAGGACGATTTACAGGT      | 2727 |
| Qy | 2076 | AGGCGTTAACCGATTTATGAAGTGAATCAAGCGGCAAACTTTAGTGGAAATCCCTATCGGATGA | 2135 |
| Db | 2728 | AAATGTGACAGATTATCAAGTGCACCAAGCGGCMAATTTAGTGTCAATGTCCTTATCCGATGA  | 2787 |
| Qy | 2136 | TTTGTATCCAAATTCMAAAACGATGTGTTATTTGATGCAGTGCAGAGAGCGCAAAACGCTCAG  | 2195 |
| Db | 2788 | ACAAATATGGGCATGACAAAAAGATGTTATTTGAAGCGGTAAAGAGCGCAAAACGCTCAG     | 2847 |
| Qy | 2196 | TGAGGCACGTAAATTTGCTTCAAGATCCAGATTTTCCAAGAGATAAAT-----CGAGAAA     | 2249 |
| Db | 2848 | CCGCGAAGCGCACTTACTTCAAGATCCAGATTTTAAATCAATCAATAGTACAGAAAGAA      | 2907 |
| Qy | 2250 | TGCGTGAACGCGCAAGTACGCGAATTCAGGTTATAGAAGGGATGCTTTATTTCAAAGCGCG    | 2309 |
| Db | 2908 | TGGCTGGAAGCGCAAGTAAACGGTGTACTATTAGCGAGGGCGGTCCATTTCTTTAAAGTCTG   | 2967 |
| Qy | 2310 | TTATCTACGCGCTACAGGTGCGAGAGAAATAGATACGGAACGTTATCCAAAGTATCTGTA     | 2369 |
| Db | 2968 | TGCATCTTCAGTTAGTAGAAGCGCAAG-----GAAAAATATCCAAATACATATTTA         | 3015 |
| Qy | 2370 | TCAAAAAGTAGAGAGAGGTGTATTAAAAACATACACAGATATAGTTAGAGAGGGTTGT       | 2429 |
| Db | 3016 | TCMAAAAGTAGATGCATCGGTGTAAAGCCTTATACCGCTATAGACTAGATGGAATTTGT      | 3075 |
| Qy | 2430 | CGGAAGCAGTCAAGGATTTGAAATTTTCAAAATTCGTATCAACAGAACCGAAATGTAAA      | 2489 |
| Db | 3076 | GAAGAGTAGTCAAGATTTAGAAATTCATCTCATCCACCATCAATAAGTCCATCTTGTAAA     | 3135 |
| Qy | 2490 | AAATGTACCGGATGANTTTGCTGCAGATGTATCTCTGTGTTAACTCGGATGGTAGTATCAA    | 2549 |
| Db | 3136 | AAATGTACCAAGATAATTTAGTATCTCATCTTACTCAGATGGTCTTTCAGCGGNAACAA      | 3195 |
| Qy | 2550 | TCCATGCGAGCAACAAAGATGTGTGAATAGCCGTTTGAAGTAGAAGTAGAAGAACCGT-----  | 2601 |
| Db | 3196 | CCGTTGTGATGAACAGCATCAGGTAGATATGAGCTAGATGCGGAGCATCATCAATGGA       | 3255 |
| Qy | 2602 | -----TCTGGTGAAGCGCATCAGATTCTTATTCCTATTGTATACAGGTGAATTCGA         | 2651 |
| Db | 3256 | TTGCTGTGAAGCGGCTCAAAACATGAGTTTCTTCTTATTTAATACAGGGGATCTAAA        | 3315 |
| Qy | 2652 | TTCAATGAAAAATGCAAGGAATATGGGTTCCGATTTAAGATTTACGGACCCAGAGGATATGC   | 2711 |
| Db | 3316 | TGCAAGTGTAGATCAGGGCATTTGGGTTGCTATTTAAAAGTTTCGAAACACAGATGGTATGC   | 3375 |
| Qy | 2712 | AACACTCGGAAAACCTAGAATTGCTCGAAGAGGACCTTTATTCAGGAGACGATTTAGAACG    | 2771 |
| Db | 3376 | GACGTTAGGAAATCTTTGAATTTGTTAGAGGTTGGGGCATTTATCGGGTGAATCTCTAGAACG  | 3435 |
| Qy | 2772 | CTTTCMAAGAGAGAAACAAACAGTGAAGATTCMAATGACAGAGAGCTGGAAGAAACAGA      | 2831 |
| Db | 3436 | GGAAACAAAGAGATANTCGGAAATGGAAATTCGAGCTAGGAGAGAAACGTCGAGAAATAGA    | 3495 |
| Qy | 2832 | TAGAAGGTATATGGCATTCGAAAACAGCGGTAGATCGTTTATATGCGGATTTATCAGGATCA   | 2891 |
| Db | 3496 | TCGTGTGTATTTTAGTCTCGGAAAACAGCAATTAATCATCTGTTTGTAGACTATCAAGATCA   | 3555 |
| Qy | 2892 | GCAACTGAATCTCGATGTGAGATTAAGATCTTATCTGCGGCCCCAAGATCTGATACAGTC     | 2951 |
| Db | 3556 | ACAAATTAATTCAGAAATTTGGGCTAGCAGAAATTAATGAAGCTTCAAAATCTTGTAGAGTC   | 3615 |

|    |      |   |      |
|----|------|---|------|
| Qy | 2952 | CATTCCTTAGTATATAACGAAATGTTCCCGAANAATACAGGGATGAACATATACGAAGTT      | 3011 |
| Db | 3616 | AAITTCGGGTGATATATAGTGATACACTATTTACAGATTCTCGGATTAACACGAAATTTA      | 3675 |
| Qy | 3012 | TACAGAAATTAACAGATCGACTCCACAACGCGTGGAGTTTGATGATCAGCGGAATGCCAT      | 3071 |
| Db | 3676 | CACAGAGTTATCCGATCGCTTACACAGAGATCGTATCTGTATAGTCTAGAAATCGGT         | 3735 |
| Qy | 3072 | ACCAATATGSGATATTTTCGAAATGGGTTAAGTAATTTGGAATCAACCGCTGGCGTAGAAGT    | 3131 |
| Db | 3736 | GCAGAAATGGAGACTTTTAAACAGTGGTCTAGATAGTTTGGAAATACAACTATGGATGCATCGGT | 3795 |
| Qy | 3132 | ACACAAATCAATCATACATCTGCTCTTGATTTCCAACTGGCGATGAGCAAGTTTCGCA        | 3191 |
| Db | 3796 | TCAGCAAGATGGCAATATGCAATCTCTTAGTCTCTTCGCAATGGGATGCAACAAGTTTCCCA    | 3855 |
| Qy | 3192 | ACAGTTTACAGTTTCAACCGAATCAAGATATGTGTTACGAGTTACTGCGAGAAAAGAAGG      | 3251 |
| Db | 3856 | ACAATTCAGAGTAAATCCGAATTTGAATGTCTTAGTGTGACAGCAAGAAAATGAGG          | 3915 |
| Qy | 3252 | GGTAGAAATGGATATGTAAGTATCCGTGATGGTGGAAATCAACAGAAACGCTTACTTT        | 3311 |
| Db | 3916 | AGCGGAGATGGATACGTCACAATCCGAGATGGCGCTCATCACCAAGAAACTCTTTACATT      | 3975 |
| Qy | 3312 | TAGTCAGAGCGATTATGATACAAATGGAAATGTATATACGCAAGTGTCCAAATACAAATGG     | 3371 |
| Db | 3976 | TAATGCAATGTGACTACGATGTAATGGTACGTTATGTCATGCAATTCGTATATACAGACAG     | 4035 |
| Qy | 3372 | ATA 3374  |      |
| Db | 4036 | AGA 4038  |      |

RESULT 10  
 US-08-379-656B-4  
 ; Sequence 4, Application US/08379656B  
 ; Patent No. 5885571  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lambert Bart  
 ; APPLICANT: Jansens, Stefan  
 ; APPLICANT: Van Audenhove, Katrien  
 ; APPLICANT: Peferoen, Marxix  
 ; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND  
 ; TITLE OF INVENTION: THEIR INSECTICIDAL PROTEINS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSES: BIRCH, STEWART, KOLASCH & BIRCH  
 ; STREET: 8110 Gatehouse Road, Suite 500 East  
 ; CITY: Falls Church  
 ; STATE: Virginia  
 ; COUNTRY: U.S.A.  
 ; ZIP: 22042  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC Compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/379,656B  
 ; FILING DATE: 23-MAR-1995  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/EP93/01820  
 ; FILING DATE: 12-JULY-1993  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 93400949.9  
 ; FILING DATE: 09-APR-1993  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 92402358.8  
 ; FILING DATE: 27-AUG-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Svensson, Leonard R.  
 ; REGISTRATION NUMBER: 30.330





QY 1608 GTTCTGTCAGGTGTAAGAGCCAGGACATACAGAGGGGATTTATTACAGTATAATAG 1667  
DB 2251 GGGTACTACGGTCTTAAAGGTCAGGATTTACAGAGGGGTATCTCC---GAAGAAC 2307  
QY 1668 AAGTACTGCTCTGAGGACCTTATTCTAGCTCGATATGCGCTAGCATTTAGAAAAGC 1727  
DB 2308 AACTAATGGCAATTTGGAACGTTAAGAGTAACGGTTAATCCACATTAACACAACATA 2367  
QY 1728 AGGGAATATCGTGTAGACTGAGATATGCTACTGATGAGATATTTGATTGCATGTAAA 1787  
DB 2368 TCGCTTAGAGTTCTGTTTGGCTCAACAGGAATTTCAATATAGGGTACTCCGTGGAG 2427  
QY 1788 CGATGC-----TCAGATTAGATGCCAAAACAATGAACCCAGGTGAGGATCTGACATC 1841  
DB 2428 GGTTCCTATCGGTGATGTAGATTAGGAGGACAAATGAACAGAGGCGGAGGAATTA 2487  
QY 1842 TAAACCTTTAAAGTTGAGATGCTATCACACA-----TTAAATTTAGCACAGATAG 1895  
DB 2488 CGAATCCCTTTTTCACAGAGAGTTTACTACTCGGTCCGTTCAATCCGCCCTTTTACATT 2547  
QY 1896 TTCGCTAGCATTTGAAACATAATTTAGGTGAAGACCCCTAATTCACATTTATCTGGTATAGT 1955  
DB 2548 TACACAGCTCAAGAGATTCTAAGGTGAGTGCAGAGGTGTAGCACCGGTGGTGAATA 2607  
QY 1956 TTACGTTGACCGAATCGAATTCATCCAGTAGAGACATATGAAGCGGAAACAAGATTT 2015  
DB 2608 TTATATAGATAGAAATTGAATTTGCTCTGTGAATCCGCGCAGCAGAGGCGGAAGGATTT 2667  
QY 2016 AGAGCAGCGAAGAGCAGTGAATGCTTTTACGATACAAAAGATGCGTTAGGACC 2075  
DB 2668 AGAAGCGCGAAGAGCGGTGGCGAGCTTTGTTTACAGTACAGGCGGAGATTAACAGT 2727  
QY 2076 AGGCGTTAACGATTTAGAGTGAATCAAGCGGCAATTTAGTGAATGCTATCGATGA 2135  
DB 2728 AATGTGACAGATTATCAAGTGGACCAAGCGGCAATTTAGTGTCACTTATCCGATGA 2787  
QY 2136 TTTGTATCCAAATGAAAACGATTTGTTATTTGATGACGTGAGAGGCAAAACGCTCAG 2195  
DB 2788 ACAATATGGCGATGACAAAAGATGTTATGGAAGCGGTAGAGCGGCAAAACGCTCAG 2847  
QY 2196 TGAGCAGTATTTGCTTCAAGTCCAGATTTTCAAGATTAAT-----GGHAAAA 2249  
DB 2848 CCGGAAAGCGCACTTACTTCAAGATCCAGTCTTATTAACAATGATACAGAGAGAA 2907  
QY 2250 TGGCTGAGCGCAAGTACGGCAATTTGAGTTATGAAGCGGATGCTTTATTCAAGGCGG 2309  
DB 2908 TGGCTGGAAGCGAAGTACGGTTTACTATTAGCGGCGGTCCATTTCTTAAAGGTCG 2967  
QY 2310 TTATCTACGCTACAGGTGCGAGAGAAATAGATACGGAACGATCCAAAGTATCTGTA 2369  
DB 2968 TGCACCTTCAGTTAGCAAGCGCAAGA-----GAAATTTCCACATACATTTTA 3015  
QY 2370 TCAAAAGTAGAGGAGGTGTTAAACCATACACAGATATAGATTGAGAGGGTTTGT 2429  
DB 3016 TCAAAAGTAGATGATCGGTGTTAAAGCCTTTATACAGCTATAGACTAGATGATTTGT 3075  
QY 2430 CGGAAGCAGTCAAGATTGGAATTTTCCAAATTCGTATCAACCGAAGCGAATTTGTA 2489  
DB 3076 GAAGAGTAGTCAAGATTGGAATTTGATCTCATCAACCGAATCAATGTTGTA 3135  
QY 2490 AAATGTACCGGATGTTTGTGCGCAGATGTTATCTCTGTTAACTCGGATGTTAGTATCA 2549  
DB 3136 AAATGTACCAATAATTTAGTATCTGATCTACTTACTCAGATGTTCTTTCAGCGGAATCA 3195  
QY 2550 TCGATGACGCAACAAAGTATGTAATGAGTTCGTTTGAAGTAGAATAACCGT----- 2601  
DB 3196 CCGTTGTGATGAACAGCATCAGGTAGTATGAGCTAGATGCGGAGCATCATCCAAATGGA 3255  
QY 2602 -----TCTGTGAGCGCATGAGTTCTTCTATTCTTATTGATACAGGTGAATCGA 2651  
DB 3256 TTGCTGTGAGCGGCTCAACACATGAGTTTCTTCTTATTAATACAGGGGATCTAAA 3315  
QY 2652 TTACAATGAAAATGAGGAATATGGGTTTGAATTTAAGATTTACGGACCCAGAGGGATATGC 2711

DB 3316 TGCAAGTGTAGATCAGGGCATTTGGGTTGTATTAAAAAGTTTCGAACAACAGATGGGTATGC 3375  
QY 2712 AACACTCGGAACCTTAGAATTTGGTTCGAAGAGGAGCCTTTATCAGGAGCGCATTTAGAACG 2771  
DB 3376 GACGTTTAGGAAATCTTGAATTTGGTAGAGGTTGGGCCAATATTCGGGTGAATCTCTAGAACG 3435  
QY 2772 CTTTCAAGAGAGAACAACAACAGTGGAGAGATTCAATGACAAGAGAGCGTGAAGAAACAGA 2831  
DB 3436 GGAACAAGAGATATTCGGAATTCGAATGCAAGCTAGGAAGAAAACGTGCAGAAATAGA 3495  
QY 2832 TAGAAGGTATATGCGCATCGAAACAAGCGGTAGATCGTTTATATATCCCGATTTATCAGGATCA 2891  
DB 3496 TCGGTGTATTAGCTCGGAACAAGCAATTAATCATCTGTTGTAGACTATCAAGATCA 3555  
QY 2892 GCACTGAATCCTGATGATAGATTAACAGATCTTACTCGGCCCAAGATCTGATACAGTC 2951  
DB 3556 ACAATTAATCCAGAAATTCGGCTAGCAGAAATTAATGAAGCTTTCAAACTCTGTAGAGTC 3615  
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DB 3616 AATTCGGGTGTATATAGTATGATACACTATTACAGATTTCTGGGATTAACCTACGAATTTA 3675  
QY 3012 TACAGAAATTAACAGATCGATCTCAACAAGCGGTGGAGTTTGTATGATCAGCGAAATGCGAT 3071  
DB 3676 CACAGAGTTTACCGATCGCTTACAAACAGCATCGTATCTGTATACGCTCTAGAAATGCGGT 3735  
QY 3072 ACCAAATGCGTATTTCCGAATGCGTTAAGTAAATGGAATGCAACGCTGCGGTAGAGT 3131  
DB 3736 GCAAAATGGAAGACTTTAAACAGTGGTCTAGATAGTTGGAATACAACTATGATGATCGGT 3795  
QY 3132 ACAACAAATCAATCATACATCTGCTCTGTTGATTCCAAACCTGGGATGAGCAAGTTTCGCA 3191  
DB 3796 TCACAGATGCGCATATGATTTCTTAGTTCTTTCGATTTGGATGCAACAAGTTTCCCA 3855  
QY 3192 ACAGTTTACAGTTTCAACCGAATCAAGATATGTTTACGAGTTACTCGGAGAAAAGAGG 3251  
DB 3856 ACAATTCAGAGTAAATCCGAATTTGAAGTATGCTTACGTTGTGACAGCAAGAAAAGTAGG 3915  
QY 3252 GGTAGGAATGGAATGATTAAGTATCCGTGATGCGGAAATGGAATCAACAGAAAGCTTACTTT 3311  
DB 3916 AGCGGAGATGGAATGATCTCAATCCAGATGCGGCTCCTCCCAAGAAAAGCTTTTACAT 3975  
QY 3312 TAGTGAAGCGATTTATGATACAAATGGAATGTATAACGCAAGTGTCCCAATACAAATGG 3371  
DB 3976 TAATGATGTGACTACGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 4035  
QY 3372 ATA 3374  
DB 4036 AGA 4038

RESULT 11  
US-08-455-838-4  
; Sequence 4, Application US/08455838  
; Patent No. 6028246  
; GENERAL INFORMATION:  
; APPLICANT: Lambert Bart  
; APPLICANT: Jansens, Stefan  
; APPLICANT: Van Audenhove, Katrien  
; APPLICANT: Peferoen, Marix  
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND  
; THEIR INSECTICIDAL PROTEINS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH  
; STREET: 8110 Gatehouse Road, Suite 500 East  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22042  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,838  
FILING DATE: 31-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 'PCT/EP93/01820  
FILING DATE: 12-JULY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93400949.9  
FILING DATE: 09-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92402358.8  
FILING DATE: 27-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 2121-106P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4344 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 668..4141  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: 1..4344  
OTHER INFORMATION: /note= "encompasses entire sequence  
OTHER INFORMATION: of SEQ ID NO (SID) 2: from nt position 474 to 2034 in SID 4"

|    |      |   |      |
|----|------|---|------|
| Db | 908  | CTCGGGCTTTTAGTGGTTCCGGTTTCTCGGACAAATAGTGAAGTTTTATCAATTCCTTTTA     | 967  |
| Qy | 301  | GATATTTCTGTGGCCTTCAGGGGMAAAGAGTCAATAGTGGGAAATTTTATGGAACAAGTAGAA   | 360  |
| Db | 968  | AATACACTGTGGCCAGTTAAATGATACACTATATGSGAAGCTTTCATGCGCAGGTGGAG       | 1027 |
| Qy | 361  | GAATCATTTAATCAAAAATATGACAGATATGCAAGGAATTAAGCGCTTTCGGAATTAGAA      | 420  |
| Db | 1028 | GAACTTTGTCAATCAACAATATACAGAAATTCGAAGAATCAGGCACCTTGCAGATATGCAA     | 1087 |
| Qy | 421  | GGATTAGGTAATAATTTACCAATTTATCTAACTCGCTTGAAGAAATCGGAAGAAATCCCA      | 480  |
| Db | 1088 | GGATTAGGAGACTCTTTTAAATGATATCAAGCTTCCCTTCAAATTTGGTTGGCTGATCGA      | 1147 |
| Qy | 481  | AATGGTTTCAAGAGCCTTACGAGATGTGGGAAATCGATTTGAAATCCTGGGATAGTTATTT     | 540  |
| Db | 1148 | AATGATACACGAAATTAAGTGTGTTCTGCTCAATTTATAGCTTTAGACCTTGATTTT         | 1207 |
| Qy | 541  | ACGCAATATATGCGCACTTTTATAGTGTGACAAATTTTGAAGTACCAATTCCTTACTGTATAT   | 600  |
| Db | 1208 | GTTAATGCTATTCCATTTGTTTGCAGTAAATGACACAGCAGGTTCCATTTACTGTCAGTATAT   | 1267 |
| Qy | 601  | GCAATGGCAGCCAACTTTCATTTACTGTTATTAAGACGCGTCAATTTTGGAGAGAA          | 660  |
| Db | 1268 | GCAACAAGCTGTGAATTTACATTTGTATTATTTAAAGATGTCATCTCTTTTGGAGAGGA       | 1327 |
| Qy | 661  | TGGGGAATGGTCAACAACACTACTAATTAATTAATTTATGATCGTCAAAATGAAACTTTACTGCA | 720  |
| Db | 1328 | TGGGGAATTCACACAGGGGGAATTTCCACATATTTATGACCGTCAATTTGGAATCAACCGCT    | 1387 |
| Qy | 721  | GAATATTTCTGATCCTGTGTAAAGTGTATGAAACTGGTTTATAGCAAAATTTAAAGGCACG     | 780  |
| Db | 1388 | AAGTACACTAAATTTACTGTGAAACTTGGTATAATACAGGTTTAGATCGTTTAAGAGGAACA    | 1447 |
| Qy | 781  | AGCGCTAAACAATGGGTGCACTAATCAACCAATTCGTGTAGAGAAATGACACTGGCGGTTTTA   | 840  |
| Db | 1448 | AATACTGAAAGTTGGTTAAGATATCATCAATTCGGTGTAGAGAAATGACTTTAGTGGTATTA    | 1507 |
| Qy | 841  | GATGTTGTTGTCATTTATCCCAATTTATGACACACGACGTACCCAAATGGGAAACGGAAGCA    | 900  |
| Db | 1508 | GATGTTGTGGCGTATTTCCATTTATGATGTACGACTTTATCCACGGGATCAACCCCA         | 1567 |
| Qy | 901  | CAACTAACAGGGAAGTATATACAGATCCACTGGGCGCGGTAAACGTTCTTCAATTG--        | 958  |
| Db | 1568 | CAGCTTACAGTGAAGTATATACAGATCCGATGTTATTTAATCCACGACTAATGTTGA         | 1627 |
| Qy | 959  | -----GTTCTGGTATGCAAAAGCACCTTCTTTCGGAGTGTAGAAATCATCCGTT            | 1008 |
| Db | 1628 | CTTTGGCGACGTTGGGGTACTAATCCCTATATACTTTTCTGAGCTCGAAAATGCGCTTC       | 1687 |
| Qy | 1009 | ATTTCGACACCCCATGTATTTGATTTATATAACGGGACTCACAGTGTATACAAATCAAGA      | 1068 |
| Db | 1688 | ATTTCGCCACCACTTTTGTATAGGTGTAATGCTTTAACTACAGAGTAATTCGATTT          | 1747 |
| Qy | 1069 | AGCATTTCTTCGCTCGCTATATAAGACATTTGGGCTGGTCAATCAAAATAGCTACATCGT      | 1128 |
| Db | 1748 | CCAGTTTCACTAAT---TTTATGATTTATTTGGTCAGACATACGTTACGCCGTAGTTAT       | 1804 |
| Qy | 1129 | GTCAGTAGGGGTAGTAATCTTCAACAATATGTATGGAACATAAATAATCTACACAGCACT      | 1188 |
| Db | 1805 | CTGAACGATTCAGCAGTACAAGAATAGTTATGSG-----CCTAAATTACAACCACAAGA       | 1858 |
| Qy | 1189 | AGTACCTTTGATTTTACGAATTTATGATATTTTACAAGACTCTATCAAAAGGATGCG-TACT    | 1247 |
| Db | 1859 | GCAACAATTTAATCCCGAGTTGATAGGAAACAACCGCATAGAGTCAACCGCAGTAGATTTT     | 1918 |
| Qy | 1248 | CCTTGATTTGTTTACCCTGGTTTATACGTATATATTTTTCGAATGCCAAGATCGAGTT        | 1307 |
| Db | 1919 | CGTTCTGCAATGATAGGTATATATCGCGGTGAATGAGCTTCTTTTGTCCAGGAGGCTTG       | 1978 |
| Qy | 1308 | TTTTCATGTTAAACCAATGGAATAATACCAAGAAAGCACTTAAGATATTAATCCAGTTTCCAA   | 1367 |

Db 1979 TTTAATGGT-----ACGATCTTCCTGCTAATCGAGATGTAG 2016  
QY 1368 AGATATTATACGAGTCAAGAGATTCCGAATTAGAATTACCTCCAGAACTTCAGATCA 1427  
Db 2017 AGATCTCTATGATACAAATGATGAATTACCCAGATGAAGTACCGGAATTCACCCA 2076  
QY 1428 ACCAAATTATGATCATATAGCCATAGATTATGTATATACCAAGTATTCGCCGACGGG 1487  
Db 2077 TAGCATATCTCATGTACCTTTTATAGCTT-----TCAAACTAATCAGGCTGGATCTAT 2130  
QY 1488 TAACACTACCGGATAGTACTGTATTTCTTGGACATACGAGTGCAGATTTAACAA 1547  
Db 2131 AGCTAATGAGGAAGTGTACTTATGTGTGGACCGGTGATGTGACCTTAATAA 2190  
QY 1548 TACAATATATTCAGATAAAATCACTCAAAATTCGGCCGTTAAATGTGGGATAATTAC 1607  
Db 2191 TACGATTACCCCAATAGAATTACAAATTACCATTGGTAAAGGCATCTGCACCTGTTTC 2250  
QY 1608 GTTTGTTCCAGTGGTAAAGGACAGGACATACAGGAGGGATTTATTAAGTATATATAG 1667  
Db 2251 GGGTACTACGGTCTTAAAGGTCAGGATTTACAGGAGGGGTATACCTCC---GAAGAAC 2307  
QY 1668 AAGTACTGGTTCGTAGGAACCTTTATTTCTAGCTCGATATGGCTAGCATTAAGAAAGC 1727  
Db 2308 AACTAATGGACATATTTGGAACGTTAAGAGTAACGGTTAATTCACCATTAACAAACAATA 2367  
QY 1728 AGGGAATATCGTGAAGACTGAGATATGCTACTGTAGTGCAGATATTGTAATGATGTAAA 1787  
Db 2368 TCGCCTAAGAGTTCGTTTTCCTCAACAGGAAATTCAGTATAGGGTACTTCGTGGAGG 2427  
QY 1788 CGATGC-----TCAGATTCCAGATGCCAAAAACAATGAACCCAGGTGAGGATCTGACATC 1841  
Db 2428 GGTTCCTATCGGTGATGTAGATTAGGGAGCACAATGAACAGAGGCGCAGGAACCTTA 2487  
QY 1842 TAAAACTTTTAAAGTTCAGATGCTATCAACA-----TTAAATTTACCAACAGATAG 1895  
Db 2488 CGAATCCTTTTCAAGAGAGTTTACTACTACTGGTCCGTTCAATCCGCTTTTACATT 2547  
QY 1896 TTCGCTAGCAATGAACATAAATTTAGTGAAGACCCCTAAATTCACATTTATCTGTATAGT 1955  
Db 2548 TACACAGCTCAAGAGATTTCTACAGTGAATGCAAGGTGTTAGCACCGGTGGTGAATA 2607  
QY 1956 TTACGTTGACCGAATCGAATTCATCCAGTATGATGAGACATATGAAGCGGAACAAGATTT 2015  
Db 2608 TTATATAGATAGAAATTTGAATTTGCTCTGTGAATCCGCGCAGAGAGCGGAGAGGATTT 2667  
QY 2016 AGAAGCAGCGAAGAAACGATGATGCTTTTACGATATCAAAAGATCGCTTACGACC 2075  
Db 2668 AGAAGCGGCGAAGAAACGCGTGGAGCTTTGTTTACACGTCACAGGAGCGGATTTACAGGT 2727  
QY 2076 AGCGGTAAACGGATTATGAAGTGAATCAAGCGCAAACTTAGTGAATGCCCTATCGGATGA 2135  
Db 2728 AATGTGACAGATTATCAAGTGGACCAAGCGGCANATTTAGTGTGATGCTTTATCCGATGA 2787  
QY 2136 TTTGTTATCCAAATGAATAACGATTTGTTATTTGATGAGTGAAGAGGCAAAACCGCTCAG 2195  
Db 2788 ACAATATGGGCATGACAAAAGATGTTATTTGAAGCGGTAAAGCGGCAAAACCGCTCAG 2847  
QY 2196 TGAGGCACGTAATTTGCTTCAAGATCCAGATTTTCCAGAGATAAAT-----GGAGAAA 2249  
Db 2848 CCGCAACCGCACTTACTTCAGATCCAGATTTTAAATCAATCAATAGTACAGAGAGAA 2907  
QY 2250 TGCGTGGACGGCAAGTACGGGAATTGAGTTTATAGAGGGGATGCTTTTATCAAGGGCG 2309  
Db 2908 TGCGTGGAGGCAAGTAAACGGTGTACTATTAGCGAGGCGGTCCATCTTTTAAAGTGC 2967  
QY 2310 TTATCTACGCTTACCGGTGCGAGAGAAATAGATACCGAAACCGTATCCAAAGTATCTGTA 2369  
Db 2968 TGCATTTCACTTAGCAAGCGCAAG-----GAAATTTATCCAAACATACATTTA 3015  
QY 2370 TCAAAAGTATAGAGAGGTGTATTTAAACCATACACAGATATAGATTGAGAGGTTGT 2429  
Db 3016 TCAAAAGTATAGATGCTCGGTGTTAAAGCCTTATACACGCTATAGACTAGATGATGTTGT 3075

QY 2430 CGGAAGCAGTCAAGGATTCGAAATTTTCAAAATTCGTCAATCAAAACGAAACCGAATTCGTAAA 2489  
Db 3076 GAAGAGTAGTCAAGATTTAGAAATTTGATCTCATCCACCATCATAAAGTCCATCTTGTAAA 3135  
QY 2490 AAATGPAACGGATGATTTGCTGCCAGATGATCTCTCTGTTAACTCGATGGGTAGTATCAA 2549  
Db 3136 AAATGTACAGATAATTTAGTATCTGATATCTTACTCAGATGGTCTTTGCGAGGGAATCAA 3195  
QY 2550 TCGATCAGCGGACAAAAGTATGTGAATAGCCGTTTGAAGTAGAATAACCGT-----2601  
Db 3196 CCGTTGTGATGAACAGCATCAGTAGATATGAGCTAGATGCGGAGCATCATCCAATGGA 3255  
QY 2602 -----TCTGTGGAAGCGCATGAGTTCTTATTCCTATTGATACAGGTGAAATCGA 2651  
Db 3256 TTGCTGTGGAAGCGCTCAAAACACATGAGTTTCTTCTATATTAATACAGGGATCTAAA 3315  
QY 2652 TTACAATGAAATGCAAGAAATATGGTTTGGATTTAAGATTACGGACCCAGAGGATATGC 2711  
Db 3316 TGCAGTGTAGATCAGGGCATTTGGGTTGTTATTAAGAGTTTCAAAACAGATGGGTATGC 3375  
QY 2712 AACACTCGGAAACCTAGAAATTCGTGGAAGGACCTTTTATCAGGAGACGCAATTAGAAG 2771  
Db 3376 GACGTTAGGAATCTTTGAATTTGAGAGTTGGGCCATTTATCGGTGAATCTCTAGAACG 3435  
QY 2772 CTTGCAAAAGAGAAACAAACAGTGGGAAGATTCAAATGACAAGAACGCTGAAGAAACAGA 2831  
Db 3436 GGAAACAAAGAGATAATCGGAATGGATTCAGAGCTAGGAAGAAACGTTGCAGAAATAGA 3495  
QY 2832 TAGAAGTATATGGCATTCGAAACAAAGCGGTAGATCGTTTATATGCGGATATACAGATCA 2891  
Db 3496 TCGTGTGTTATTTAGCTGCGAAACAAAGCAATTAATCATCTGTTTGTAGACTATCAAGATCA 3555  
QY 2892 GCACTGATCTGATGTAGATTTACAGATCTTACTGCGGCCCBAGATCTGATACAGTC 2951  
Db 3556 ACAATTTAAATTCAGAAATTTGGGCTAGCAGAAATTAATGAAGCTTCAAAATCTTGTAGAGTC 3615  
QY 2952 CATTCCTTACGTATATAACGAAATGTTCCAGAAATATCCAGGATGAACTATACGAAGTT 3011  
Db 3616 AATTTCCGGGTGATATAGTGTATACACTATTACAGATTCCTGGGATTAATACGAATTTA 3675  
QY 3012 TACAGAAATTAACAGATTCGACTCCAAACAGCGGTGAGTTTGTATGATCAGCGAAATGCCAT 3071  
Db 3676 CACAGAGTTATCCGATCGCTTACAAACAGCATCGTATCTGTATACGCTCTAGAAATCGCGT 3735  
QY 3072 ACCAAATGCTGATTTTGAATGGGTAGTAAATTTGGAATGCAACGCCCTGGCGTAGAAGT 3131  
Db 3736 GCAAAATGGAGACTTTAAACAGTGGTCTAGATAGTTGGAATACAACTATGGATGCTCGGT 3795  
QY 3132 ACAACAAATCAATCATACATCTGTCCTTGTGATTCGAACTGGGATGAGCAAGTTTCGCA 3191  
Db 3796 TCAGCAGATGCGAATATGCAATTTCTTAGTTCTTTCGCAATGGGATGCAAGTTTCCCA 3855  
QY 3192 ACAGTTTACAGTTTCAACCGAATCAAGATATGTGTTTACGAGTTTACGCGAGAAAAGAGG 3251  
Db 3856 ACAATTTGAGAGTAAATCCGAATTTGAAGTATGCTTTACGTTGACAGCAAGAAAAGTAGG 3915  
QY 3252 GGTAGAAATGATATGTAAAGTATCCGTGATCGTGAATCAACAGAAACCGCTTACTTT 3311  
Db 3916 AGCGGAGATGAGTACGTCACAAATCCGAGATGGCGCTCATCCCAAGAAATCTTTACATT 3975  
QY 3312 TAGTCAACCGGATTAATGATACAAATGGAATGTATTAATAGCAAGTCTCAATCAAAATGG 3371  
Db 3976 TAATGATGTGATAGTACGATGAATAGTAAAGTGTAGTATGTCAATGACAAATTCGTATATACAGA 4035  
QY 3372 ATA 3374  
Db 4036 AGA 4038

RESULT 12  
US-09-019-809-4  
; Sequence 4, Application US/09019809

Patent No. 6143550  
GENERAL INFORMATION:  
APPLICANT: LAMBERT, BART  
APPLICANT: JANSSENS, STEPAN  
APPLICANT: VAN AUDENHOVE, KATRIEN  
APPLICANT: PEPEROEN, MARNIX  
APPLICANT: VAN RIE, JEROEN  
APPLICANT: VAN AARSEN, ROEL  
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR  
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/019,809

FILING DATE: 02-FEB-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

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REFERENCE/DOCKET NUMBER: 2121-135P

TELECOMMUNICATION INFORMATION:

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TELEX: 248345

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 4344 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 668..4141

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1..4344

OTHER INFORMATION: /note= "encompasses entire sequence

of SEQ ID NO (SID) 2: from nt position 474 to 2034

OTHER INFORMATION: in SID 4"

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1..4344

OTHER INFORMATION: /note= "also encompasses part of

OTHER INFORMATION: the sequence of SID 3: from nt position 2994 to

OTHER INFORMATION: 4344 in SID 4"

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1..4344

OTHER INFORMATION: /note= "SID 3 shows additional

OTHER INFORMATION: nucleotides, located 3' from the sequence shown in

OTHER INFORMATION: SID 4 (1352-1554 in SID 4)"

US-09-019-809-4

Query Match 24.4%; Score 883.4; DB 3; Length 4344;

Best Local Similarity 56.6%; Pred. No. 1.5e-183;

Matches 1936; Conservative 0; Mismatches 1386; Indels 101; Gaps 12;

QY 1 ATGAGTCCAAATATCAAAATGAATATGAATATAGATGGACACCTTCTACTTCTGTA 60

DB 668 ATGAATCGAAATATCAAAATGAATATGAATATAGATGGACACCTTCTACTTCTGTA 727

QY 61 TCCAAATGATTCTAACAGATACCCCTTTTGGCAATGAGCCAAACAAATGCGCTACAAAATATG 120  
DB 728 TCAGATGACGATGTGAGGTATCCTTTGGCAAGTGACCCAAATGCGCGTTTACAAAATATG 787  
QY 121 GATTATAAGATATTATAAAATGTCTGCGGGAATGCTAGTAGTGAATACCTGGTTCACCT 180  
DB 788 AACTATAAGATATTACTTTACAAATGACAGATGAGGACTACACTGATCTTTATATAAATCCCT 847  
QY 181 GAAGTACTCTGTAGCGGACAGATGACAGCTTAAGGCCCAATTCGATATAGTAGGTAATAA 240  
DB 848 AGTTTATCTATTAGTGTAGAGATGAGTTTACAGCTGCGCTTACTGTTGTTGGAGATA 907  
QY 241 CTATCAGTTTGGGGTCCCATTTGTTGGCCCGATAGTAGTCTTTATATCTCAACTTATT 300  
DB 908 CTCGGGCTTTTAGGTGTTCCGTTTCTGGAACAATAGTAGGTTTATCAATTCCTTTTA 967  
QY 301 GATATCTGTGGCTTCAGGGGAAAGAGTCATGGAATTTTATGGAACAAGTAGAA 360  
DB 968 AATACACTGTGGCCAGTTAATGATACAGCTATATGGAAGCTTTTCATGCGACAGGTGAG 1027  
QY 361 GAATCAATTAATCAAAATAAGCAGATATGCAAGGAATAAAGCGCTTCGGAATTAGAA 420  
DB 1028 GAATCTGCAATCAACAAATACAGAAATTTGCAAGAAATCAGGCACTTGCAAGATTGCA 1087  
QY 421 GGATTAGGTAAATTAACCAATTAATCTAACTGCGCTTGAAGAATGGGAAGAAATCCA 480  
DB 1088 GGATTAGGAGACTCTTTTAATGATATCAAGTTCCCTTCAAAATTCGTTGGCTGATCGA 1147  
QY 481 AATGGTTCAAGAGCTTACGAGATGCGGAATTCGATTTGAAATCCTGGATAGTTTATT 540  
DB 1148 AATGATACACGAAATTTAAGTGTGTTGCTGCTCAATTTATAGCTTTAGACCTTTGATT 1207  
QY 541 ACGCAATATATGCCATCTTTTAGAGTCACAAATTTTGAAGTACCATTCTTACTGTATAT 600  
DB 1208 GTTAATGCTATTCATTTGTTGCAAGTAATGAGCAGCAGGTTCCATTTACTGTCTAGTAT 1267  
QY 601 GCAATGGCAGCAACCTTCAATTTACTGTTTAAAGGACGCTCAATTTTGGAGAAGAA 660  
DB 1268 GCACAAGCTGTGAATTTTACATTTGTTTATTAATAAAGATCATCTCTTTTGGAGAAGAA 1327  
QY 661 TGGGATGGTCAACACTACTATTATAACTATTATGATCGTCAATGAATGAATCTTACTGCA 720  
DB 1328 TGGGATTTCAACAGGGGGAATTTCCACATATTTATGACCGTCAATTTGGAATCAACCG 1387  
QY 721 GAATATTTCTGATCACTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGT 780  
DB 1388 AATACACTAATTTACTGTGAACCTTGGTATTAATACAGTTTAGATCGTTTAAAGGAACA 1447  
QY 781 AGCGCTAAACAAATGGGTTGACTATAACCAATTCGTTAGAGAAATGACACTGGCGGTTTA 840  
DB 1448 AATACCTGAAAGTTGGTTAAGATATCATCAATTCGTTAGAGAAATGACTTTTAGTGTATTA 1507  
QY 841 GATGTTGTTGATTTTCCCAATTTATGACACAGCAGTACCCCAATGGAAACGAAAGCA 900  
DB 1508 GATGTTGTTGCGCTTATTTCCATATTTATGATGTACGCTTTTATCCACGGGATCAAAACCA 1567  
QY 901 CAACATAACAGGAGACTATATACAGATCCACTGGCGCGGTAAACGTTCTTCAATTG-- 958  
DB 1568 CAGCTTACAGGTGAGGTATATACAGATCCGATTTGTTAATTAATCCACAGCTAATGTTTGA 1627  
QY 959 -----GTTCTCTGATGACAAAGACCTTCTTTTGGAGGTGATAGATCATCCGTT 1008  
DB 1628 CTTTGGCGAGCTTGGGTACTTAATCCCTATAATACTTTTCTGAGCTCGAAATGCGCTTC 1687  
QY 1009 ATTCCAGCACCCCATGTTTGAATTTATTAACCGGACTCTCAGTGTATACAAATCAAGA 1068  
DB 1688 ATTCGCCACCCACATCTTTTGTAGTGTGATGCTGAATAGCTTAACAATCAGCAGTAATCGATTT 1747  
QY 1069 AGCATTTCTTCGCTCCGTATATAAGACATTTGGCTGGTCTGATCAATTAAGTACCATCGT 1128  
DB 1748 CCAGTTTCTCATCTAAT--TTTATGGATTTATGGTCAGGACATACGTTACGCGGTGTTAT 1804  
QY 1129 GTCAGTAGGGGTAGTAATCTTTCAACAAATGATGGAACATAATCAAAATCTACACAGCACT 1188

Db 1805 CTGAACGATTCAGAGTCAACAGAGTATAGTTATGG-----CTAATTAACAACCAACA 1858  
Qy 1189 AGTACTCTTGTATTTTACGAATTTATCATTTTACAGAGCTCTATCAAGAGTACAG-TACT 1247  
Db 1859 GCAACAATTAATCCCGAGTTGATGGACCAACCGCATAGATCAACGGCAGTAGATTTT 1918  
Qy 1248 CTTGATATGTTTACCCTGGTTATACGPATATATTTTGGAAATGCCAGAGTCGAGTT 1307  
Db 1919 GGTTCGTATGATAGGTATATATGCGGTGAATAGAGCTTCTTTGTCCAGAGGCTTG 1978  
Qy 1308 TTTCAATGTAACCAATTCGAATTAATACCAAGAGAGGTAAAGTATTAATTCAGTTCCNA 1367  
Db 1979 TTTAATGTT-----ACGACTCTCTCGCTAAATGGAGGTAG 2016  
Qy 1368 AGATATTATAGCGAGTCAAGAGATTTCGGAAATTAGAAATTACCTCCAGAACTTCAGATCA 1427  
Db 2017 AGATCTCTATGATACAAATGATGAATACCACCAAGATGAAGTACCGAGATTCAACCA 2076  
Qy 1428 ACCAAATTATGATCATATAGCCATAGATTAATGTATATCAAGTATTTCCCGCAGCGG 1487  
Db 2077 TAGACTATCTCATGTTACCTTTTATAGCTT-----TCAAACTAATCAGGCTGGATCTAT 2130  
Qy 1488 TAACACTACCGGATTAGTACCTGTATTTCTTTGGACACATCGAAGTGCAGATTTAAACA 1547  
Db 2131 AGCTAATGCGAGAGTGTACCTACTTATATGTTTGGACCCGCTCGTGTATGTGGACCTTAATAA 2190  
Qy 1548 TACAATATATTACAGATAAAATCACTCAAAATCCGCGCTTAAATGTGGGTAATTTTACC 1607  
Db 2191 TACGNATTACCCAAATAGAAATTACAAATTACNTTGGTAAAGGCATCTGCACCTGTTTC 2250  
Qy 1608 GTTTGTTCCAGTGTGTAAGGACAGAGACATACAGAGGGGATTTTATACAGATAAATAG 1667  
Db 2251 GGGTACTACGGTCTTAAAGGTTCCAGGATTTTACAGAGGGGGTATACTCC---GAAGAAC 2307  
Qy 1668 AAGTACTGGTCTGTAGGAACCTTATTTCTAGCTCGATATGGCCCTAGCAATTAAGAAAAAGC 1727  
Db 2308 AACTAATGGCAATTTGGAAACGTTAAGAGTAAACGGTTAAATTCACCAATTAAACAACAATA 2367  
Qy 1728 AGGAAATATCGTGTAGAGTACAGATATGCTACTGATGCAGATATGTTATTCATGTAA 1787  
Db 2368 TCGCTAAGAGTTCGTTTGGCTCAACAGGAATTTTCAGTATAGGGTACTCCGTGGAGG 2427  
Qy 1788 CGATGC-----TCAGATTTCAGATGCCAAAAACAATGAACCCAGGTGAGGATCTGACATC 1841  
Db 2428 GGTTCCTATCGGTGATGTAGATTAGGAGCAACATGAACAGAGGCGCAGGACACTAATTA 2487  
Qy 1842 TAAACTTTTAAAGTTCAGATGCTATCAACA-----TTAAATTTAGCAACAGATAG 1895  
Db 2488 CGAATCCCTTTTCAACAGAGAGTTTACTACTGCTCGGTTCATTCGCGCTTTTACATTT 2547  
Qy 1896 TTCGCTAGCATTTGAACATAATTTAGGTGAAGACCCTTAATTCACATTTATCTGTTATAGT 1955  
Db 2548 TACAACAGCTCAAGAGATTTCAAGTGAATGCAGAGGTGTAGACCGGTGGTGAATA 2607  
Qy 1956 TTACGTTGACCGAATTCGAATTCATCCAGTATAGACATATGAAGCGGACCAAGATTT 2015  
Db 2608 TTATATAGATAGATTGAATTTGCTCTGTTGATCCGCAACGAGAGCGGAGAGATTT 2667  
Qy 2016 AGAAGCAGGAGAAAGCAGTGAATGCCCTTGTATAGATACAAAGATGGCTTACGACC 2075  
Db 2668 AGAAGCGCGAAGAAAGCGGTGGCGAGCTTGTTTACACGTACAAGGGACGATTACAGGT 2727  
Qy 2076 AGCGGTACGATTTAGTGAATCAAGCGCAACTTAGTGGAAATCGCTATCGGATGA 2135  
Db 2728 AATGTGACAGATTATCAAGTGGACCAAGCGCAAAATTTAGTGTCTATTCGATGA 2787  
Qy 2136 TTTGTATCCAAATGAAAAACGATTTGTTATTTGATGCAAGAGAGGCAAAACGCTCAG 2195  
Db 2788 ACAATATGGCATGACAAAAGATGTTATTTGAAAGGTTAAGAGCGGCAAAACGCTCAG 2847  
Qy 2196 TGAGGCAGTAAATTTGCTTCAAGATCCAGATTTTCAAGAGATTAAT-----GGAGAAAA 2249

Db 2848 CCGGAAACGCAACTTACTTCAAGATCCAGATTTTAAATACAATCAATAGTACAGAAGAA 2907  
Qy 2250 TGGCTGGACGCGCAAGTACGGGAATTTAGAGGTTATAGAGGGGATCTTTATTTCAAGGGCG 2309  
Db 2908 TGGCTGGAGGCAAGTACGGGTGTACTATTAGCGAGGCGGTCCATTTCTTTAAAGGTGCG 2967  
Qy 2310 TTATCTACGCTTACCAGGTGCGAGAGAAATAGATACGGAAACGTATCCAAAGTATCTGTA 2369  
Db 2968 TGCACCTTCAGTTAGCAAGCGCAAGA-----GAAAAATTCCACATACATTTA 3015  
Qy 2370 TCAAAAGTAGAGAGAGGTGTATTAATAACCATACACAAGATATAGATTGAGAGGTTTGT 2429  
Db 3016 TCAAAAAGTAGATCGATCGGTGTTAAAGCCCTTATACACGCTATAGACTTAGATGATTTGT 3075  
Qy 2430 CCGAAGCAGTCAAGGATTTGGAAATTTTTCACAAATTCGTATCAAAACGAACCGAATTTGTA 2489  
Db 3076 GAAGATGATCAGATTTAGAAATTTGATCTCATCCACATCATAAAGTCCATCTTTGTA 3135  
Qy 2490 AAATGTACCGGATGATTTGCTGCCAGATGTATCTCTGTTAACTCGGATGGTAGTATCAA 2549  
Db 3136 AAATGTACAGATAATTTAGTATCTGATACITTTACTCAGATGGTCTTTCAGCGGAATCAA 3195  
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Qy 2602 -----TCTGCTGAAGCGCATGATCTCTATTCCTATTGATACAGGTGAATCGA 2651  
Db 3256 TTGCTGTGAAGCGCTCAACACATGAGTTTCTTCTATTAATTAACAGGGATCTAAA 3315  
Qy 2652 TTACAATGAATAATCAGGAATATGGGTTGGATTTAAGATTACGGACCCAGAGGATATGC 2711  
Db 3316 TGCAAGTGTAGATCAGGSCATTTGGGTTGTATTAAGAGTTCGAACACAGATGGGTATGC 3375  
Qy 2712 AACACTCGGAAACCTAGAAATTTGGTCGAAGAGGACCTTTATCAGAGACGCAATTAGAAG 2771  
Db 3376 GACGTTAGGAAATCTTGAATTTGGTAGAGTTGGGCCATTTATCGGGTGAATCTCTAGAAGC 3435  
Qy 2772 CTTCCAAGAGAGAACAAACAAGTGGAGATTCAAATGACAGAGAGAGCTGAAGAACAGA 2831  
Db 3436 GGAACAAGAGATTAATCGAAATGGAATGCAGAGCTAGGAAGAAACCGTGAGAAATAGA 3495  
Qy 2832 TAGAAGGTATATGGCATCGAAACAAAGCGGTAGATCGTTTATATCCGATTAATCAGGATCA 2891  
Db 3496 TCGTGTGTATTTAGCTCGAAACAAAGCAATTAATCACTGTTTGTAGACTATCAAGATCA 3555  
Qy 2892 GCAACTGAACTCCTGATGTAGAGATTAAGATCTTACTTCGGGCCCAAGATCTGTACAGTC 2951  
Db 3556 ACAATTAATCCAGAAATTTGGGCTAGCAGAAATTAATGAAGCTTCAAAATCTTTAGAGTC 3615  
Qy 2952 CATTCCTTACGTATATAACGAATTTCCCAAGAAATACCGGGATGAATATACGAACTT 3011  
Db 3616 AATTTCCGGGTGTATATAGTGATACATTTACAGATTCCTGGGATTAATCAGAAATTTA 3675  
Qy 3012 TACAGAAATTAACAGATCGACTCCCAACAGCGGTGGAGTTTGTATGATCAGCGAAATTCGCA 3071  
Db 3676 CACAGAGTTATCCGATCGCTTACAAACAGCATCGTATCTGTATAGCTGTAGAAATTCGGT 3735  
Qy 3072 ACCAAATGGTGATTTTCGAATGGGTTAAGTAAATTTGGAATGCAACGCTTCGGTAGAAGT 3131  
Db 3736 GCAAAATGGAGACTTTAAACAGTGGCTAGATAGTTGGAAATCAAACTATGGATGCATCGGT 3795  
Qy 3132 ACAACAAATCAATCATCATCTGCTTCTGTTGATTTCCAACTGGGATGAGCAAGTTTCGCA 3191  
Db 3796 TCAGCAAGATGGCAATATGCAATTTCTTAGTTCCTTCGCAATTTGGGATGCAAAAGTTTCCA 3855  
Qy 3192 ACAGTTTACAGTTTCAACCGAATCAAGATATGTTACAGAGTTACTGCGAGAAAAGAGG 3251  
Db 3856 ACATTTGAGAGTAAATCCGAATTTCTAGTATGTTTACGTTGTGACAGCAAGAAAGTAGG 3915  
Qy 3252 GGTAGGAAATGGATATGTAAAGTATCCGTTGATGGTGGAAATCAACAGAAACGCTTACTTT 3311  
Db 3916 AGCGGAGATGGATCGTCACAATCCGAGATGGCGCTCATCCCAAGAAACTCTTACATT 3975

QY 3312 TAGTCACAGCATTATGATACAAATGGAATGTATATATACCGAAGTGTCCCAATCAAAATGG 3371  
Db 3976 TAATGCATGTGACTAGGATGTAATAGTACGATATGTCAATGACAATTCGTATATACAGA 4035

QY 3372 ATA 3374

Db 4036 AGA 4038

## RESULT 13

US-09-471-177-4

; Sequence 4, Application US/09471177

; Patent No. 6448226

; GENERAL INFORMATION:

; APPLICANT: LAMBERT, BART

; APPLICANT: JANSSEN, STEFAN

; APPLICANT: VAN AUDENHOVE, KATRIEN

; APPLICANT: PEFFEROEN, MARNIX

; APPLICANT: VAN RIE, JEROEN

; APPLICANT: VAN AARSSEN, ROEL

; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR

; TITLE OF INVENTION: INSECTICIDAL PROTEINS.

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Birch, Stewart, Kolasch &amp; Birch, LLP

; STREET: P.O. Box 747

; CITY: Falls Church

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22040-0747

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/471,177

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/019,809

; FILING DATE: 02-FEB-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: SVENSSON, LEONARD R.

; REGISTRATION NUMBER: 30,330

; REFERENCE/DOCKET NUMBER: 2121-135P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 205-8000

; TELEFAX: (703) 205-8050

; TELEX: 248345

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4344 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 668..4141

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 1..4344

; OTHER INFORMATION: /note= "encompasses entire sequence

; OTHER INFORMATION: of SEQ ID NO (SID) 2: from nt position 474 to 2034

; OTHER INFORMATION: in SID 4"

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 1..4344

; OTHER INFORMATION: /note= "also encompasses part of

; OTHER INFORMATION: the sequence of SID 3: from nt position 2994 to

; OTHER INFORMATION: 4344 in SID 4"

; OTHER INFORMATION:

## FEATURE:

; NAME/KEY: misc feature

; LOCATION: 1..4344

; OTHER INFORMATION: /note= "SID 3 shows additional

; OTHER INFORMATION: nucleotides, located 3' from the sequence shown in

; OTHER INFORMATION: SID 4 (1352-1554 in SID 4)"

US-09-471-177-4

Query Match 24.4%; Score 883.4; DB 4; Length 4344;

Best Local Similarity 56.6%; Pred. No. 1.5e-183;

Matches 1936; Conservative 0; Mismatches 1386; Indels 101; Gaps 12;

QY 1 ATGAGTCCTCAAAATCAAAATGAATATCAAAATATAGATGCGACACCTTCTACTTCTGTA 60

Db 668 ATGATCGAATATCAAAATGAATATGAATATGATGCCCCCATTTGGTGTGCA 727

QY 61 TCCAAATGATTTCAAGATACCCCTTTGCGAATAGGCAACAAATGCGCTACAAATATG 120

Db 728 TCAGATGACGATGTGAGGTATCCCTTTGGCAAGTGACCCAAATGCGAGCGTTACAAATATG 787

QY 121 GATTATAAGATTATTTAAATATGCTCGGGAATGCTAGTGAATACCTCGTTCCACT 180

Db 788 AACTATAAGATTACTTACAAATGACAGATGAGGACTACACTGATTTCTTATAATAATCT 847

QY 181 GAAATGACTTTGTAGCGGACAAGATGAGTAAAGCGCGCAATTTGATATAGTAGTAAATTA 240

Db 848 AGTTTATCTATTAGTGTAGAGATGAGTTCAGACTGCGCTTACTGTTGTTGGGAGATA 907

QY 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCGGATGATGAGTCTTTTATACTCAACTTATT 300

Db 908 CTCGGGGCTTTAGGTGTTCCGTTTCTGSCAAATAGTAGGTTTATCAATTCCTTTTA 967

QY 301 GATATTCTGTGGCTTCAGGGGAAAAGAGTCAATCGGGAATTTTATGGAACAAGTAGBA 360

Db 968 AATACACTGTGGCAGTTAATGATACAGTATATGGGAGCTTTTCATGCGACAGTGGAG 1027

QY 361 GAACTCATTAATCAAAATATAGCAGATATGCAAGATATGAAAGCGTTTCGGAAATTAGAA 420

Db 1028 GAACTTGTCATCAACAATATACAGATTTGCAAGATATGAGGACTTTCAGAGATGCAA 1087

QY 421 GGATTAGGTAATTAACCAATTTATCTAACTGCGCTTGAAGAAATGGAAGAAATCCA 480

Db 1088 GGATTAGGAGACTCTTTTAAATGATATCAACGTTCCCTTCAAAATTTGGTGGTGTATCGA 1147

QY 481 AATGTTCAAGAGCTTACGAGATGCGGAATTCATTTGAATCTCTGGATAGTTTATT 540

Db 1148 AATGATACACAGAAATTTAAGTGTGTCGTCCTCAATTTATAGCTTTAGACCTTGATTT 1207

QY 541 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATTCCTTACTGTATAT 600

Db 1208 GTTATGCTATTCCATTTGTTGCAATATGAGCAGCAGGTTCCATTTCTGCTGATATAT 1267

QY 601 GCAATGGCAGCCACTTTCATTTTACTGTTTATTAAGGACGCGTCAATTTTGGAGAGAA 660

Db 1268 GCACAAGCTGTGAATTTACATTTGTTTATTTAAAGATGTCATCTCTTTTGGAGAGGA 1327

QY 661 TGGGATGTCACAACTACTATTAACTATTATGATGCTCAATGAAATGAACTTACTGCA 720

Db 1328 TGGGGATTCCACACAGGGGAAATTTCCACATATTATGACCGTCAATTTGGAACCTGCT 1387

QY 721 GAATATTTCTGATCAGTGTGTAAGTGGTATGAACTGTTTATAGCAAAATTTAAAGGCAG 780

Db 1388 AAGTACACTAATTAATGTAAGAACTTTGGTATATATACAGTTTATAGTGTGTAAGAGAA 1447

QY 781 AGCGCTAAACAAATGGTGTGACTATTAACCAATTTCCGTAGAGAAATGACACTGGCGTTTA 840

Db 1448 AATACTGAAAGTTGGTTAAGATATCATCAATTTCCGTAGAGAAATGACTTTAGTGTATTA 1507

QY 841 GATGTTGTCATTTATTTCCAAATTTATGACACGACGCTACCCATGGAAGAAAGCA 900

Db 1508 GATGTTGTGGCGCTATTTCATATTATGATGATGACTTTTATCCACGCGGATCAAAACCA 1567

QY 901 CAACTAACAGGGAGTATATACAGATCCACTGGGCGCGTAAACGCTGCTTCAATTTG-- 958

Db 1568 CAGCTTTACAGTGGAGTATATACAGATCCGATTTGTAATCCACGACGTAATGTTGGA 1627  
Qy 959 -----GTTCTCGGTATGACAAAGCACCTTCTTCGGAGTGATAGATCATCGGTT 1008  
Db 1628 CTTTGGCGAGGTTGGGTACTAATCCGTATATACCTTTCTGAGCTCGAAATGCGCTTC 1687  
Qy 1009 ATTTCGACACCCCATGATTTGATATATTAACGGGACTCACAGTGATATACAAATCAAGA 1068  
Db 1688 ATTGCGCCACCATCTTTTGTATAGGCTGATATAGCTTAACATCAGCAGTATCGATTT 1747  
Qy 1069 AGCATTTCTCCGCTCGCTATATTAAGACATGCGGTGCTCATCAATATAGCTACCATCGT 1128  
Db 1748 CCAGTTTCTATCTAAT---TTTATGGAATTTATGCTCAGGACATACGTTACGCCGTAGTTAT 1804  
Qy 1129 GTCAGTAGGGGTAGTAACTTTCAACAAATGATGGAAGTAACTTAATCAAAATCTACACGACT 1188  
Db 1805 CTGAACGATTCAGCAGTACAAGAAGATAGTTATGG-----CCTAATTAACACCAAGA 1858  
Qy 1189 AGTACCTTTGATTTTACGAATATGATATTTACAAGACTCTATCAAGAGTACAG-TACT 1247  
Db 1859 GCAACAAATTAATCCCGAGTTGATGNAACAAACCGCATAGAGTCAACGGCAGTAGATTT 1918  
Qy 1248 CTTTGATATTTGTTTACCTGGTTATACGTATATATTTTTTGGAAATGCCAGAAGTCGAGTT 1307  
Db 1919 CGTCTCGCATGTAGTATATATGCGGTGAATAGAGCTTCTTTTGTCCAGGAGGCTTG 1978  
Qy 1308 TTTTCAGTAAACCAATGNAATATACCAGAAAGAGCTTAAGATATATCCAGTTTCCAA 1367  
Db 1979 TTTAATGGT-----ACGATTTCTCTCGCTTAATGGAGGATGTAG 2016  
Qy 1368 AGATATATAGCGAGTACAAGATTCGGAAATAGAAATTAACCTCCAGAACTTCAGATCA 1427  
Db 2017 AGATCTATGATACAAATGATGAATTAACACGAGTAGAAGTACCGAGTTCAACCCA 2076  
Qy 1428 ACCAAATATAGTCAATATAGCCATAGATTAATGTCATATACAAAGTATTTCCCGCGAGG 1487  
Db 2077 TAGACTATCTCATGTACCTTTTCTTTTAGCTT-----TCAACTTAATCAGGCTGATCTAT 2130  
Qy 1488 TAACACTACCGGATAGTACTGTATTTCTTGACACATACGAAATGTCAGATTTAAACAA 1547  
Db 2131 AGCTAATGAGGAAGTGTACTTACTTATGTTTGGACCGCTCGTGATGTGGACCTTAATA 2190  
Qy 1548 TACAATATATTCAGATAAATCACTCAAAATTCGCGCGTTAAATGTTGGATAATTTACC 1607  
Db 2191 TAGATATACCCAAATAGATATACAAATTAACCATTTGGTAAAGGCACTGCACTGTTTC 2250  
Qy 1608 GTTTGTTCCAGTGGTAAAGGACAGGACATACAGGAGGGGATTTATTAAGTATATAG 1667  
Db 2251 GGCTACTACGCTTTAAAGTCCAGATTTTACAGAGGGGATTAATCTCC---GAGAAC 2307  
Qy 1668 AGTACTGGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCTAGCATTAAGAAAGC 1727  
Db 2308 AACTAATGGCACATTTGGAACGTTAAGAGTAAACGGTTAATTCACCATTAACACAAATA 2367  
Qy 1728 AGGGAATATCGTGAAGTACGATATGCTACTGATGACAGATATTTGATTTGATGATTA 1787  
Db 2368 TCGCTTAAGAGTTCTGTTTGGCTTCAACAGGAATTTTCAATTAAGGGTACTCCGTGGAGG 2427  
Qy 1788 CGATGC-----TCAGATTCAGATGCCMAAACAATGAACCCAGAGTGAGGATCTGACATC 1841  
Db 2428 GGTTCCTATCGGTGATGTTAGATTAGGAGCACATGACAGAGGGGAGGACTAATCTTA 2487  
Qy 1842 TAAACCTTTAAAGTTGCGATGCTATCAACA-----TTAAATTTAGCAACAGATAG 1895  
Db 2488 CGAATCCTTTTCAAGAGAGTTTACTACTACTGCTCGCTTCAATCCGCGCTTTTACATT 2547  
Qy 1896 TTCGCTAGCATTTGAACATATTTTGTGTGAGACCCCTAATTTCAACATATCTGCTATAGT 1955  
Db 2548 TACACAGCTCAAGAGATTTCAACAGTGAATGACAGAGGTGTTAGCACCGGTGTTGAATA 2607  
Qy 1956 TTAACGTTGACCGAATCGAATTTTCACTCCAGTATGACATATGAAGCGGAACAGATTT 2015

Db 2608 TTATATAGATAGATTTGAAATTTGCTCCTGTGAATCCGGCACGAGAAGCGGAAGAGATTT 2667  
Qy 2016 AGAACGACGGAAGAAGCAGATGAATGCTTGTGTTTACGAATACAAAGATGGCTTACGACC 2075  
Db 2668 AGAACGCGGAAGAAGCGGTGGAGCTTGTGTTTACGTAACAGGACGGAATACAGGT 2727  
Qy 2076 AGCGCTAACCGGATTTAAGTGAATCAAGCGGCAAACTTTAGTGAATGCTTATCCGATGA 2135  
Db 2728 AATGTGACAGATTTAAGTGAACCAAGCGGCAAAATTTAGTGTCTATCCGATGA 2787  
Qy 2136 TTTGTATCCAATGAAACAGATTTGTTATGTCGAGTGAAGAGGCAAAACGCTCTAG 2195  
Db 2788 ACAATATGGGATGACAAAAAGATGTTATGGAAGCGGTAAAGCGGCAAAACGCTCTAG 2847  
Qy 2196 TGAGGCACTAATTTGCTTCAAGATCCAGATTTCCAGAGATAT-----GGAGAAA 2249  
Db 2848 CCGCAACGCAACTTACTTCAAGATCCAGATTTTAAATCAATATAGTACAGAGAGAA 2907  
Qy 2250 TGGCTGGACCGCAAGTACGGGAATTTGAGTTATAGAAAGGAGTCTTTTATTCAAAAGGCG 2309  
Db 2908 TGGCTGGAAGCAAGTAAACGGTGTACTATTAGCGAGGCGGTCCATTTCTTTAAGGTG 2967  
Qy 2310 TTATCTACGCCCTACAGGTGCGAGAGAAATAGATACGGAACGATCCAAAGCTATCTGTA 2369  
Db 2968 TGCACCTTCAGTTAGCAAGCGCAAGA-----GAAAATTTATCCAACTATCATTTA 3015  
Qy 2370 TCAAAAGTGAAGGAGGTGTTAATAAACCATACACAGATATAGATTCAGAGGCTTTGT 2429  
Db 3016 TCAAAAGTGAAGTATCGGTGTTAAAGCTTTATACGCTATAGACTAGATGGATTTGT 3075  
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Qy 2490 AAATGTACCGGATGATTTGCTGCCAGATGATCTCTCTGTTAACTCGGATGGTATCAA 2549  
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Qy 2602 -----TCTGTGAGCGCATGAGTTCTCTATTCTCTATTGATACAGGTGAATCGA 2651  
Db 3256 TTGCTGTGAGCGGCTCAACACATGAGTTTCTCTCTATATATACAGGGAATCAA 3315  
Qy 2652 TTACAATGAAATGCGGAATATGGGTTTGAATTTAAGATTTACGGAACCCAGAGGATATGC 2711  
Db 3316 TGCAAGTGTAGATCAGGCAATTTGGGTTGTTAATAAAGTTGGAACAAACAGATGGGTATGC 3375  
Qy 2712 AACACTCGGAAACCTTAGAATTTGGTCAAGAGGACCTTTATCAGGAGACGATTTAGAAGC 2771  
Db 3376 GACGTTAGGAAATCTTGAATTTGGTAGAGGTTTGGGCAATTTATCGGGTGAATCTCTAGAAGC 3435  
Qy 2772 CTTGCAAGAGAGAACCAACAGTGAAGATTTCAATGACAAAGACCGTGAAGAACACA 2831  
Db 3436 GGAACAAGAGATATATGCGAAATGGAATGAGAGCTAGAGAGAAACCGTGAAGAAATGA 3495  
Qy 2832 TAGAAGGTATATGGCATCGAAACAAAGCGGTATGATCGTTTATATGCGGATTTACAGATCA 2891  
Db 3496 TCGTGTGATTTAGCTGGAACAGCAATTTAATCATCTGTTTGTAGACTATCAAGATCA 3555  
Qy 2892 GCACTGAATCTGATGATAGATTTACAGATCTTACTGCGGCGCCCAAGATCTGATACAGTC 2951  
Db 3556 ACAATTTAAATCAGAAATTTGGGCTAGCAGAAATTAATGAAGCTTCAAAATCTTTGTAGAGTC 3615  
Qy 2952 CATTCCTTACGTATATAAGAAATGTTCCGAAATACAGGAGTGAACCTATACCAAGTT 3011  
Db 3616 AATTTCCGGGTGATATAGTATACACTATTACAGATTTCTCGGATTAACCTAGAAATTTA 3675  
Qy 3012 TACAGAAATTAACAGATCGACTCCAAACAGCGGTGAGTTTGTATGATCAGCGAAATGCCAT 3071  
Db 3676 CACAGGTTATCCGATCGCTTACACAGCATCGTATCTGTATACGTCTAGAAATGCGGT 3735





Db 961 CTTTGGCGAGTTGGGGTACTAATCCCTATAATACCTTTTCTGAGCTCGAATAATGCCTTC 1020  
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Qy 1069 AGCATTTCTTCGCTCGCTATATAAGACATTTGGGCTCGTCAATCAATAAGCTACCATCGT 1128  
Db 1081 CCAGTTTCACTAAT---TTTATGGATTAATTTGGTCAGGACATAGCTTTACGCGTAGTTAT 1137  
Qy 1129 GTCAAGTAGGGGTAGTAACTTTCACAAATGTATGGAAGTAACTAATCAAAATCTACACAGACT 1188  
Db 1138 CTGAACGATTCAGCAGTACAGAAGATAGTTATGG-----CCTAATTAACAACCAAGA 1191  
Qy 1189 AGTACCTTTGATTTACGAATTAATGATTTTACAAGACTCTATCAAGAGTATGAG-TACT 1247  
Db 1192 GCACAAATTAATCTGGAGTTGATGGAAACAAACCGCATAGAGTCAACGGCAGTAGATTTT 1251  
Qy 1248 CCTTGATATTTGTTTACCTCGTTATACGTATATATATTTTGGAAATGCCAGAAGTCGAGTT 1307  
Db 1252 CGTCTGCAATGATAGTATATATGGGTGAATAGACTTCTTTTGGTCCAGAGGCTTG 1311  
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Db 1524 TAGGATATACCCAAATAGAAATTAACAATTAACCAATTTGGTAAAGGCATCTGCACCTGTTTC 1583  
Qy 1608 GTTTGTTCCAGTGGTAAAGGACGAGACATACAGAGGAGGATTTTATTAAGTATATATAG 1667  
Db 1584 GGGTACTACGGTCTTAAAGGTTCCAGATTTACAGAGGGGGTATATCTCC---GAAGAAC 1640  
Qy 1668 AAGTACTGTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCTAGCATTTAGAAAAGC 1727  
Db 1641 AACTAATGGCACATTTGGAACTTAAAGATTAACAGTTAATTCACCATTAACACAAAGATA 1700  
Qy 1728 AGGGAATATCGTGAAGTACAGATATGCTACTGATGCGAGATTTGTATGTGATGTAA 1787  
Db 1701 TCGGTAAGAGTTCTGTTTCTTCAATCAGGAATTTTTCAGCATTAAGGATATCTGCGTGAAA 1760  
Qy 1788 CGATGCTCAGATTCAG-----ATGCCMAAACAATGNAACCCAGGTGAGGATCTGCATC 1841  
Db 1761 TACCTCTATAGCTTATCAAGATTTGGAGTACATGAAACAGAGGACAGGAACTTA 1820  
Qy 1842 TAAACTTTTAAAGTTGCGAGTCTATCAACATTAATTAATTTAGCAACAGATATGCTGCT 1901  
Db 1821 CGAATCATTTGTCAAGTGAGTTCTACTAATCAAGAGGCTGCTGCTTTTACATTTAC 1880  
Qy 1902 AGCATTTGAACATAAATTTAGTGAAGACCTTAATTCACATTAATCTGTTATAGTTTACGT 1961  
Db 1881 ACAAGCTCAAGAAAATTTAAACATCTCTGCAAGAGGTTGTAGCACCGGTAGTGAATTTT 1940  
Qy 1962 T---GACCGAATCGAATTCATCCAGTAGATGAGACATATGAAGCGGAACAAGATTTAGA 2018  
Db 1941 TATAGTAGAATTTGAATCATCTCTGTGAACCCGCGACGGAAGCAGAGGATTTAGA 2000  
Qy 2019 AGCAGCGAAGAACGATGAATCCCTTGTGTTTACGAATACAAAAGATGGCTTACGACCAGG 2078  
|||||

Db 2001 AGCAGCGAAGAAAGCGGTGGCGAATCTTGTTTACAGTACAGGACGGATTTACAGGTAAA 2060  
Qy 2079 CGTAAACGGATTTAAGATGAATCAAGCGGCAAACTTTAGTGGAAATGCTATCGGATGATTT 2138  
Db 2061 TGTGACAGATTTATCAAGTGGACCAAGCGCAAAATTTAGTGTCTATGCTTATCCGATGAACA 2120  
Qy 2139 GTATCCAAATGAAAACGATTTGTTATTTGATGCAAGTGAAGAGGCAAAAACGCTCTAGTGA 2198  
Db 2121 ATATGGGCAATGACAAAAGATGTTATGGAAGCGGTGAAGCGGCAAAAACGCTCTAGCCG 2180  
Qy 2199 GGCACGTAAATTTGCTTTCAAGATCCAGATTTCCAAGAGATAAAT-----GGAGAAAATGG 2252  
Db 2181 CGAAACCACTTACTTTCAAGATCCAGATTTTAATACAATCAATAGTACAGAAGAGATGG 2240  
Qy 2253 CTGGACGGCAAGTACCGGAAATGAGGTTATAGAAGGGATGCTTTATTTCAAAGGGGCTTA 2312  
Db 2241 CTGGAAGGCAAGTAAACGGTGTACTATTAGCGAGGCGGTCCATTTCTTTAAAGGCTGTCG 2300  
Qy 2313 TCTACGCTTACCAGGTGCGAGAGAAATAGATACGGAAACGTTATCCAACGCTATCTGTATCA 2372  
Db 2301 ACTTCAGTTAGCAAGCGCAAGA-----GAAAATTTATCCAACATACATTTATCA 2348  
Qy 2373 AAAAGTAGAGGAGGTGTTATTAACCAATACATACAGATATAGATTCGAGAGGTTTCTCGG 2432  
Db 2349 AAAAGTAGATGATCGGTGTTAAAGCTTTATACAGCTATAGACTAGATGGATTTCTGAA 2408  
Qy 2433 AAGCAGTCAAGATTTGGAATTTTCAATTTCTGTCATCAAAACGAAACCGAATTTGTTAAAAA 2492  
Db 2409 GAGTAGTCAAGATTTAGAAATTTGATCTCATCCACCATCAATAAGTCCATCTTTGTTAAAAA 2468  
Qy 2493 TGTACCGGATGTTTGTCTGCCAGATGATCTCTCTGTTAACTCGGATGTTAGTATCAATCG 2552  
Db 2469 TGTACAGATATTTAGTATCTGATCTACTTACAGATGTTCTTTCGACGGGAATCAACCG 2528  
Qy 2553 ATGACGCGAACAAGATATGTAATAGCCGTTTAGAAGTAGAAAAACCGT-----2601  
Db 2529 TTGTGATGAACAGCATCAGSTAGATATGATGATGCGAGCATCATCCAATGCGATTG 2588  
Qy 2602 -----TCTGGTGAAGCGCATGATTTCTTATTTCTTATGATACAGGTGAATTCGATTA 2654  
Db 2589 CTGTGAAGCGGCTCAACACATGATGTTTTCTTCTATATTAATACAGGGGATCTAAATGC 2648  
Qy 2655 CAATGAAATGACAGAAATATGTTGATTTAAGATTTACGGACCCAGGAGGATATCAAC 2714  
Db 2649 AAGTGTAGATCAGGCAATTTGGGTTGTTTAAAGTTTGAACAACAGATGGGTATCGGAC 2708  
Qy 2715 ACTCGGAAACCTAGAAATTTGGTGAAGAGGACCTTTTATCAGGAGAGCGATTTAGAACGTT 2774  
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Db 2769 ACAAAAGAGATAATGGAATGGAATGCAAGCTAGGAGAAAGAAACGTCGAGAAATAGATCG 2828  
Qy 2835 AAGGTATATGCGATCGAAACAAGCGGTAGATCTTTATATGCGGATTTACAGATCAGCA 2894  
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Qy 2895 ACTGAATCTGTATGAGATTAAGATCTTACTCGGCGCCCAAGATCTGATACAGTCCAT 2954  
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Db 2949 TTTCCGGTGTATATAGTGATACATTTACAGATTTCTCGGATTAACACGAAATTTTACAC 3008  
Qy 3015 AGAATTTAACAGATCCACTCCAAACAGCGTGGAGTTTGTATGATCAGCGGAAATGCCATACC 3074  
Db 3009 AGAGTTATCCGATCCGTTTACAAACAGCATTCGATCTGTATACGTCTAGAAATTCGGGTGCA 3068  
Qy 3075 AAATGCTGATTTTGAATTTGGGTTAAGTAAATTTGGAATGCAACGCTGCGGTGAGAGTACA 3134  
Db 3069 AAATGGAGACTTTACAGTGGTCTAGATAGTTGGAAATACAACTATGATGTCATCGGTTCA 3128  
|||||

QY 3135 ACAAATCAATCATCATCTGCTCTTGTGATTCCTCAAACTGGGATGAGCAAGTTTCGCAACA 3194  
DB 3129 GCAAGATGCAATATGCAATTTCTTAGTTCTTTCGATTTGGGATGCAAGTTTCCTCAACA 3188  
QY 3195 GTTACAGTTCAACCGAATCAAGATATGTGTTACGATTTACTGCGAGAAAGAGGGGT 3254  
DB 3189 ATTGAGAGTAAATCCGAATTTGTAAGTATGTTTACGTTGTGACAGCAAGAAAGTAGGAGG 3248  
QY 3255 AGGAATGGRATGTAAAGTATCCGATGATGGTGGAAATCAACAGCAAGCACTTACTTTTAG 3314  
DB 3249 CGGAGATGATACGTCACAAATCCGAGATGGCGCTCATCACCAGAAACTCTTACATTTAA 3308  
QY 3315 TCGAAGCGATTATGATACAAATCGGAATGTATAATACGCAAGTGTCCAATACAAATGGATA 3374  
DB 3309 TGCATGTGACTACGATGTAATGGTACGTATGCTCAATGACAAATTCGTATATACAGAGA 3368

## RESULT 15

US-08-542-921-1  
; Sequence 1, Application US/08542921  
; Patent No. 5736514  
; GENERAL INFORMATION:  
; APPLICANT: IIZUKA, TOSHIHIKO  
; APPLICANT: TAGAWA, MICHIO  
; APPLICANT: ARAI, SATOSHI  
; APPLICANT: NIIZEKI, MASATSUGU  
; APPLICANT: MIYAKE, TOSHIRO  
; TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL  
; TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/542,921  
; FILING DATE: 13-OCT-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 276082/94  
; FILING DATE: 14-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 49-209-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3759 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis var. japonensis  
; STRAIN: N141  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 47..3556  
US-08-542-921-1

Query Match 23.4%; Score 848.6; DB 1; Length 3759;  
Best Local Similarity 56.2%; Pred. No. 5.4e-176;  
Matches 1930; Conservative 0; Mismatches 1414; Indels 93; Gaps 14;

QY 1 ATGAGTCCAATATCAAAATGAATATGAATATATAGATGGGACACCTTCTACTTCTGTA 60  
DB 47 ATGAATCGAAATATCAAAATGAATATGAATATATAGATGGGACACCTTCTACTTCTGTA 106  
QY 61 TCCAATGATTTCAACAGATCCCTTTTGGCGAATGAGCGCAACAAATGCGCTACAAATATG 120  
DB 107 GCAGATGATTTGTAATATATCCCTTTCACAGATGATCCGATGCTGGATGCGAAATATG 166  
QY 121 GATTATAAGATTTATTTAAATATGTCGCGGAAATCTAGTGAATACCCCTGGTTCACCT 180  
DB 167 AACTATAAGGAATTTTACAAACGATATGCTGGAGACTATACAGATCCCTTCTATTAACT 226  
QY 181 GAAGTACTTGTAGCGGACAGATGAGCTAAGCGCGCAATGAGCGCAATGATATAGTAGGTAATTA 240  
DB 227 AACTTATCTGTTAGTGGAAAGATGTAATACAACTTGGAAATTAATATGTTAGGGAGATTA 286  
QY 241 CTATCAGGTTTGGGCTCCCAATTTGTTGGGCGGATAGTGTCTTTATATCTCAACTTATT 300  
DB 287 CTAAGCTTTTGGATTTCCCTTTCTAGTCAATGGGTTACTGTATATACCTATCTTTTA 346  
QY 301 GATATTCTGTGGCTTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360  
DB 347 AACAGCTTGTGGCGGATGACGAGAAATCTGTATGGGACGCTTTTATGGAGAGTAGAA 406  
QY 361 GAATCTAATTAATCAAAATATAGCAGAAATATGCAAGGAATAAAGCGCTTTCGGAATGAA 420  
DB 407 GAACTTATGATCAAAATATCTCAGAGCAGTAAGGAGTAGGCAATGGATGACCTAACT 466  
QY 421 GGATAGTATTAATTAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480  
DB 467 GGATTAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 526  
QY 481 AATGGTTCAAGAGCTTTACGAGATGTCGGAATCGAATTTGAAATCCTGGATAGTTTATT 540  
DB 527 AATGGCGCAAGGCACTCTTAGTTTCTC---AGCGATTTAACTTTTAGATAGCTATT 583  
QY 541 ACGCAATATATGCCATCTTTTA-----GAGTGACAAATTTTGAAGTACCATT 588  
DB 584 ACACAATTTATGCCAAGCTTTGGCTCTGGTCTCGGAAAGTCAAAATTTATGCAACTATATTA 643  
QY 589 CTTACTGTATATGCAATGGCGACCAACCTTCATTTACTGTTATTAAAGGACGCTCAATT 648  
DB 644 CTTCCAGTATATGCAACAGCAGCAAACTTCATTTGTTATTATTAAAGAGTGCAGACAT 703  
QY 649 TTTGGAGAAAGATGGGATGGTCAACAACTACTATTAACTATTATGATCGTCAAAATG 708  
DB 704 TATGGAGCTAGATGGGCTGAAATCAAACTCAATAGATCAATTCCTCTCGTCAACA 763  
QY 709 AAATTTACTGCAGAAATATCTGATCACTGTGTAAAGTGGTATGAACTGGTTTACGAAAA 768  
DB 764 AGCTTACTCAGACTTATACAAATCAATTTGTTTACTGCGTATATGATGATGAGGAA 823  
QY 769 TTAAGGCGCAGCGCTTAACAACTGGTGGTGACTATACCAATTCGCTAGAGAAATGACA 828  
DB 824 TTAAGAGGCAACACCGCTGAGAGTTGGTTAAATACAACTCAATATCGTAGAGAAATGACT 883  
QY 829 CTGGCGGTTTTAGATGTTGTCATTTCCCAATTTATGACACACGACCGCTACCCAATG 888  
DB 884 TTGACGGCAATGGATTTAGTGGCAATTTCCCATTTATTAATTTACGCAATATCCAGAT 943  
QY 889 GAAACGAAAGCAACAACTAAAGGAAAGTATATACA-----GATCCACTG 933  
DB 944 GGGACAAATCTCAACTTACACGCTGAGGCTTATACAGATCCGATGCGATTTGATCCACTG 1003  
QY 934 GCGCGGTAAACGTTCTTCAATTTGGTTCCTGGTATGCAAGACACCTTCTTTTGGAGTG 993  
DB 1004 GAACAACCAACTACTCAATTTATGCGATCATGGTACATTAACCCAGCTTTTCGAAATCAT 1063  
QY 994 ATGAATCATCCGTTATTTCGACACCACCCCATGTTTGTATTATATAACGGGACTCACAGTG 1053

|    |      |  |      |
|----|------|--|------|
| Db | 1064 | TTGAAATTCCTCTGTACTAGAAATTCATTGAATTCGTCGCCCGCACCTTTTGTGAAGGTTA      | 1123 |
| Qy | 1054 | TATACACAATCAAGAAGCATTTCTTCGCGTCGTATATAAGACATTTGGGCTGTCATCAA        | 1113 |
| Db | 1124 | AGTAATTTGCCAAATTTTAGTTAATTAACCAACAACGAGTAGCGCTTGGCGTGGGTCAAGG      | 1183 |
| Qy | 1114 | ATAAGCTACCATCGTCTCAGTAGGGGTAGTAATCTTCAACAANAATGATGAACTAATCAA       | 1173 |
| Db | 1184 | GTAAGATACCAATTAATTTGCATAGTCTCTATAATACAGGAAAAAGTTACGCGCTCCTCAGT     | 1243 |
| Qy | 1174 | AATCTACACAGCACTAGTACCTTTTGATTTTACGAAATTTATGATATTTTACAGACTCTATCA    | 1233 |
| Db | 1244 | GATCCGTTGGAGCTAATA---TCAATGTTCAAAATAATGATATTTATCAGATTAATTCG        | 1300 |
| Qy | 1234 | AAGGAT-GCAGTACTCCTTGTGATATGTTTACCCTGGTTATACGTATATATTTTTCGGAAT      | 1292 |
| Db | 1301 | CAGGTTAGCAATTTTGCTAGTCTCTGTTGGCTCATCATATAGTGTGTTGGGACACTAATTTT     | 1360 |
| Qy | 1293 | GCCAGAAGTCGAGTTTTTTCATGTGTAAACCAATTTGAATAATACAGAAAGAGTTAAAGTA      | 1352 |
| Db | 1361 | TATTTGAGTTTCAGGACAAGTAAGTGGGATTTCCAGGATATATACACGAAGGTATACCAGCA     | 1420 |
| Qy | 1353 | TAATCCAGTTTCCAAAGATATATATAGCGAGTAC-AAGAGATTCGGAAATAGAAATTTACCTC    | 1411 |
| Db | 1421 | GTTTGTCTTCAACACGAAATTCACCTGATGAGTTACCAAGCTTTAATCCGGAAGGAGAT        | 1480 |
| Qy | 1412 | CAGAAACTTTCAGATCAACCAAAATTTATGAGTCATATAGCCATAGATATGTCATATCACAA     | 1471 |
| Db | 1481 | ATCATTAGAATAATATAGTCAATAGGTTATCTCATATAACCAATATCGTTTCAAGCACT        | 1540 |
| Qy | 1472 | GTATTCGCCGACGGGTAACT-ACTCCGGAATAGTACCTGTATTTTCTTGGACACATCGA        | 1530 |
| Db | 1541 | CAAAAGTGTAGTCCATCAACTGTTAGCGCAAAATTTTACCTACTTGTGTATGGAACGATCGA     | 1600 |
| Qy | 1531 | AGTCAGAGTTTAAACAATACATATATTCAGATAAATCACTCAAAATTCGGCCGCTTAAA        | 1590 |
| Db | 1601 | GATGTGGACCTTGATTAATACCAATTTACTGCGAAATCAAAATTCACAACTACCAATTTAGTAAAG | 1660 |
| Qy | 1591 | TGTTGGGATAATTTTACCGTTTGTTCAGTGGTAAAAAGGACCGAGCATACAGCAGAGGGAT      | 1650 |
| Db | 1661 | GCATATGACTAAGTAGTGTGTCTACTGTGCTGGAAGTCCAGANTTCAAGGAGAGAT           | 1720 |
| Qy | 1651 | TTATTAAGTATAATAGAAAGTACTGTGTTCTGTAGGAACCTTATTTCTAGCTCGATATGCG      | 1710 |
| Db | 1721 | GTAAATCCGAAGAAACAAATCTGTGTGATTCGGAGCAATRAAGGTGTGCGTCACTGGACCG      | 1780 |
| Qy | 1711 | CTAGCAATTAGAAAAGCAGGGAATATCGTGTGAAGCTGAGATATGCTACTGATCGAGAT        | 1770 |
| Db | 1781 | CTAAACACACGATATCGCATAAAGTTCCGTTATGCTTTCGACAAATAGATTTTGTGATTTCTTT   | 1840 |
| Qy | 1771 | ATTGTATTGCATGTAAACGATG---CTCAGATTAGATGCCCCAAAAACAATGAACCCAGGT      | 1827 |
| Db | 1841 | GTAAACCGTGGAGGAATCTACTATAAATAATTTTAGATTTACAGTCAATGAACAGGGGA        | 1900 |
| Qy | 1828 | GAGGATCTGACATCTAAAACTTTTAAAGTTGACAGATGCTATCAACAATTTAAATTTAGCA      | 1887 |
| Db | 1901 | CAGGAATCAAGATATGAAATCTTATCGTACTGTAGAGTTTACAATCTCTTTTAATTTTACA      | 1960 |
| Qy | 1888 | ACAGATAGTTTCGTAGCATTTGAAACATAATTTTAGTGTGAAGACCCTAATTCACAAATATCT    | 1947 |
| Db | 1961 | CAAAAGTC--AAGATATAATTCGAACATCTATCCAGGA-----CTTAGTGGAAAT            | 2008 |
| Qy | 1948 | GGTATGTTTACTGTTGACCGGAATCGAATTCATCCAGTAGATGAGACATATGAAGCGGA        | 2007 |
| Db | 2009 | GGGGAAGTATACTTGATAGAAATTTGAATTCATCCCTGTGAAACCCGCAACGGAAGCAGAA      | 2068 |
| Qy | 2008 | CAAGATTTAGAAACGACGGAAGAAAGCAG---TGAATGCTTTTGTATACGAATACAAAGAT      | 2064 |
| Db | 2069 | GAGGATTTAGAGACGGAAGAAAGCGGTAGSCAGNACTTGTGTTTACAGTCAAGGGAC          | 2128 |
| Qy | 2065 | GGCTTACGACCGGCGTAAACGGATTAATGAAGTGAATCAAGCGGCNAATCTTAGTGGAAATGC    | 2124 |

|    |      |   |      |
|----|------|---|------|
| Db | 2129 | GGATTACAGGTAAATGTGACAGATTATCAAGTGGACCAAGCGCGAAATTTAGTGTCAATGC   | 2189 |
| Qy | 2125 | CTATCGGATGATTTGTATCCAAATCAAAAACGATTGTTATTTTGATGTCAGTGGAGAGGCA   | 2184 |
| Db | 2189 | TTATCCGATGAACATATGGGCAATGACAAAGAAGATGTTATTCGAGCGGTAGAGCGGCA     | 2248 |
| Qy | 2185 | AAACGCCTCAGTGGAGCGCACTAAATTTGCTTCAAGATCCAGATTTTCCAGAGATAAAT---  | 2241 |
| Db | 2249 | AAACGCCTCAGCGCGGAAACGCAACTTACTTCAAGATCCAGATTTTAAATCAACATCAATAGT | 2308 |
| Qy | 2242 | ---GGAGAAAATGGCTGGACCGCAAGTACGGGAAATGGAGTTTATAGAAGGGATGCTTTA    | 2298 |
| Db | 2309 | ACAGAAGAGATGGCTGGAGGCAAGTAAACGGTGTACTATTTAGCGAGGCGGTCCATTC      | 2368 |
| Qy | 2299 | TTCAAAGGCGGTATCTACGCCCTACCAAGTGCAGAGAAATAGATACGGAACGATATCCA     | 2358 |
| Db | 2369 | TTTTAAGGTCGTCACCTTCAGTTAGCAGCGCAAG-----GAAATTTATCCA             | 2416 |
| Qy | 2359 | ACGTATCTGTATCAAAAAAGTAGAGGAGGTGTTATTAACCATAACAAGATATAGATTG      | 2418 |
| Db | 2417 | ACATACATTTATCAAAAAAGTAGATGCATCGGTGTTAAAGCCTTATACACGCTATAGACTG   | 2476 |
| Qy | 2419 | AGAGGGTTGTCCGAGACGATCAAGGATGGGAAATTTTACAAATTCGTATCAAAACGAAC     | 2478 |
| Db | 2477 | GATGGGTCGTGAAGAGTAGTCARGATTTAGAAATTTGATCTCATTCACATCATATAAGTC    | 2536 |
| Qy | 2479 | CGAAATTTGAAAAATGTACCGCATGATTTGCTGCCAGATGTATCCTCTTAACTCGGAT      | 2538 |
| Db | 2537 | CATCTTGTGAAAAATGTACCAATATTTAGTATCCGATACCTTCTCGGATGGTCTTGC       | 2596 |
| Qy | 2539 | GGTAGTATCAATCGATGCGAGCGAAACAAAGATATGTGAATAGCCGTTTAGAAGTAGAAAAAC | 2598 |
| Db | 2597 | ACTGGAATGAATCGATGTGAGGAAACAAACAGATGGTAAATGCCAACTGCAACACAGAAT    | 2656 |
| Qy | 2599 | CGT-----TCTGGTGAAGCGCATGAGTTCTCTATTCTTATTGAT                    | 2637 |
| Db | 2657 | CATCATCCGATGGATTTGCTGGAACGGCTCAAAACACATGAGTTTCTTCTTATATTAAT     | 2716 |
| Qy | 2638 | ACAGGTGAAATCGATTACAAATCGAGGAATATGGTTGGATTTAAGATTACGGAC          | 2697 |
| Db | 2717 | ACAGGGGATCTAAATGCAAGTGTAGATCAGGGCATTTGGGTTGTATTAAGAATTGCAACA    | 2776 |
| Qy | 2698 | CCAGAGGGATATGCAACACTCGGAAACCTAGAAATTTGGTCGAAGAGGGACCTTTATCAGGA  | 2757 |
| Db | 2777 | ACAGATGGGTATGCGACGTTAGGAAATCTTGAATTTGGTAGAGTTGGGCCATTTATCGGT    | 2836 |
| Qy | 2758 | GAGCGATTAGAACGCTTCCAAAGAGAGAAACAAAGTGGAGATTCAAATGACAGAGAAGA     | 2817 |
| Db | 2837 | GAATCTCTAGAACCGGAAACAAAGAGATTAATGCGAAATGGAAATGCGAGAGCTAGGAAGAAA | 2896 |
| Qy | 2818 | CGTGAAGAAAACAGATAGAAGGTATATGGCATCGAAACAGCGGTAGATCGTTTATATGCC    | 2877 |
| Db | 2897 | CGTGCAAAAATAGATCGTGTGTATTTAGCTGCAAAACAGCAATTAATCATCTGTTTGT      | 2956 |
| Qy | 2878 | GATTATCAGGATCAGCAACTGAATCCTGATGTAGAGATTTACAGATCTTTACTCGCGCCAA   | 2937 |
| Db | 2957 | GACTATCAAGATCAACAATTAATCCAGAAATTTGGGTAGCAGAGAAATTAATGAAGCTTCA   | 3016 |
| Qy | 2938 | GATCTGATACAGTCCATTCCTTACGTATATACGAATAATGTTCCCAAGAAATACACAGGATG  | 2997 |
| Db | 3017 | AATCTTGTAGAGTCAATTTCCGGTGTATATAGTGTATACACTATTACAGATTCCTCGGAT    | 3076 |
| Qy | 2998 | AACTATACGAGTTTACAGATTTACAGATCCAGCTCCAAACAGCGTGGAGTTTGTATGAT     | 3057 |
| Db | 3077 | AACTACGAAATTTACAGAGTTATCCGATCGCTTACAAACAGCATCGTATCTGTATACG      | 3136 |
| Qy | 3058 | CAGCGAAATGCCATACCAATCGGTGATTTTCGAAATGGGTTAAGTAAATTTGGAATGCAACG  | 3117 |
| Db | 3137 | TCTCGAATCGGTCGAAATGAGACTTTAACAGTGGTCTAGATAGTTGGAATACAACT        | 3196 |
| Qy | 3118 | CCTGCGGTAGAAGTACAAACAATCAATCATACATCTGCTCTTGTGATTCCAAACCTGGAT    | 3177 |
| Db | 3197 | ACGGATGATCGGTTTCAGCAAGATGGCAATATGCAATTTCTTAGTTCTTTTCGCAATCGGAT  | 3256 |



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2003, 00:48:42 ; Search time 6104 Seconds  
(without alignments)  
17264.295 Million cell updates/sec

Title: US-10-032-717-1  
Perfect score: 3621  
Sequence: 1 atgagtccaaataatcaaaa.....tgattgtagacgtagagtaa 3621

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_scs.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_on.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pin.\*
- 35: em\_htg\_rtd.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Match | Length | DB | ID         | Description         |
|------------|--------|-------|--------|----|------------|---------------------|
| 1          | 2565.2 | 70.8  | 3507   | 1  | BTU04365   | U04365 Bacillus th  |
| 2          | 2565.2 | 70.8  | 3507   | 6  | I25972     | I25972 Sequence 3   |
| 3          | 1812.2 | 50.0  | 3471   | 1  | BTU04364   | U04364 Bacillus th  |
| 4          | 1812.2 | 50.0  | 3471   | 6  | I25971     | I25971 Sequence 1   |
| 5          | 1185.6 | 32.7  | 3435   | 1  | AB089299   | AB089299 Bacillus   |
| 6          | 1180   | 32.6  | 3483   | 1  | BTU04366   | U04366 Bacillus th  |
| 7          | 1180   | 32.6  | 3797   | 6  | AR005118   | AR005118 Sequence   |
| 8          | 1180   | 32.6  | 3797   | 6  | AR050172   | AR050172 Sequence   |
| 9          | 1180   | 32.6  | 3797   | 6  | E06830     | E06830 DNA sequence |
| 10         | 900    | 24.9  | 3459   | 6  | AX189653   | AX189653 Sequence   |
| 11         | 883.4  | 24.4  | 3474   | 6  | AX100532   | AX100532 Sequence   |
| 12         | 883.4  | 24.4  | 4344   | 6  | A73540     | A73540 Sequence 4   |
| 13         | 883.4  | 24.4  | 4344   | 6  | AR031103   | AR031103 Sequence   |
| 14         | 883.4  | 24.4  | 5772   | 1  | BTCRV9COP  | BTCRV9COP           |
| 15         | 882.8  | 24.4  | 3471   | 6  | AR205864   | AR205864 Sequence   |
| 16         | 882.8  | 24.4  | 3471   | 6  | AX098657   | AX098657 Sequence   |
| 17         | 881.8  | 24.4  | 4344   | 6  | A73785     | A73785 Sequence 4   |
| 18         | 848.6  | 23.4  | 3759   | 1  | BACN141    | D85560 Bacillus th  |
| 19         | 848.6  | 23.4  | 3759   | 6  | AR000568   | AR000568 Sequence   |
| 20         | 848.6  | 23.4  | 3759   | 6  | AR053979   | AR053979 Sequence   |
| 21         | 848.6  | 23.4  | 3759   | 6  | AR055735   | AR055735 Sequence   |
| 22         | 848.6  | 23.4  | 3759   | 6  | E11968     | E11968 gDNA encodi  |
| 23         | 822.2  | 22.7  | 3453   | 6  | AR205865   | AR205865 Sequence   |
| 24         | 822.2  | 22.7  | 3867   | 1  | AB011496   | AB011496 Bacillus   |
| 25         | 740.4  | 20.4  | 4000   | 1  | BTCRVIX    | X75019 B.thuringie  |
| 26         | 740.4  | 20.4  | 12579  | 1  | BTCRVIX    | X58120 B.thuringie  |
| 27         | 734.2  | 20.3  | 3411   | 6  | AR205866   | AR205866 Sequence   |
| 28         | 733.6  | 20.3  | 3414   | 1  | BTU04368   | U04368 Bacillus th  |
| 29         | 731.4  | 20.2  | 3414   | 1  | BTU04367   | U04367 Bacillus th  |
| 30         | 726.6  | 20.1  | 4623   | 1  | BTU28801   | U28801 Bacillus th  |
| 31         | 726    | 20.0  | 3651   | 6  | AX138576   | AX138576 Sequence   |
| 32         | 726    | 20.0  | 3651   | 6  | AX146768   | AX146768 Sequence   |
| 33         | 721.4  | 19.9  | 3663   | 6  | AX088010   | AX088010 Sequence   |
| 34         | 721.4  | 19.9  | 3663   | 6  | AX088012   | AX088012 Sequence   |
| 35         | 718.2  | 19.8  | 3627   | 6  | AX138580   | AX138580 Sequence   |
| 36         | 718.2  | 19.8  | 3627   | 6  | AX146772   | AX146772 Sequence   |
| 37         | 712    | 19.7  | 4004   | 1  | BACCRVILIC | M64478 Bacillus th  |
| 38         | 712    | 19.7  | 4004   | 6  | A07236     | A07236 B.thuringie  |
| 39         | 706.8  | 19.5  | 3624   | 6  | AX138578   | AX138578 Sequence   |
| 40         | 706.8  | 19.5  | 3624   | 6  | AX146770   | AX146770 Sequence   |
| 41         | 681.6  | 18.8  | 3687   | 6  | AX189649   | AX189649 Sequence   |
| 42         | 681.6  | 18.8  | 4173   | 6  | AX098667   | AX098667 Sequence   |
| 43         | 678    | 18.7  | 3934   | 1  | BACCRVIE   | L32020 Bacillus th  |
| 44         | 678    | 18.7  | 3934   | 6  | AR068828   | AR068828 Sequence   |
| 45         | 678    | 18.7  | 3934   | 6  | I38760     | I38760 Sequence 3   |

ALIGNMENTS

RESULT 1  
LOCUS BTU04365  
DEFINITION Bacillus thuringiensis kumamotoensis PS50C(b) CryIII  
ACCESSION U04365  
VERSION U04365.1  
KEYWORDS GI:436834  
SOURCE  
ORGANISM Bacillus thuringiensis.  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 3507)  
AUTHORS Narva,K.E. and Fu,J.  
TITLE Novel Coleopteran-Active Toxins from Bacillus thuringiensis

BTU04365 3507 bp DNA linear BCT 27-AUG-1994  
Bacillus thuringiensis kumamotoensis PS50C(b) CryIII  
delta-endotoxin gene, partial cds.





Db 1441 TCATATAGCCATAGATTAGGTCATATTAACATTAATTAATCTCCA---GTTCAACTAGCACG 1497  
Qy 1501 TTAGTACCTGTTATTTCTTGGACACATCGAAGTCGAGATTTAAACAATAATATATCA 1560  
Db 1498 TATGTACCTGTTATTTCTTGGACACATCGAAGTCGAGATTTAAACAATAATATATCA 1557  
Qy 1561 GATAAATACATCAAAATCCCGCCGTTAAATGTTGGGATAATTTACCGTTTGTTCAGTG 1620  
Db 1558 GCGGAATCACCATAATACACGGGGCGAAGTCTAGCACCATAGGCGAATACTTATATA 1617  
Qy 1621 GTAAAGACACAGGACATACAGAGGGGATTTATACAGTATAATAAGAGTACTGGTTCT 1680  
Db 1618 ATAAAGGGCGGTGTTATACAGGGGGAGACTTAGTGGCTTTTAAACGACCGCATCGGAAGT 1677  
Qy 1681 GTAGGAACCTTATTTCTAGCTCATATGSCCTAGCATATAGAAAGACGAGGGAATATCGT 1740  
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LOCUS 125972 3507 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 3 from patent US 5554534.  
ACCESSION 125972  
VERSION 125972.1 GI:1605842  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3507)  
AUTHORS Michaels,T.E., Narva,K.E. and Fonceerrada,L.  
TITLE Bacillus thuringiensis toxins active against scarab pests  
JOURNAL Patent: US 5554534-A 3 10-SEP-1996;  
FEATURES Location/Qualifiers

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ACCESSION
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VERSION
  U04364.1 GI:436832
KEYWORDS
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SOURCE
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  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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  Narva, K.E. and Fu, J.
  Novel Coleopteran-Active Toxins from Bacillus thuringiensis
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REFERENCE
  2 (bases 1 to 3471)
  Feitelson, J.S.
  Direct Submission
  Submitted (15-DEC-1993) Jerald S. Feitelson, Molecular Biology,
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CDS
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ORIGIN

Query Match 50.0%; Score 1812.2; DB 1; Length 3471;

Best Local Similarity 72.2%; Pred. No. 0;

Matches 2504; Conservative 0; Mismatches 908; Indels 57; Gaps 9;

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DEFINITION Sequence 1 from patent US 5554534.  
ACCESSION 125971  
VERSION 125971.1 GI:1605841  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3471)  
AUTHORS Michaels,T.E., Narva,K.E. and Poncerrada,L.  
TITLE Bacillus thuringiensis toxins active against scarab pests  
JOURNAL Patent: US 5554534-A 1 10-SEP-1996;  
FEATURES  
Location/Qualifiers  
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source /organism="unknown"

BASE COUNT 1200 a 567 c 751 g 953 t  
ORIGIN

Query Match 50.0%; Score 1812.2; DB 6; Length 3471;  
Best Local Similarity 72.2%; Pred. No. 0;  
Matches 2504; Conservative 0; Mismatches 908; Indels 57; Gaps 9;

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## RESULT 6

BTU04366

LOCUS

DEFINITION

Bacillus thuringiensis japonensis Buibui CryIII delta-endotoxin

gene, complete cds.

ACCESSION

U04366

VERSION

U04366.1

KEYWORDS

3483 bp DNA linear BCT 27-AUG-1994

BTU04366

Bacillus thuringiensis japonensis Buibui CryIII delta-endotoxin

gene, complete cds.

ACCESSION

U04366

VERSION

U04366.1

KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## CDS

Bacillus thuringiensis.  
Bacillus thuringiensis  
Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus; Bacillus cereus group.  
1 (bases 1 to 3483)  
Sato, R., Takeuchi, K., Ogiwara, K., Minami, M., Kaji, Y., Suzuki, N., Hori, H., Asano, S., Ohba, M. and Iwahana, H.  
Cloning, heterologous expression, and localization of a novel crystal protein gene from Bacillus thuringiensis serovar japonensis strain buibui toxic to scarabaeid insects  
Curr. Microbiol. 28 (1), 15-19 (1994)  
94100786  
7764305  
2 (bases 1 to 3483)  
Feitelson, J.S.  
Direct Submission  
Submitted (15-DEC-1993) Jerald S. Feitelson, Molecular Biology, Mycogen Corporation, 4980 Carroll Canyon Road, San Diego, CA 92121, USA  
On Aug 27, 1994 this sequence version replaced gi:436836.

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RESULT 7

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AR005118
LOCUS AR005118 3797 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 1 from patent US 5747450.
ACCESSION AR005118
VERSION AR005118.1 GI:3965997
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3797)
AUTHORS Ohba,M., Iwahana,H., Sato,R., Suzuki,N., Ogiwara,K., Sakanaka,K.,
Hori,H., Asano,S. and Kawasugi,T.
TITLE Microorganism and insecticide
JOURNAL Patent: US 5747450-A 1 05-MAY-1998;
FEATURES
source 1..3797
/organism="unknown"
BASE COUNT 1345 a 606 c 776 g 1070 t
ORIGIN
Query Match 32.6%; Score 1180; DB 6; Length 3797;
Best Local Similarity 61.4%; Pred. No. 1.1e-226;
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RESULT 9

E06830

LOCUS

DEFINITION DNA sequence encoding insecticidal protein against coleopteran

3797 bp

DNA

linear

PAT 29-SEP-1997



larvae.  
 ACCESSION E06830  
 VERSION GI:2175012  
 KEYWORDS JP 1994065292-A/1.  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 REFERENCE artificial sequences.  
 AUTHORS 1 (bases 1 to 3797)  
 Ogiwara, K., Minami, M., Suzuki, N., Hori, H., Asano, M., Kawabuchi, T.,  
 Sato, R., Oba, M. and Iwabana, S.  
 TITLE INSECTICIDAL PROTEIN AGAINST LARVA OF COLEOPTERAN INSECT AND NEW  
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 Patent: JP 1994065292-A 1 08-MAR-1994;  
 KUBOTA CORP  
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 OC Artificial sequence; Genes.  
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 PN JP 1994065292-A/1  
 PD 08-MAR-1994  
 PF 11-AUG-1992 JP 1992213886  
 PI OGIIWARA KATSUTOSHI, MINAMI MASAYOSHI, SUZUKI NOBUKAZU, PI  
 HORI HIDEAKA,  
 ASANO MASASHI, KAWASUGI TADAOKI, SATO REIICHI, OBA MICHIO, PI  
 IWABANA SHIYUUSUKE  
 PC C07K13/00, A01H5/00, A01N63/02, C12N1/21, C12N5/10, C12N15/32, PC  
 C12N15/70,  
 PC C12N15/75, C12N15/78//C12P21/02, (C12N1/21, C12R1:19), (C12N1/21,  
 C12R1:38),  
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 CC \*source: clone=E.C. JM109 strain transformed with a plasmid;  
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 FT /product='insecticidal protein against FT  
 Coleoptera'.  
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## RESULT 10

AX189653

LOCUS

DEFINITION Sequence 5 from Patent WO0147952.

ACCESSION AX189653

VERSION AX189653.1 GI:15143042

KEYWORDS

SOURCE

ORGANISM

Bacillus thuringiensis.

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus

cereus group.

REFERENCE

AUTHORS

1 (bases 1 to 3459)

Arnaut, G., Boets, A., Damme, N., Mathieu, E., Vanneste, S. and van

Rie, J.

AX189653 3459 bp DNA linear PAT 08-AUG-2001

TITLE Insecticidal proteins from *Bacillus thuringiensis*  
JOURNAL Patent: WO 0147952-A 5 05-JUL-2001;  
Aventis CropScience N.V. (BE)

FEATURES  
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Location/Qualifiers

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Matches 1937; Conservative 0; Mismatches 1335; Indels 126; Gaps 11;

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## RESULT 11

AX100532 3474 bp DNA linear PAT 10-APR-2001  
LOCUS Sequence 1 from Patent WO0121821.  
DEFINITION AX100532  
ACCESSION AX100532  
VERSION AX100532.1 GI:13619536  
KEYWORDS  
SOURCE Bacillus thuringiensis.  
ORGANISM Bacillus thuringiensis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.  
REFERENCE 1 (bases 1 to 3474)  
AUTHORS Michiels, F., Jansens, S., Kumar, H., Lobo, D. and Samson, J.  
TITLE Insect-resistant rice plants  
JOURNAL Patent: WO 0121821-A 1 29-MAR-2001;  
Aventis CropScience N.V. (BE)  
FEATURES  
source Location/Qualifiers  
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BASE COUNT 1114 a 600 c 769 g 991 t

ORIGIN

Query Match 24.4%; Score 883.4; DB 6; Length 3474;  
Best Local Similarity 56.6%; Pred. No. 3.6e-167;  
Matches 1936; Conservative 0; Mismatches 1386; Indels 101; Gaps 12;

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QY 121 GATTATAAGATTAATTAATAATGTCTGGGGAATGCTAGTGAATACCCCTGGTTCACCT 180  
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DB 241 CTCGGGCTTTAGGTCTTCOGTTTTCTGGACAAATAGTGTGATTTTATCAATTCCTTTTA 300

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QY 1189 AGTACCTTTGATTTTACGNAATTTATGATTTTACAAGACTCTATCAAGAGTGCAG-TACT 1247

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QY 1308 TTTTCATGGTAAACCAATTGAATTAATCCAGAAAGACGTTTAAAGTATTAATCCAGTTTCCA 1367

DB 1312 TTTAATGGT-----ACGACTTCTCTGCTAATGGAGGATGTAG 1349

QY 1368 AGATATTATAGCGAGTACAAGAGTTCCGAATTTAGAAATTTACCTCCAGAACTTCAGATCA 1427

DB 1350 AGATCTCTATGATCAAAATGATGAATTTACCACAGATGAAGTACCGGAAGTTTCAACCCA 1409

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DB 1410 TAGACTATCTCATGTACCTTTTGTAGCTT-----TCAAACTAATCAGGCTGGATCTAT 1463

QY 1488 TAACTACTCCGGATTAGTACCTGTATTTTCTTTGGACACATCGAAGTGCAGATTTTAAACAA 1547

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QY 1548 TACATATATTAGATAAAATCATCTCAAAATTCGGGCCGTTAAATGTTGGGTAATTTTACC 1607

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[illegible]

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| Db | 2769 | GGAAACAAAGAGATTAATGCGAAATGGAAATGCGAGCTAGGAGAAACCGTCAGNAATAGA     | 2828 |
| Qy | 2832 | TAGAAGGTATATGGCATCGAAACCAAGCCGTAGATCGTTTTATATGCCGATTATCAGGATCA   | 2891 |
| Db | 2829 | TCGTGTGTATTAGCTGCGAAACCAAGCAATTAATCATCTGTTGTAGACTATCAAGATCA      | 2888 |
| Qy | 2892 | GCAACTGAATCCTGATGTAGAGATTAACAGATCTTACTCGGCCCAAGATCTGATACAGTC     | 2951 |
| Db | 2889 | ACAAATTAATCCAGAAATGGCGTAGCAGAAATTAATGAAGCTTCACAAATCTTGTAGAGTC    | 2948 |
| Qy | 2952 | CATTCTTACGTATATACGAATGTTCCCGAANAATACAGGGATGCACTATACGAAGTT        | 3011 |
| Db | 2949 | AAATTCGGGTATATATGTGATACACTATTACAGATTCCTGGGATTAACCTACGAATTTA      | 3008 |
| Qy | 3012 | TACAGAAATTAACAGATCGACTCCAAACAAGCGTGAGTTTGTATGATCAGCGAAATGCCAT    | 3071 |
| Db | 3009 | CACAGATTATCCGATCGCTTACACAAGCATCGTATCTGTATACGTCTAGAAAATCGCGT      | 3068 |
| Qy | 3072 | ACCAATCGGTGATTTTTCGAAATGGGTTAAGTTAATTTGGAAATGC AACCGCTGGCGTGAAGT | 3131 |
| Db | 3069 | GCAAAATGGAGACTTTAAACAGTGGTCTAGATAGTTTGGAAATCAACTATGGATGCATCGGT   | 3128 |
| Qy | 3132 | ACACAATCAATCATATCATCTGTCTCTGTGATTCCCAATCCGGATGAGCAAGTTTTCGCA     | 3191 |
| Db | 3129 | TACGACAGATGGCAATATGCATTTCTTTAGTTCTTTTCGCATTTGGGATGCAAGTTTTCCTCA  | 3188 |
| Qy | 3192 | CACAGTTTACAGTTTCAACCGAATCAAGATATGTGTTACGAGTTATCTCGCAGAGAAAAGAGG  | 3251 |
| Db | 3189 | ACAATTGAGAGTAAATCCGAATTGTAAGTATGTTCTTACGTGTGACAGCAAGAAAAGTAGG    | 3248 |
| Qy | 3252 | GGTAGAAATGGATATGTAAGTATCCGTGATGGTGGAAATCAAAACAGAAACGGTTACTTTT    | 3311 |
| Db | 3249 | AGCGCGAGATGGATACGTACAAATCCGAGATGGCGCTCATCCCAAGAAACTCTTACATT      | 3308 |
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| Db | 3309 | TAATGCAATGTGACTACGATGTAATGGTACGTATGTCAATGACAAATTCGTATATATACAGA   | 3368 |
| Qy | 3372 | ATA 3374   |      |
| Db | 3369 | AGA 3371   |      |

RESULT 12

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| A73540 | LOCUS      | A73540   | 4344 bp    | DNA | linear | PAT 15-OCT-1999 |
|        | DEFINITION | Sequence 4 from Patent WO9424264.                                  |            |     |        |                 |
|        | ACCESSION  | A73540   |            |     |        |                 |
|        | VERSION    | A73540.1   | GI:6064159 |     |        |                 |
|        | KEYWORDS   | .  |            |     |        |                 |
|        | SOURCE     | unidentified.  |            |     |        |                 |
|        | ORGANISM   | unclassified.  |            |     |        |                 |
|        | REFERENCE  | 1 (bases 1 to 4344)  |            |     |        |                 |
|        | AUTHORS    | Lambert, B. and Jansens, S.  |            |     |        |                 |
|        | TITLE      | NEW BACILLUS THURINGIENSIS STRAINS AND THEIR INSECTICIDAL PROTEINS |            |     |        |                 |
|        | JOURNAL    | Patent: WO 9424264-A 4 27-OCT-1994;                                |            |     |        |                 |
|        |            | PLANT GENETIC SYSTEMS NV (BE) ; LAMBERT BART (BE)                  |            |     |        |                 |

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BASE COUNT 1436 a 713 c 936 g 1259 t  
ORIGIN

Query Match 24.4%; Score 883.4; DB 6; Length 4344;  
Best Local Similarity 56.6%; Pred. No. 3.5e-167;  
Matches 1936; Conservative 0; Mismatches 1386; Indels 101; Gaps 12;

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| Qy | 61   | TCCATGATTTCAACAGATACCTTTTGGGAATGAGCCAAACAAATGCGCTACAAATATG       | 120  |
| Db | 728  | TCAGATGCGATGTGAGGTATCTCTTTGGCAATGACCCAAATAGCGCGTTACAAATATG       | 787  |
| Qy | 121  | GATTATAAGATTAATTTAAATATGCTCGGGAATGCTAGTGAATACCTTGTTCACT          | 180  |
| Db | 788  | AACATATAAGATTAATTTAAATATGACATGAGGACTACACTGATTTCTTATATTAATCT      | 847  |
| Qy | 181  | GAAGTACTTGTGTAGCGGCAACAGATGAGTAAAGCGCGCAATTTGATATAGTAGTAAATTA    | 240  |
| Db | 848  | AGTTTATCTATGTGTAGATGAGTACGATTCAGATGCGCTTACTGTTGTGGGAGATA         | 907  |
| Qy | 241  | CTATCAGGTTTATGAGGTGCCATTTGTGGCGGATGAGTGTGAGTCTTTATATCTCAACTAT    | 300  |
| Db | 908  | CTCGGGCTTTAGTGTTCGGTCTTCTGCAAAATAGTGTGAGTCTTTATCAATTCCTTTTA      | 967  |
| Qy | 301  | GATATTCTGTGCGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAGTAGNA       | 360  |
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| Qy | 361  | GAACTCATTAATCAAAATATGACAGAAATATGCAAGGAATATAAGCGCTTTTCGGAAATTAGAA | 420  |
| Db | 1028 | GAACTTGTCAATCAACAAATATGAGAAATTTGCAAGAAATCAGGCACTTGCAGATGTCNA     | 1087 |
| Qy | 421  | GGATTAGTATAATTAACAAATATATCTAACTGGCTTGAAGATGGGAAGAAATCA           | 480  |
| Db | 1088 | GGATTAGGAGACTCTTTTAAATGATATCAACCTTCCCTTCAAAATTTGGTGTGCTGATCGA    | 1147 |
| Qy | 481  | AATGTTTCAAGAGCTTACGAGATGCGGAATCGATTTGAAATCCTGTGATAGTTATTT        | 540  |
| Db | 1148 | ANTGATACAGAAATTTAAGTGTGTGTGCTCAATTTATAGCTTTAGACCTTGATTTT         | 1207 |
| Qy | 541  | ACGCAATATAGCCATCTTTTAGGTGACAAATTTTGAAGTACCAATCTCTTACTGTATAT      | 600  |
| Db | 1208 | GTTAATGCTATTCATTTGTTGAGTAAATGACAGCAGGTTCATTTACTGTGATATAT         | 1267 |
| Qy | 601  | GCAATGGCAGCAACCTTCATTTACTGTTATTAAGGACGCGTCAATTTTGGAGAGAA         | 660  |
| Db | 1268 | GCACAAAGCTGTGAATTTTACATTTGTTATTTATTAAGATGCACTCTTTTGGAGAGGA       | 1327 |
| Qy | 661  | TGGGATGGTCAACAACTACTATTAATTAATGATATGATCGTCAATGAACTTACTGCA        | 720  |
| Db | 1328 | TGGGATTTCAACACAGGGGAAATTTCCATATATGACCGTCAATTTGGAATTAACCGCT       | 1387 |

|    |      |  |      |
|----|------|--|------|
| Qy | 721  | GAATATTCGTGATCACTGTGTAAAGTGGTATGAAACTGGTTAGTCAAAATTTAAAGCCAG     | 780  |
| Db | 1388 | AAGTACACTTAATTAATCTGTGAACCTTGGTATTAATACAGGTTAGTTCGTTTAAAGAGCA    | 1447 |
| Qy | 781  | AGCGCTAAACAAATGGTGTGACTATAACCAATTCCTGTAGAGAAATGACACTGGCGGTTTA    | 840  |
| Db | 1448 | AATACTGAAAGTTGGTTAAGATATCATCAATTCCTGTAGAGAAATGACTTTTAGTGTATTA    | 1507 |
| Qy | 841  | GATGTTGTGCTATTATCCCAAAATTTATGACACAGCAGCTACCCCAATCGAAACGAAAGCA    | 900  |
| Db | 1508 | GATGTTGTGGCGCTATTTCCTAATTTATGATGACACTTTTATCCAAACGGGATCAAAACCA    | 1567 |
| Qy | 901  | CAACTAAACAGGGAAGTATATACAGATCCACTGGCGCGGTAAACGCTGCTTCTCAATTC      | 958  |
| Db | 1568 | CAGCTTACACGCTGAGGTATATACAGATCCGATTTGTTATTAATCCACAGCTAATGTTGA     | 1627 |
| Qy | 959  | -----GTTCTGTGTATGACAAAGCACCTTCTTTCGGAGTGATAGAAATCATCCGTT         | 1008 |
| Db | 1628 | CTTTGCCGACGTTGGGGTACTAATCCCTATTAATACTTTTCTGAGCTCGAAATGCCTTC      | 1687 |
| Qy | 1009 | ATTCGACCAACCCCATGTATTGTTTATATATAACGGGACTCACAGTGTATACACAAATCAAGA  | 1068 |
| Db | 1688 | ATTCGCCCAACCATATCTTTTGTAGAGCTGATAGCTTAAACAATCAGCAGTAATCGATTT     | 1747 |
| Qy | 1069 | AGCATTTCTTCGCTCGCTATATATAAGACATTTGGGCTGCTCATCAAAATAGCTTACCATCGT  | 1128 |
| Db | 1748 | CCAGTTTCATCTAAT---TTTATGGAATTTTGGTCAGGACATACGTTACCGCGTAGTTAT     | 1804 |
| Qy | 1129 | GTCACTAGGGGTAGTAATCTTCAACAAATGTATGGAACATAAATCAAAATCTACACAGCT     | 1188 |
| Db | 1805 | CTGAACGATTCAGCAGTACAAGAGATAGTTATGG-----CCTAATTTACACCAACAAGA      | 1858 |
| Qy | 1189 | AGTACCTTTGATTTTACGAATTTATGATTTTCAAGACTCTTCAAGAGTCAACGAGTATGATTTT | 1247 |
| Db | 1859 | GCAACAATTAATCCCGGAGTTGATGGAACAAACCCGATAGAGTCAACGCGAGTAGTTT       | 1918 |
| Qy | 1248 | CTTGTATATGTTTACCTCGTATATACGTATATATTTTTCGAAATGCCAGAGTCCGAGTT      | 1307 |
| Db | 1919 | CGTTCTGCAATGTAGGTATATATGCGGTGATAGAGCTTCTTTTGTCCAGGAGCTTG         | 1978 |
| Qy | 1308 | TTTCATGTGTAAACCAATTTGAATAATACAGAAAGACGTAAAGTATAATTCAGTTTCCAA     | 1367 |
| Db | 1979 | TTTAAATGGT-----ACGACTTCTCTGCTAATGGAGGATGAG                       | 2016 |
| Qy | 1368 | AGATATATAGCGAGTACAAGATTCGGAATTAAGAAATCTCCAGAACTTCAGATCA          | 1427 |
| Db | 2017 | AGATCTCTATGATACAAATGATGAATTTACCACCAAGTAAAGTACCGGAAGTTCAACCCA     | 2076 |
| Qy | 1428 | ACCAAAATATGAGTCAATATAGCCATAGATTTATGTCATATCACAAGTATTTCCCGCAGCGG   | 1487 |
| Db | 2077 | TAGACTATCTCATGTTACCTTTTGTAGCTT-----TCAAACTAATCAGGCTGGATCTAT      | 2130 |
| Qy | 1488 | TAACTACTACCGGATTTAGTACCTGTTATTTTCTTGGACACATCGAAGTGCAGATTTAAACAA  | 1547 |
| Db | 2131 | AGCTAATGCGAGAAAGTGTACCTTACTTATGTTTGGACCGCTGCTGATGTGGACCTTAATAA   | 2190 |
| Qy | 1548 | TACATATATTTTCAGATAAATCACTCAAAATTCGCGCGGTAAATGTTGGGTAAATTTTACC    | 1607 |
| Db | 2191 | TACGATTAACCAATGAATTTACAAATACCATTGGTAAAGGCATCTGCACCTGTTTC         | 2250 |
| Qy | 1608 | GTTTGTTCAGGTGTAAAGGACGAGGACATACAGAGGGGATTTTATTAAGTATAATAG        | 1667 |
| Db | 2251 | GGGTACTACGGTCTTAAAGGTCAGGATTTTACAGGAGGGGTATCTCC---GAAGAAC        | 2307 |
| Qy | 1668 | AAGTACTGGTTCGTAGGAACTTATTTCTAGCTCGATATGCGCCCTAGCATTTAGAAAAAGC    | 1727 |
| Db | 2308 | AACATAATGGCAATTTGGAACTTAAAGAGTAAACGTTAATTCACCATTAACACAAATA       | 2367 |
| Qy | 1728 | AGGGAATATCGTGTAGAGTGTAGATATGCTACTGATCGAGATTTGTTATTCATGTAA        | 1787 |
| Db | 2368 | TCGCTTAAGAGTTCGTTTGTGCTCAACAGGAAATTTTCAAGTATAAGGGTACTCCGCGAGG    | 2427 |
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RESULT 13
AR031103
LOCUS AR031103 4344 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5861543.
ACCESSION AR031103
VERSION AR031103.1 GI:5944317
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4344)
AUTHORS Lambert, B., Jansens, S., Van Audenhove, K., Referoen, M., Van Rie, J.
and Van Aarseen, R.
TITLE Bacillus thuringiensis strains and their insecticidal proteins
JOURNAL Patent: US 5861543-A 4 19-JAN-1999;
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Location/Qualifiers
source 1. 4344
/organism="unknown"
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ORIGIN
Query Match 24.4%; Score 883.4; DB 6; Length 4344;
Best Local Similarity 56.6%; Pred. No. 3.5e-167;
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Db 4036 AGA 4038

BTCRY9COP
LOCUS Bthuringiensis DNA for cry9Ca1 operon.
DEFINITION Bthuringiensis DNA for cry9Ca1 operon.
ACCESSION Z37527
VERSION Z37527.1 GI:547554
KEYWORDS cry9Ca1 operon.
SOURCE Bacillus thuringiensis.
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 5772)
AUTHORS Lambert, B., Buyse, L., Decock, C., Janssens, S., Piens, C., Saey, B., Seurinck, J., Van Audenhove, K., Van Rie, J., van Vliet, A. and Peferoen, M.
TITLE A Bacillus thuringiensis insecticidal crystal protein with a high activity against members of the family Noctuidae
JOURNAL Appl. Environ. Microbiol. 62 (1), 80-86 (1996)
MEDLINE 96141404
PUBMED 8572715
REMARK 2 (bases 1 to 5772)
AUTHORS Lambert, B.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-1994) EMBL Data Library by: Lambert B. Plant Genetic Systems N.V. Jozef Plateastraat 22 Ghent Belgium
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| DEFINITION | Sequence 73 from patent US 6369213.                              |   |                        |
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| VERSION    | AR205864.1   | GI:21503554   |                        |
| KEYWORDS   | Unknown.   |   |                        |
| SOURCE     | Unknown.   |   |                        |
| ORGANISM   | Unclassified.  |   |                        |
| REFERENCE  | 1 (bases 1 to 3471)  |   |                        |
| AUTHORS    | Schneppf H.Ernest., Wicker,C., Narva,K.E., Walz,M., Stockhoff,B. |   |                        |
| TITLE      | Toxins active against pests                                      |   |                        |
| JOURNAL    | Patent: US 6369213-A 73 09-APR-2002;                             |   |                        |
| FEATURES   | Location/Qualifiers  |   |                        |
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2003, 00:39:12 ; Search time 479 Seconds

(without alignments)  
17023.979 Million cell updates/sec

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Perfect score: 3621

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 101002.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 2          | 3621   | 100.0       | 4874   | 24 | Bacillus thuringie |
| 3          | 3151.8 | 87.0        | 3633   | 24 | Bacillus thuringie |
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| 5          | 2565.2 | 70.8        | 3507   | 17 | Antiscarab pest to |
| 6          | 2008.4 | 55.5        | 2010   | 24 | Bacillus thuringie |
| 7          | 2003   | 55.3        | 2003   | 24 | Bacillus thuringie |
| 8          | 1987.4 | 54.9        | 2013   | 24 | Bacillus thuringie |
| 9          | 1986.4 | 54.9        | 2022   | 24 | Bacillus thuringie |

|    |        |      |      |    |           |                    |
|----|--------|------|------|----|-----------|--------------------|
| 10 | 1986.4 | 54.9 | 2022 | 24 | ABK87244  | Bacillus thuringie |
| 11 | 1986.4 | 54.9 | 2022 | 24 | ABK87256  | Bacillus thuringie |
| 12 | 1985.8 | 54.8 | 2013 | 24 | ABK87258  | Bacillus thuringie |
| 13 | 1848.4 | 51.0 | 1860 | 24 | ABK87243  | Bacillus thuringie |
| 14 | 1827.4 | 50.5 | 1854 | 24 | ABK87251  | Bacillus thuringie |
| 15 | 1826.4 | 50.4 | 1863 | 24 | ABK87249  | Bacillus thuringie |
| 16 | 1825.8 | 50.4 | 1854 | 24 | ABK87259  | Bacillus thuringie |
| 17 | 1824.8 | 50.4 | 1863 | 24 | ABK87250  | Bacillus thuringie |
| 18 | 1821.6 | 50.3 | 1863 | 24 | ABK87257  | Bacillus thuringie |
| 19 | 1813.8 | 50.1 | 3471 | 13 | AAQ30821  | Toxin 50C. Bacill  |
| 20 | 1812.2 | 50.0 | 3471 | 13 | AAQ27167  | Delta-endotoxin ge |
| 21 | 1812.2 | 50.0 | 3471 | 13 | AAQ28940  | B.thuringiensis PS |
| 22 | 1812.2 | 50.0 | 3471 | 14 | AAQ38653  | Bt isolate P850C c |
| 23 | 1812.2 | 50.0 | 3471 | 17 | AAQ43222  | Antiscarab pest to |
| 24 | 1807.4 | 49.9 | 3471 | 14 | AAQ51704  | Bacillus thuringie |
| 25 | 1539.2 | 42.5 | 2022 | 24 | ABK87242  | Bacillus thuringie |
| 26 | 1521.8 | 42.0 | 2003 | 24 | ABK87237  | Bacillus thuringie |
| 27 | 1317.6 | 36.4 | 3690 | 24 | ABK51132  | cDNA encoding Baci |
| 28 | 1180   | 32.6 | 3797 | 14 | AAQ38666  | Coeloptera toxin f |
| 29 | 983.6  | 27.2 | 3797 | 15 | AAQ58975  | B.thuringiensis se |
| 30 | 900    | 24.9 | 3459 | 22 | AAH28242  | Maize optimised B. |
| 31 | 883.4  | 24.4 | 3474 | 22 | AAH19323  | Nucleotide sequenc |
| 32 | 883.4  | 24.4 | 4344 | 20 | AAV99986  | Nucleotide sequenc |
| 33 | 882.8  | 24.4 | 3471 | 19 | AAV16516  | DNA encoding a Bac |
| 34 | 882.8  | 24.4 | 3471 | 20 | AAH83877  | Bacillus thuringie |
| 35 | 882.8  | 24.4 | 3471 | 22 | AAQ502477 | B. thuringiensis D |
| 36 | 882.8  | 24.4 | 3471 | 22 | AAQ56782  | Insecticidal toxin |
| 37 | 881.8  | 23.4 | 3759 | 17 | AAH27148  | Bacillus thuringie |
| 38 | 848.6  | 22.7 | 3453 | 19 | AAV16517  | DNA encoding a Bac |
| 39 | 822.2  | 22.7 | 3453 | 20 | AAH83878  | Bacillus thuringie |
| 40 | 822.2  | 22.7 | 3667 | 19 | AAV38466  | DNA encoding a Bac |
| 41 | 822.2  | 22.7 | 3667 | 19 | AAV38466  | DNA encoding a Bac |
| 42 | 734.2  | 20.3 | 3411 | 19 | AAV15518  | DNA encoding a Bac |
| 43 | 734.2  | 20.3 | 3411 | 20 | AAH83879  | Bacillus thuringie |
| 44 | 732    | 20.2 | 3414 | 14 | AAQ41745  | DNA encoding B.t.  |
| 45 | 732    | 20.2 | 3414 | 15 | AAQ56922  | Bacillus thuringie |

#### ALIGNMENTS

#### RESULT 1

ABK87234

ID ABK87234 standard; DNA; 3621 BP.

XX AC ABK87234;

XX AC ABK87234;

DT 07-OCT-2002 (first entry)

DE Bacillus thuringiensis Cry1218-1 gene sequence.

XX KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;

XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;

XX KW insect target range; endotoxin; Cry1218; gene; ds.

XX OS Bacillus thuringiensis.

XX XX WO200234774-A2.

XX PD 02-MAY-2002.

XX PF 24-OCT-2001; 2001WO-US45468.

XX PR 24-OCT-2000; 2000US-242838P.

XX PR 23-OCT-2001; 2001US-0032717.

XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.

XX PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;

XX XX WPI; 2002-519178/55.

XX DR P-PSDB; AAU99255.

XX XX

PT New isolated pesticidal polypeptide useful for impacting insect pest  
PT e.g. Colorado potato beetle -

PS Claim 1; Page 91-96; 176pp; English.

XX The present invention relates to a new pesticidal polypeptide. The  
CC invention is useful for impacting an insect pest by applying the  
CC the molecules of the invention to the environment of the insect pest by  
CC spraying, dusting, broadcasting, or seed coating, where the insect pest  
CC is selected from Colorado potato beetle, western corn rootworm or  
CC southern corn rootworm. The invention is also useful for increasing  
CC insect target range and for producing transgenic microorganisms and  
CC plants that express the pesticidal polypeptide. The invention is also  
CC useful for producing transformed plants and in transforming any organism  
CC to produce the pesticidal polypeptide of the invention. The present  
CC nucleic acid sequence encodes a Bacillus thuringiensis wild-type  
CC Cry12I8 endotoxin protein.

XX Sequence 3621 BP; 1277 A; 608 C; 771 G; 965 T; 0 other;

Query Match 100.0%; Score 3621; DB 24; Length 3621;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | ATGAGTCCAAATAATCAAAATGAATATGAATATATAGATGCGACACCTTCTACTTCTGTA | 60  |
| Db | 1   | ATGAGTCCAAATAATCAAAATGAATATGAATATATAGATGCGACACCTTCTACTTCTGTA | 60  |
| Qy | 61  | TCCAATGATTTCAAGATACCTTTTGGGAATGAGCCAAATGCGCTACAAATATG        | 120 |
| Db | 61  | TCCAATGATTTCAAGATACCTTTTGGGAATGAGCCAAATGCGCTACAAATATG        | 120 |
| Qy | 121 | GATTATAAGATTTATTAATAATGTCGCGGAATGCTAGTGAATACCTCGTTCACCT      | 180 |
| Db | 121 | GATTATAAGATTTATTAATAATGTCGCGGAATGCTAGTGAATACCTCGTTCACCT      | 180 |
| Qy | 181 | GAACTACTTTAGCGGCAAGATGACGCTAAGCGCGCAATTTGATATAGTAAATTA       | 240 |
| Db | 181 | GAACTACTTTAGCGGCAAGATGACGCTAAGCGCGCAATTTGATATAGTAAATTA       | 240 |
| Qy | 241 | CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTGAGTCTTATCTCACTTAT       | 300 |
| Db | 241 | CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTGAGTCTTATCTCACTTAT       | 300 |
| Qy | 301 | GATATCTGTGCGCTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAACAAGTAGAA   | 360 |
| Db | 301 | GATATCTGTGCGCTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAACAAGTAGAA   | 360 |
| Qy | 361 | GAACTCATTAATCAAAAATAGCAGAATATGCAAGGAATAAAGCGCTTCGGAATTAGAA   | 420 |
| Db | 361 | GAACTCATTAATCAAAAATAGCAGAATATGCAAGGAATAAAGCGCTTCGGAATTAGAA   | 420 |
| Qy | 421 | GGATTAGTAAATTAATCAATATATCTAACTGCGCTTGAAGATGGGAAGAAATCCA      | 480 |
| Db | 421 | GGATTAGTAAATTAATCAATATATCTAACTGCGCTTGAAGATGGGAAGAAATCCA      | 480 |
| Qy | 481 | AATGGTTCAAGAGCCTTACGAGATGCGAAATCGAATTTGAAATCCTGATAGTTTATTT   | 540 |
| Db | 481 | AATGGTTCAAGAGCCTTACGAGATGCGAAATCGAATTTGAAATCCTGATAGTTTATTT   | 540 |
| Qy | 541 | ACGCAATATATGCCATCTTTTATAGATGACAATTTTGAAGTACCAATCTCTATGATAT   | 600 |
| Db | 541 | ACGCAATATATGCCATCTTTTATAGATGACAATTTTGAAGTACCAATCTCTATGATAT   | 600 |
| Qy | 601 | GCAATGGGAGCAACCTTCATTTACTGTTTAAAGGACGCGTCAATTTTGGAGAGAA      | 660 |
| Db | 601 | GCAATGGGAGCAACCTTCATTTACTGTTTAAAGGACGCGTCAATTTTGGAGAGAA      | 660 |
| Qy | 661 | TGGGATGTCACCAACTACTTATTAATACTATTATGATCGTCAAAATGAACTTACTGCA   | 720 |
| Db | 661 | TGGGATGTCACCAACTACTTATTAATACTATTATGATCGTCAAAATGAACTTACTGCA   | 720 |
| Qy | 721 | GAATATTTCTGATCACTGTGTAAAGTGTATGAACTGGTTTATGCAAAATTTAAAGGCACG | 780 |

|    |      |   |      |
|----|------|---|------|
| Db | 721  | GAATATTTCTGATCACTGTGTAAAGTGTATGAACTGGTTTATGCAAAATTTAAAGGCACG  | 780  |
| Qy | 781  | AGCCTTAAACAATGGGTTGACTATAACAATTCCTGTAGAGAAATGACACTGCGGTTTAA   | 840  |
| Db | 781  | AGCCTTAAACAATGGGTTGACTATAACAATTCCTGTAGAGAAATGACACTGCGGTTTAA   | 840  |
| Qy | 841  | GATGTGTGTGATTTATTTCCCAATTTATGACACACGACGTAACCAATGGAACGAAAGCA   | 900  |
| Db | 841  | GATGTGTGTGATTTATTTCCCAATTTATGACACACGACGTAACCAATGGAACGAAAGCA   | 900  |
| Qy | 901  | CAACTAACAGGGAAGTATATACAGATCCACTGGGCGGGTAAACGTCCTCTCAATTTGGT   | 960  |
| Db | 901  | CAACTAACAGGGAAGTATATACAGATCCACTGGGCGGGTAAACGTCCTCTCAATTTGGT   | 960  |
| Qy | 961  | TCCGTGTATGACAAAGCACCTTCTTTCGGAGTGATAGAATCATCCGTTTATTCGACACCC  | 1020 |
| Db | 961  | TCCGTGTATGACAAAGCACCTTCTTTCGGAGTGATAGAATCATCCGTTTATTCGACACCC  | 1020 |
| Qy | 1021 | CATGTATTTGATTTATATAACGGGACTCAACAGTGTATACAAATCAAGAACATTTCTTCC  | 1080 |
| Db | 1021 | CATGTATTTGATTTATATAACGGGACTCAACAGTGTATACAAATCAAGAACATTTCTTCC  | 1080 |
| Qy | 1081 | GCTCGCTATATAAGACATTTGGGCTGGTCAATCAATTAAGCTACCATCGTGTCAATGGGGT | 1140 |
| Db | 1081 | GCTCGCTATATAAGACATTTGGGCTGGTCAATCAATTAAGCTACCATCGTGTCAATGGGGT | 1140 |
| Qy | 1141 | AGTAATCTTCAACAATAATGATGGAACCTAATCAAAATCTACACAGCAGTACCTTTGAT   | 1200 |
| Db | 1141 | AGTAATCTTCAACAATAATGATGGAACCTAATCAAAATCTACACAGCAGTACCTTTGAT   | 1200 |
| Qy | 1201 | TTTACGAATTTATGATTTTATCAAGACTCTATCAAGGATGCACTCTCTTGTGATTTGTT   | 1260 |
| Db | 1201 | TTTACGAATTTATGATTTTATCAAGACTCTATCAAGGATGCACTCTCTTGTGATTTGTT   | 1260 |
| Qy | 1261 | TACCTCGTGTATACGTATATATTTTGGAAATGCGAAGTTCGAGTTCATGTGTAAC       | 1320 |
| Db | 1261 | TACCTCGTGTATACGTATATATTTTGGAAATGCGAAGTTCGAGTTCATGTGTAAC       | 1320 |
| Qy | 1321 | CAATTTGAATATACAGAAAGAGTAAAGTATTAATCCAGTTTCCAAAGATATTATAGCG    | 1380 |
| Db | 1321 | CAATTTGAATATACAGAAAGAGTAAAGTATTAATCCAGTTTCCAAAGATATTATAGCG    | 1380 |
| Qy | 1381 | AGTACAAGAGATTCGGAATTAGAATTTACCTCCAGAACTTCAGATCAACCAAAATATGAG  | 1440 |
| Db | 1381 | AGTACAAGAGATTCGGAATTAGAATTTACCTCCAGAACTTCAGATCAACCAAAATATGAG  | 1440 |
| Qy | 1441 | TCATATAGCCATAGATTTATGTCATATCAAGATTTCCCGGACGCGGTAAACCTACCGGA   | 1500 |
| Db | 1441 | TCATATAGCCATAGATTTATGTCATATCAAGATTTCCCGGACGCGGTAAACCTACCGGA   | 1500 |
| Qy | 1501 | TTAGTACCTGTATTTTCTTGGACACATCGAAGTGCAGATTTAAACAATACATATATTTCA  | 1560 |
| Db | 1501 | TTAGTACCTGTATTTTCTTGGACACATCGAAGTGCAGATTTAAACAATACATATATTTCA  | 1560 |
| Qy | 1561 | GATAAATCACTCAAAATCCCGCGGTTAAATTTGGGATAATTTACCGTTTGTCCAGTG     | 1620 |
| Db | 1561 | GATAAATCACTCAAAATCCCGCGGTTAAATTTGGGATAATTTACCGTTTGTCCAGTG     | 1620 |
| Qy | 1621 | GTAAAGGACCAAGNACATACAGGAGGGATTTATACAGTATATAGAGTACTCGTTCT      | 1680 |
| Db | 1621 | GTAAAGGACCAAGNACATACAGGAGGGATTTATTTACAGTATATAGAGTACTCGTTCT    | 1680 |
| Qy | 1681 | GTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAAGAGGGAATATCGT   | 1740 |
| Db | 1681 | GTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAAGAGGGAATATCGT   | 1740 |
| Qy | 1741 | GTAAAGCTGAGATATGCTACTGATGAGATTTGATTTGTCATGTAAACGATCTCAGATT    | 1800 |
| Db | 1741 | GTAAAGCTGAGATATGCTACTGATGAGATTTGATTTGTCATGTAAACGATCTCAGATT    | 1800 |
| Qy | 1801 | CAGATGCCAAAAACAATGAACCCAGGTGAGGATCTGAATCTTAAACCTTTTAAAGTTGCA  | 1860 |
| Db | 1801 | CAGATGCCAAAAACAATGAACCCAGGTGAGGATCTGAATCTTAAACCTTTTAAAGTTGCA  | 1860 |

Db 1801 CAGATGCCAAAAAACAATGAACCCAGGTGAGGATCTGACATCTTAAACTTTTAAAGTTGCA 1860  
Qy 1861 GATGCTATCAACAATTAATTTAGCAACAGATAGTTCGCTAGCATTTGAAACATATTTA 1920  
Db 1861 GATGCTATCAACAATTAATTTAGCAACAGATAGTTCGCTAGCATTTGAAACATATTTA 1920  
Qy 1921 GGTGAAGACCTTAATCAACATATCTGTATAGTTTACGTTGACCGAATCGAATTCATC 1980  
Db 1921 GGTGAAGACCTTAATCAACATATCTGTATAGTTTACGTTGACCGAATCGAATTCATC 1980  
Qy 1981 CCAGTAGATGAGACATATCAAGCGGAACAAGATTTTAAAGACGCGAAGAAACAGTGAAT 2040  
Db 1981 CCAGTAGATGAGACATATCAAGCGGAACAAGATTTTAAAGACGCGAAGAAACAGTGAAT 2040  
Qy 2041 GCCTTTGTTTACGAATACAAAAGATGCTTTACGACGAGGCGTAACGATTTATGAAGTGAAT 2100  
Db 2041 GCCTTTGTTTACGAATACAAAAGATGCTTTACGACGAGGCGTAACGATTTATGAAGTGAAT 2100  
Qy 2101 CAAGCGGCAAACTTAGTGAATGCCCTATCGGATGATTTGTATCCAAATGAATAACGATTTG 2160  
Db 2101 CAAGCGGCAAACTTAGTGAATGCCCTATCGGATGATTTGTATCCAAATGAATAACGATTTG 2160  
Qy 2161 TTATTTGATGCAAGTGAAGAGGCAAAACGCTCAGTGAGGCGAAGTAAATTTGCTTCAAGAT 2220  
Db 2161 TTATTTGATGCAAGTGAAGAGGCAAAACGCTCAGTGAGGCGAAGTAAATTTGCTTCAAGAT 2220  
Qy 2221 CCAGATTTTCCAAAGAGATAAATGAGAAATATGGCTGACGCGCAAGTACGGGAATTTGAGGTT 2280  
Db 2221 CCAGATTTTCCAAAGAGATAAATGAGAAATATGGCTGACGCGCAAGTACGGGAATTTGAGGTT 2280  
Qy 2281 ATAGAAGGGGATGCTTTATTTCAAAGGGCGTTATCTACGCTTACAGGTCGCGAGAGAAATA 2340  
Db 2281 ATAGAAGGGGATGCTTTATTTCAAAGGGCGTTATCTACGCTTACAGGTCGCGAGAGAAATA 2340  
Qy 2341 GATACGGAACGTAATCCACGATCTGTATCAAAAAGTAGAGGAAGGTGTATTAACCA 2400  
Db 2341 GATACGGAACGTAATCCACGATCTGTATCAAAAAGTAGAGGAAGGTGTATTAACCA 2400  
Qy 2401 TACACAAGATATAGATTTGAGAGGGTTTGTCCGAAGCAGTCAAGGATTTGAAATTTTCA 2460  
Db 2401 TACACAAGATATAGATTTGAGAGGGTTTGTCCGAAGCAGTCAAGGATTTGAAATTTTCA 2460  
Qy 2461 ATTGCTCATCAACGAAACCGAATTTGAAATAATGTAACCGATGATTTGCGCAGATGTA 2520  
Db 2461 ATTGCTCATCAACGAAACCGAATTTGAAATAATGTAACCGATGATTTGCGCAGATGTA 2520  
Qy 2521 TCTCTGTTTAACTCGATGGTAGTATCAATCGATGACGCGAACAAGATGTGTAATAGC 2580  
Db 2521 TCTCTGTTTAACTCGATGGTAGTATCAATCGATGACGCGAACAAGATGTGTAATAGC 2580  
Qy 2581 CGTTTAGAAGTAGAATAACCGTTCTGGTGAAGCGCATGAGTTCTTAATTCCTATTGTATACA 2640  
Db 2581 CGTTTAGAAGTAGAATAACCGTTCTGGTGAAGCGCATGAGTTCTTAATTCCTATTGTATACA 2640  
Qy 2641 GGTGAATTCGATTTACAATGAAATGACGGAATATGGGTTGGAATTAAGATTAACGACCCA 2700  
Db 2641 GGTGAATTCGATTTACAATGAAATGACGGAATATGGGTTGGAATTAAGATTAACGACCCA 2700  
Qy 2701 GAGGATATGCAACACTCGGAAACCTTAGAATTTGGTTCGAAGAGGACCTTTATCAGGAGAC 2760  
Db 2701 GAGGATATGCAACACTCGGAAACCTTAGAATTTGGTTCGAAGAGGACCTTTATCAGGAGAC 2760  
Qy 2761 GCATTAGAAGCGTTGCAAGAGAGAGAACCAACAGTGAAGTTCAAATGACAGAGACCT 2820  
Db 2761 GCATTAGAAGCGTTGCAAGAGAGAGAACCAACAGTGAAGTTCAAATGACAGAGACCT 2820  
Qy 2821 GAAGAAACAGATAGAGGTATATGGCATCGAACAAGCGGTAGATCGTTTATATGCCGAT 2880  
Db 2821 GAAGAAACAGATAGAGGTATATGGCATCGAACAAGCGGTAGATCGTTTATATGCCGAT 2880  
Qy 2881 TATCAGGATCAGCAACTGAACTCTGATGTAGAGATTAACAGATCTTACTCGGCCCAAGAT 2940  
Db 2881 TATCAGGATCAGCAACTGAACTCTGATGTAGAGATTAACAGATCTTACTCGGCCCAAGAT 2940

Qy 2941 CTGATACAGTCCATTCCTTACGTATATAACGAAATGTTCCAGAAATACCGGGATGAAC 3000  
Db 2941 CTGATACAGTCCATTCCTTACGTATATAACGAAATGTTCCAGAAATACCGGGATGAAC 3000  
Qy 3001 TATACGAAGTTTACAGAAATTAACAGATCGATCCCAACGAGCGTGGAGTTTGTATGATCAG 3060  
Db 3001 TATACGAAGTTTACAGAAATTAACAGATCGATCCCAACGAGCGTGGAGTTTGTATGATCAG 3060  
Qy 3061 CGAAATGCGATACCAATGCGTGAATTTTCGAAATGGTTTAAAGTAATTTGGAATCAACGCT 3120  
Db 3061 CGAAATGCGATACCAATGCGTGAATTTTCGAAATGGTTTAAAGTAATTTGGAATCAACGCT 3120  
Qy 3121 GCGGTAGAAGTACCAACAAATCAATCATCATCTGTCTTCTTGTGATTTCCAAATCGGGATGAG 3180  
Db 3121 GCGGTAGAAGTACCAACAAATCAATCATCATCTGTCTTCTTGTGATTTCCAAATCGGGATGAG 3180  
Qy 3181 CAGTTTTCGCAACAGTTTACAGTTTCAACCGAATCAAGATATGTTTACGAGTTACTGCG 3240  
Db 3181 CAGTTTTCGCAACAGTTTACAGTTTCAACCGAATCAAGATATGTTTACGAGTTACTGCG 3240  
Qy 3241 AGAAAGAGGCGGTAGGAAATGCGATATGTAAGTATCCGTTGATGTTGGAATTCAAACAGAA 3300  
Db 3241 AGAAAGAGGCGGTAGGAAATGCGATATGTAAGTATCCGTTGATGTTGGAATTCAAACAGAA 3300  
Qy 3301 AGCTTTACTTTTGTGCAAGCGATTTATGATACAAATGGAATGTATATAACGCAAGTGTC 3360  
Db 3301 AGCTTTACTTTTGTGCAAGCGATTTATGATACAAATGGAATGTATATAACGCAAGTGTC 3360  
Qy 3361 AATACAAATGGAATATAACAAATAATCGGTATATAACAAAGCATCGAGTACAAACGGA 3420  
Db 3361 AATACAAATGGAATATAACAAATAATCGGTATATAACAAAGCATCGAGTACAAACGGA 3420  
Qy 3421 TATACGCAAAATAATATGTAATAACGCAAGCATCGAATACAAACGGAATATAACAAAT 3480  
Db 3421 TATACGCAAAATAATATGTAATAACGCAAGCATCGAATACAAACGGAATATAACAAAT 3480  
Qy 3481 AGTGTGTCAATGATCAAAACCGGCTTATATCAAAACAGTGACATTCATCCCGTATACA 3540  
Db 3481 AGTGTGTCAATGATCAAAACCGGCTTATATCAAAACAGTGACATTCATCCCGTATACA 3540  
Qy 3541 GATCAAAATGCGATTTGAGATGAGTGAGACAGAGGTACATTTCTATATAGAAAGTGTAGAA 3600  
Db 3541 GATCAAAATGCGATTTGAGATGAGTGAGTGAGACAGAGGTACATTTCTATATAGAAAGTGTAGAA 3600  
Qy 3601 TTGATTTAGACGTAGAGTAA 3621  
Db 3601 TTGATTTAGACGTAGAGTAA 3621

## RESULT 2

ABK87247

ID ABK87247 standard; DNA; 4874 BP.

XX AC ABK87247;

XX DT 07-OCT-2002 (first entry)

XX DE *Bacillus thuringiensis* genomic Cry12I8-1 DNA sequence.  
XX KW Pesticidal; spraying; dusting; broadcasing; seed coating; insect pest;  
XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;  
XX KW insect target range; endotoxin; Cry12I8; gene; ds.  
XX OS *Bacillus thuringiensis*.

XX PN WO200234774-A2.  
XX PD 02-MAY-2002.  
XX PF 24-OCT-2001; 2001WO-US45468.  
XX PR 24-OCT-2000; 2000US-242838P.

23-OCT-2001: 2001US-0032717.

(DUPO) DU PONT DE NEMOURS & CO E I.

Abad AR. Duck NB. Feng X. Flannagan BD. Kahn TW. Sims LE.

WPI: 2002-519178/55.

New isolated pesticidal polypeptide useful for impacting insect pests and Colorado potato beetle -

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Claim 13; Page 144-145; 176pp; English.

The present invention relates to a new pesticidal polypeptide. The invention is useful for inventing an insect pest by applying the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm. The invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present nucleic acid sequence encodes a *Bacillus thuringiensis* wild-type Cry1I28 endotoxin protein.

Sequence 4874 BP: 1707 A: 787 C: 1003 G: 1377 T: 0 other:

100.0%; Score 3621; DB 24; Length 4874;

Very Match 100.0%; Score 3621; Pred. No. 0;  
Best Local Similarity 100.0%;

Local Similarity 100.0%, P-Val: 0.0000, ID: 3621, Length: 3621, Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGTCCAAATAATCAAAATGAATATGAAATTATAGATGCGACACCTTCTACTTCTGTA 60

731 ATGAGTCCAAATAATCAAAATGAAATATGAAATTATAGATGCCACACCTTCTACTTCTGTA 790

61 TCCAAATGATTCTAACAGATACCCCTTTTGCGAATGAGCCCAACAAATGCGCTACAAAATATG 120

791 TCCATTCTTAAACAGATACCCCTTTGCGAATGAGCCACAAATGCGTACAAATATG 850

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571 CTAACAGGTTAAGGGGTCCTTCATTGTGGGCGGATAGTAGAGTCTTTATATACACACCTTATT 103

301 GATAATCTGTGGCCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360

1031 GATATCTGTGGCCTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAACAAGTAGAA 109

361 GAACTCATTAATCAAAAATAGCAGAAATATGCAAGGAATAAAGCGCTTTCGGAATTAGAA 420

1091 GAACTCATTAATCAAAAAATAGCAGAAATATGCAAGGAATAAAGCGCTTTCGGAATTAGAA 115

421 GGATTAGGTAATAATTACCAATTATATCTAACTGCGCTTGAAAGAAATGGGAAGAAATCCA 480

1151 GGATTAGGTAATAATTACCAATTATCTAACTGCGCTTGAAGAATGGGAAGAAATCCA 121

481 AATGGTTCAAGAGCCCTTACGAGATGTGCGAAATCGATTTGAAATCCTGGATAGTTATT 540

1211 AATGGTTCAAGAGCCCTTACGAGATGTGCCGAATCGATTTTGAAATCCTGGATAGTTTATTT 127

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Db 2411 GTAGGAACCTTATTTCTAGCTCGATATGGCTAGCATTAGAAAAAGCAGGAAATATCGT 2470  
Qy 1741 GTAAGACTGAGATATGCTACTGATGACAGATATTTGTATTGTCATGTAAACGATGCTCAGATT 1800  
Db 2471 GTAAGACTGAGATATGCTACTGATGACAGATATTTGTATTGTCATGTAAACGATGCTCAGATT 2530  
Qy 1801 CAGATGCCAAAAAACAATGAACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCA 1860  
Db 2531 CAGATGCCAAAAAACAATGAACCCAGGTGAGGATCTGACATCTAAAACTTTTAAAGTTGCA 2590  
Qy 1861 GATGCTATCACAACATTAATTTAGCAACAGATATGTCGTAGCATGTAAGAAATTAATTTA 1920  
Db 2591 GATGCTATCACAACATTAATTTAGCAACAGATATGTCGTAGCATGTAAGAAATTAATTTA 2650  
Qy 1921 GGTGAAGACCCCTAATTTCAACATTTATCTGGTATAGTTTACGCTGACCGAATCGAATTCATC 1980  
Db 2651 GGTGAAGACCCCTAATTTCAACATTTATCTGGTATAGTTTACGCTGACCGAATCGAATTCATC 2710  
Qy 1981 CCAAGTATGAGACATATGAAGCGGAACAAGATTTAGAAGCAGCGAAGAACGAGTGAAT 2040  
Db 2711 CCAAGTATGAGACATATGAAGCGGAACAAGATTTAGAAGCAGCGAAGAACGAGTGAAT 2770  
Qy 2041 GCCTTGTTTACGATACAAAGATGCTTACGACCGAGGCTAACGATTTATGAAGTGAAT 2100  
Db 2771 GCCTTGTTTACGATACAAAGATGCTTACGACCGAGGCTAACGATTTATGAAGTGAAT 2830  
Qy 2101 CAAGCGGCAAACTTAGTGGAAATGCCCTATCGGATGATTTGATCCAAATGAAGAACGATTG 2160  
Db 2831 CAAGCGGCAAACTTAGTGGAAATGCCCTATCGGATGATTTGATCCAAATGAAGAACGATTG 2890  
Qy 2161 TTATTTGATGCTAGTGAGAGGCAAAACCGCTCAGTGAGGACGATTAATTTGCTTCAAGAT 2220  
Db 2891 TTATTTGATGCTAGTGAGAGGCAAAACCGCTCAGTGAGGACGATTAATTTGCTTCAAGAT 2950  
Qy 2221 CCAGATTTCCAGAGATAAATGAGAAAATGGCTGGACCGAAGTACGGGAATTTAGGTT 2280  
Db 2951 CCAGATTTCCAGAGATAAATGAGAAAATGGCTGGACCGAAGTACGGGAATTTAGGTT 3010  
Qy 2281 ATAGAAGGGATGCTCTTATTTCAAGGCGTTATCTACGCTCACCGTGCAGAGAAATA 2340  
Db 3011 ATAGAAGGGATGCTCTTATTTCAAGGCGTTATCTACGCTCACCGTGCAGAGAAATA 3070  
Qy 2341 GATACGGAAACGTPATCAACGATCTGTATCAAAAAGTAGAGGAAGGTGTATTTAAACCA 2400  
Db 3071 GATACGGAAACGTPATCAACGATCTGTATCAAAAAGTAGAGGAAGGTGTATTTAAACCA 3130  
Qy 2401 TACACAAGATATAGATTGAGAGGTTTGTCCGAAGCAGTCAAGATTTGAAAATTTTCACA 2460  
Db 3131 TACACAAGATATAGATTGAGAGGTTTGTCCGAAGCAGTCAAGATTTGAAAATTTTCACA 3190  
Qy 2461 ATTCTGTCATCAACGAAACCGAATTTGTAATAAATGTACCGGATGATTTGCTGCCAGATGTA 2520  
Db 3191 ATTCTGTCATCAACGAAACCGAATTTGTAATAAATGTACCGGATGATTTGCTGCCAGATGTA 3250  
Qy 2521 TCTCTCTGTTAACTCGGATGCTAGTATCAATCGATGCGAAGCAAAAGTATGTCAATAGC 2580  
Db 3251 TCTCTCTGTTAACTCGGATGCTAGTATCAATCGATGCGAAGCAAAAGTATGTCAATAGC 3310  
Qy 2581 CGTTTGAAGTAGAAAAACCGTTCTGGTGAAGCGGATGCTCTATTTCTATTTGATACATA 2640  
Db 3311 CGTTTGAAGTAGAAAAACCGTTCTGGTGAAGCGGATGCTCTATTTCTATTTGATACATA 3370  
Qy 2641 GGTGAATCGATTTACAAATGAAATGCAAGGAATATGGTTCGATTTAAGATTACGGACCCA 2700  
Db 3371 GGTGAATCGATTTACAAATGAAATGCAAGGAATATGGTTCGATTTAAGATTACGGACCCA 3430  
Qy 2701 GAGGGATATGCACACTCGGAAACCTAGAAATGCTCGAAGAGGACCTTTTATCAGGAGAC 2760  
Db 3431 GAGGGATATGCACACTCGGAAACCTAGAAATGCTCGAAGAGGACCTTTTATCAGGAGAC 3490  
Qy 2761 GCATTTAGACGCTTTCGAAGAGAGAAACAACAGTGGGAAGATTTCAATGACAAGAACGCT 2820  
Db 3491 GCATTTAGACGCTTTCGAAGAGAGAAACAACAGTGGGAAGATTTCAATGACAAGAACGCT 3550

Qy 2821 GAAGAAAACAGATAGAGAGGTATATGGCATCGAAAACGAACGCGTAGATCGTTTATATGCCGAT 2880  
Db 3551 GAAGAAAACAGATAGAGAGGTATATGGCATCGAAAACGAACGCGTAGATCGTTTATATGCCGAT 3610  
Qy 2881 TATCAGGATCAGCAACTGAATCCTGATGATGAGATTTACAGATCTTTACTCGGCGCCCAAGAT 2940  
Db 3611 TATCAGGATCAGCAACTGAATCCTGATGATGAGATTTACAGATCTTTACTCGGCGCCCAAGAT 3670  
Qy 2941 CTGATACAGTCCATTTCTTACGTATATATACGAAATGTTTCCAGAAATACACGGGATGAC 3000  
Db 3671 CTGATACAGTCCATTTCTTACGTATATATACGAAATGTTTCCAGAAATACACGGGATGAC 3730  
Qy 3001 TATACGAGTCTTACAGAAATTTACAGATCGACTCCAAACGAGCGTGGAGTTTGTATGATCAG 3060  
Db 3731 TATACGAGTCTTACAGAAATTTACAGATCGACTCCAAACGAGCGTGGAGTTTGTATGATCAG 3790  
Qy 3061 CGAAATGCCATACCAAATGGTGATTTTGGAAATGGGTTAAAGTAAATGGAAATGCAACGCCT 3120  
Db 3791 CGAAATGCCATACCAAATGGTGATTTTGGAAATGGGTTAAAGTAAATGGAAATGCAACGCCT 3850  
Qy 3121 GCGTAGAGTACAAACAAATCAATCATCATCTGCTCTGCTGATTCCTCAACCTGGGATGAG 3180  
Db 3851 GCGTAGAGTACAAACAAATCAATCATCATCTGCTCTGCTGATTCCTCAACCTGGGATGAG 3910  
Qy 3181 CAAAGTTTCGCAACAGTTTACAGTTCAAACGGAATCAAGATATGTGTTACGAGTTACTGCG 3240  
Db 3911 CAAAGTTTCGCAACAGTTTACAGTTCAAACGGAATCAAGATATGTGTTACGAGTTACTGCG 3970  
Qy 3241 AGAAAAGAGGGGTAGGAAATCGATATGATTAAGTATCCCGTGTGGTGGAAATCAAAACAGAA 3300  
Db 3971 AGAAAAGAGGGGTAGGAAATCGATATGATTAAGTATCCCGTGTGGTGGAAATCAAAACAGAA 4030  
Qy 3301 AGCCTTACTTTTGTAGTCCAGCGATTTATGATACAAATGGAAATCTATATACGCAAGTGTCC 3360  
Db 4031 AGCCTTACTTTTGTAGTCCAGCGATTTATGATACAAATGGAAATCTATATACGCAAGTGTCC 4090  
Qy 3361 AATACAAATGGATATAACAAATAATGGTATATAACAAAGCATCGAGTACAAACGGA 3420  
Db 4091 AATACAAATGGATATAACAAATAATGGTATATAACAAAGCATCGAGTACAAACGGA 4150  
Qy 3421 TATAACGCAAAATTAATGATTAATACGCAAGCATCGAATACAAACGGAATATAACAAAT 3480  
Db 4151 TATAACGCAAAATTAATGATTAATACGCAAGCATCGAATACAAACGGAATATAACAAAT 4210  
Qy 3481 AGTGTGTACAAATGATCAACCGCTATATACAAACAGTGCATTCATCCGTTATACA 3540  
Db 4211 AGTGTGTACAAATGATCAACCGCTATATACAAACAGTGCATTCATCCGTTATACA 4270  
Qy 3541 GATCAAAATGCTGATTTGAGATGAGTACAGAGAGGATGATCTATATAGAAAGTGTAGAA 3600  
Db 4271 GATCAAAATGCTGATTTGAGATGAGTACAGAGAGGATGATCTATATAGAAAGTGTAGAA 4330  
Qy 3601 TTGATTTGATAGCTAGAGTAA 3621  
Db 4331 TTGATTTGATAGCTAGAGTAA 4351

RESULT 3  
ABK87235

ID ABK87235 standard; DNA; 3633 BP.

XX AC ABK87235;

XX XX

DT 07-OCT-2002 (first entry)

XX Bacillus thuringiensis Cry1218-2 gene sequence.

DE Pesticidal; spraying; dusting; broadcasing; seed coating; insect pest;  
KW Colorado potato beetle; western corn rootworm; southern corn rootworm;  
KW insect target range; endotoxin; Cry1218; gene; ds.

OS Bacillus thuringiensis.

XX WO200234774-A2.  
 XX PD 02-MAY-2002.  
 XX 24-OCT-2001; 2001WO-US45458.  
 XX 24-OCT-2000; 2000US-242838P.  
 XX PR 23-OCT-2001; 2001US-0032717.  
 XX (DUPO) DU PONT DE NEMOURS & CO E I.  
 XX Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;  
 XX WPI; 2002-519178/55.  
 XX P-PSDB; RAU99256.  
 XX New isolated pesticidal polypeptide useful for impacting insect pest  
 PT e.g. Colorado potato beetle -  
 XX Claim 1; Page 98-103; 176pp; English.  
 XX The present invention relates to a new pesticidal polypeptide. The  
 CC invention is useful for impacting an insect pest by applying the  
 CC the molecules of the invention to the environment of the insect pest by  
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest  
 CC is selected from Colorado potato beetle, western corn rootworm or  
 CC southern corn rootworm. The invention is also useful for increasing  
 CC insect target range and for producing transgenic microorganisms and  
 CC plants that express the pesticidal polypeptide. The invention is also  
 CC useful for producing transformed plants and in transforming any organism  
 CC to produce the pesticidal polypeptide of the invention. The present  
 CC nucleic acid sequence encodes a *Bacillus thuringiensis* wild-type  
 CC Cry1218 endotoxin protein.  
 XX  
 SQ Sequence 3633 BP; 1277 A; 609 C; 767 G; 980 T; 0 other;  
 Query Match 87.0%; Score 3151.8; DB 24; Length 3633;  
 Best Local Similarity 92.1%; Pred. No. 0;  
 Matches 3353; Conservative 0; Mismatches 262; Indels 24; Gaps 2;

QY 1 ATGAGTCAAAATCAAAATGAATATGAAATATAGATGCGACACCTTCTACTCTGTA 60  
 DB 1 ATGAGTCAAAATCAAAATGAATATGAAATATAGATGCGACACCTTCTACTCTGTA 60  
 QY 61 TCCATGATCTCAACAGATACCTTTTCGATGAGCCAAACAAATGCGCTACAAATATG 120  
 DB 61 TCCATGATCTCAACAGATACCTTTTCGATGAGCCAAACAAATGCGCTACAAATATG 120  
 QY 121 GATTATAAGATTATTATAAATGCTCGGGAAATGCTAGTGAATACCGCTGGTTCACT 180  
 DB 121 GATTATAAGATTATTATAAATGCTCGGGAAATGCTAGTGAATACCGCTGGTTCACT 180  
 QY 181 GAACTCTGTTAGCGGCAAGATCAGCTAAGCGCGCAATGATATAGTAGTAAATTA 240  
 DB 181 GAACTCTGTTAGCGGCAAGATCAGCTAAGCGCGCAATGATATAGTAGTAAATTA 240  
 QY 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTAGCTTTTATCTCACTTAT 300  
 DB 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTAGCTTTTATCTCACTTAT 300  
 QY 301 GATATCTGTGCGCTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360  
 DB 301 GATATCTGTGCGCTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360  
 QY 361 GAACTCATTAATCAAAAAATAGCAGAATATCAAGGAATAAAGCGCTTTCCGAATTAGAA 420  
 DB 361 GAACTCATTAATCAAAAAATAGCAGAATATCAAGGAATAAAGCGCTTTCCGAATTAGAA 420  
 QY 421 GGATTAGGTAATAATCAAAATATATCTAATCTGAGCTGGCTTGAAGATGGGAAAGAAATCCA 480  
 DB 421 GGATTAGGTAATAATCAAAATATATCTAATCTGAGCTGGCTTGAAGATGGGAAAGAAATCCA 480  
 QY 481 AATGGTTCAAGAGCCTTACGAGATGTCGAAATCGAATTTGAAATCCTGGATAGTTATTT 540  
 DB 481 AATGGTTCAAGAGCCTTACGAGATGTCGAAATCGAATTTGAAATCCTGGATAGTTATTT 540  
 QY 541 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATTCCTTACTGTATAT 600  
 DB 541 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATTCCTTACTGTATAT 600  
 QY 601 GCAATGGCAGCCAACTTCAATTTACTGTATTAAGAGCGCTCAATTTTGGAGAGAA 660  
 DB 601 ACACAGAGCCAACTTCAATTTACTGTATTAAGAGCGCTTCAATTTTGGAGAGAA 660  
 QY 661 TGGGGATGGTCAACAACTATCTATTAATAAATATATATGATCGTCAAAATGAAACTTACTGCA 720  
 DB 661 TGGGGATGGTCAACAACTATCTATTAATAAATATATATGATCGTCAAAATGAAACTTACTGCA 720  
 QY 721 GAATATTTCTGATCACTGTGTAAGTGTATGAATCTGGTTTAGCAAAATTAAGAGCGACG 780  
 DB 721 GAATATTTCTGATCACTGTGTAAGTGTATGAATCTGGTTTAGCAAAATTAAGAGCGACG 780  
 QY 781 AGCGCTAAACAATGGGTTGACTATAACAATTCGTAGAGAAATGACACTGCGCGTTT 840  
 DB 781 AGCGCTAAACAATGGGTTGACTATAACAATTCGTAGAGAAATGACACTGCGCGTTT 840  
 QY 841 GATGTTGTTGCAATTTCCCAATTTATGACACACGACGTACCCAAATGGAACGAAAGCA 900  
 DB 841 GATGTTGTTGCAATTTCCCAATTTATGACACACGACGTACCCAAATGGAACGAAAGCA 900  
 QY 901 CAACATAAGGGAAGTATATACAGATCCACTGGGCGGTAAACGTGCTCTCAATTGGT 960  
 DB 901 CAACATAAGGGAAGTATATACAGATCCACTGGGCGGTAAACGTGCTCTCAATTGGT 960  
 QY 961 TCCTGGTATGACAAAGCACCTTCTTTCGAGTGTAGAAATCATCCGTTATTCGACCC 1020  
 DB 961 TCCTGGTATGACAAAGCACCTTCTTTCGAGTGTAGAAATCATCCGTTATTCGACCC 1020  
 QY 1021 CATGTATTTGATATATAACGGGACTCACAGTGTATACAAATCAAGAAAGCAATTTCTTCC 1080  
 DB 1021 CATGTATTTGATATATAACGGGACTCACAGTGTATACAAATCAAGAAAGCAATTTCTTCC 1080  
 QY 1081 GCTCGCTATATAAGACATTTGGGCTGGTCAATCAATAGCTACCATCGTGTAGTAGGGT 1140  
 DB 1081 GCTCGCTATATAAGACATTTGGGCTGGTCAATCAATAGCTATCATCGGATTTTAGTGAT 1140  
 QY 1141 AGTAATCTTCAACAAATGATGGAATCAATCAAAATCTACACAGCACTAGTACCTTTGAT 1200  
 DB 1141 AATATTAATAAAGAGATGATGGAATCAATCAAAATCTACACAGCACTAGTACCTTTGAT 1200  
 QY 1201 TTTACGAATTAATGATATTTTCAAGACTCTATCAAGAGTGCAGTACTCTCTTGATTTGTT 1260  
 DB 1201 TTTACGAATTAATGATATTTTCAAGAGCTTATCAAGAGTGCAGTACTCTCTTGATTTGTT 1260  
 QY 1261 TACCTGGTTATACGTATATTTTTTGGAAATGCGAAGTGCAGTCTTTTCAATGGTAAAC 1320  
 DB 1261 TTTCTCGTTATACGTATATTTTTTGGAAATGCGAAGTGCAGTCTTTTCAATGGTAAAC 1320  
 QY 1321 CAATTTGAATATACCAAGACCTTAAAGTATATCCAGTTCCTCCAAAGATATATATAGCG 1380  
 DB 1321 CAATTTGAATATACCAAGACCTTAAAGTATATCCAGTTCCTCCAAAGATATATATAGCG 1380  
 QY 1381 AGTACAAGAGATTCGGAAATAGAAATTAACCTCCAGAACTTCAGATCAACAAATATATAG 1440  
 DB 1381 GGGACAGAGATTCGGAAATAGAAATTAACCTCCAGAACTTCAGATCAACAAATATATAG 1440  
 QY 1441 TCATATAGCCATAGATTTATGTCATATCAAGATATTCGGCGACGGGTAAACACTACCGGA 1500  
 DB 1441 TCATATAGCCATAGATTTATGTCATATCAAGATATTCGGCGACGGGTTCACACTACCGGA 1500  
 QY 1501 TTAGTACCTGATTTCTTGGACACATCGAGTGCAGTTTAAACATATATATATATCA 1560  
 DB 1501 TTAGTACCTGATTTCTTGGACACATCGAGTGCAGTTTAAATATATATATATATCA 1560  
 QY 1561 GATAAATCACTCAAAATTCGCGCGGTTAAATGTTGGGATATTTTACCGTTTGT ----- 1613

Db 1561 GATAAAATTAACACAGATTCGGTTCGTAAGGTTCTGATTTGGCTCCCTCTATAACAGGA 1620  
Qy 1614 -----TCCAGTGTAAAGACGACGACATACAGAGGGGNTTTATTACAGTAT 1662  
Db 1621 GGGCCAAATAATACCCGTTGATCGGGTCTCGGATTTACAGGGGGGGGATTAATAAAGTA 1680  
Qy 1663 AATAGAAAGTATCGTTTCTGTAGGAACCTTATTTCTAGCTCGATATGGCCTPAGCATTAGAA 1722  
Db 1681 ATAAGAAATGGAGTAATATACATATCGCGTGTAAATTTTACAGACATTTACAAAGAA 1740  
Qy 1723 AAAGCGGGAATATCGTGAAGCTGAGATATGCTACTGATGAGATATGTATTGTCAT 1782  
Db 1741 TATAGTATGAGGATTCGGTATGCTTCGGCTAATAAATACTGAAATTTATATAAAATCCCTTCT 1800  
Qy 1783 GTAACGATGCTCAGATTCAGATGCGCAAAACAACTGAACCCAGCTGAGGATCTGACATCT 1842  
Db 1801 GAAGAAACGTTAAATCTCAGCTCAAAACAACTATGAATAGAGGTGAAGCTTTTAAACAT 1860  
Qy 1843 AAAAATTTTAAAGTTGACATGCTATCACAAACATTAATTTAGCAACAGATAGTTGCTTA 1902  
Db 1861 AATAAATTTAATTTATGCGACTTTGCCCCCTTATTAATTTTACGACAAACCGAACCTTTCA 1920  
Qy 1903 GCATTTGAACATTAATTTAGTGAAGACCTTAATTTCAACATTTATCTGGTATAGTTTACGTT 1962  
Db 1921 ACTTAGGGGCTATATTTGAAGCGGAAGACTTTTCTTGGAAAT-----TGAAGCTTATATA 1974  
Qy 1963 GACCGAATCGAATTCATCCAGTAGATGACATATGAAGCGGAAACAGATTTTAGAGCA 2022  
Db 1975 GACCGAATCGAATTTATCCAGTAGATGACATATGAAGCGGAAACAGATTTTAGAGCA 2034  
Qy 2023 GCGAAGAAAGCAGTGAATGCTTTGTACCAATACAAACAGATGCTTACGACACAGGCGTA 2082  
Db 2035 GCGAAGAAAGCAGTGAATGCTTTGTACCAATACAAACAGATGCTTACGACACAGGCGTA 2094  
Qy 2083 ACGGATTTGAAGTGAATCAAGCGGCAAACTTTAGTGAATGCTTATCGGATGATTTGTAT 2142  
Db 2095 ACGGATTTGAAGTGAATCAAGCGGCAAACTTTAGTGAATGCTTATCGGATGATTTGTAT 2154  
Qy 2143 CCATATGAAGAAAGATTTGATTTGATGACATGAGAGGCAAAACGCTTCACTGAGGCA 2202  
Db 2155 CCAATGAAGAAAGATTTGATTTGATGACATGAGAGGCAAAACGCTTCACTGAGGCA 2214  
Qy 2203 CGTAATTTGCTTCAAGATCCAGATTTCCAGAGATAAATGGAGAAATGCTGACGCGCA 2262  
Db 2215 CGTAATTTGCTTCAAGATCCAGATTTCCAGAGATAAATGGAGAAATGCTGACGCGCA 2274  
Qy 2263 AGTACGGGAATTCAGGTTATAGAGGGGATGCTTTATTTCAAAGGGCGTTATCTACGCTTA 2322  
Db 2275 AGTACGGGAATTCAGGTTATAGAGGGGATGCTTTATTTCAAAGGGCGTTATCTACGCTTA 2334  
Qy 2323 CCAGGTGCGAGAGAAATAGATACGGAACCTATCCACGTTATCTGTATCAAAAGTAGAG 2382  
Db 2335 CCAGGTGCGAGAGAAATAGATACGGAACCTATCCACGTTATCTGTATCAAAAGTAGAG 2394  
Qy 2383 GAAGTGTATTAATAACCATACACAGATATAGATTGAGAGGTTTGTTCGGAAGCAGTCAA 2442  
Db 2395 GAAGTGTATTAATAACCATACACAGATATAGATTGAGAGGTTTGTTCGGAAGCAGTCAA 2454  
Qy 2443 GGATTCGAAATTTTCAATTCGTTCATCAAACCGAATGTTAAATAATGTACCGGAT 2502  
Db 2455 GGATTCGAAATTTTCAATTCGTTCATCAAACCGAATGTTAAATAATGTACCGGAT 2514  
Qy 2503 GATTTGCTGCCAGATGATCTCTGTTAACTCGGATGTTAGTATCAATCGATGAGCGAA 2562  
Db 2515 GATTTGCTGCCAGATGATCTCTGTTAACTCGGATGTTAGTATCAATCGATGAGCGAA 2574  
Qy 2563 CAAAAGTATGTAATAGCCGTTTAGAAGTAGTGAAGAACCGTTCTGCTGAAGCGATGAGTTC 2622  
Db 2575 CAAAAGTATGTAATAGCCGTTTAGAAGTAGTGAAGAACCGTTCTGCTGAAGCGATGAGTTC 2634  
Qy 2623 TCTATTCTTATGATACAGGTGAATCGATTACAATGAAATTCAGGAATATGGGTTGGA 2682

Db 2635 TCTATTCTTATGATACAGGTGAATCGATTCAATGAAATTCAGGAATATCGGTTGGA 2694  
Qy 2683 TTTTAAGATTTACGAGACCCAGAGGGATATCAACACTCGGAAACCTAGAAATTTGGTTCGAAGAG 2742  
Db 2695 TTTTAAGATTTACGAGACCCAGAGGGATATCAACACTCGGAAACCTAGAAATTTGGTTCGAAGAG 2754  
Qy 2743 GGAACCTTTATCAGGAGACGCAATTTAGAACCTTTGCAAGAGAAACAAACAGTTCGAAGATT 2802  
Db 2755 GGAACCTTTATCAGGAGACGCAATTTAGAACCTTTGCAAGAGAAACAAACAGTTCGAAGATT 2814  
Qy 2803 CAAATGCAAGAGAGAGCTGAAGAAACAGATAGAGGTATATGCGATCGAAACAGGCGTA 2862  
Db 2815 CAAATGCAAGAGAGAGCTGAAGAAACAGATAGAGGTATATGCGATCGAAACAGGCGTA 2874  
Qy 2863 GATCGTTTATATGCGGATTTATCAGGATCAGCAACTCAATCTCTGATGTAGAGATTACAGAT 2922  
Db 2875 GATCGTTTATATGCGGATTTATCAGGATCAGCAACTCAATCTCTGATGTAGAGATTACAGAT 2934  
Qy 2923 CTTTACTGCGGCCCAAGATCTGATACAGTCCATTCCTTACGTATATTAACGAAATGTTCCCA 2982  
Db 2935 CTTTACTGCGGCCCAAGATCTGATACAGTCCATTCCTTACGTATATTAACGAAATGTTCCCA 2994  
Qy 2983 GAAATACCAAGGATGAACTTATACGAAGTTTACAGAAATTAACAGATCGACTCCCAACAGCG 3042  
Db 2995 GAAATACCAAGGATGAACTTATACGAAGTTTACAGAAATTAACAGATCGACTCCCAACAGCG 3054  
Qy 3043 TGGAGTTTGTATGATCAGCGAAATGCCATACCAAAATGGTGATTTTCGAAATGGTTAAAGT 3102  
Db 3055 TGGAGTTTGTATGATCAGCGAAATGCCATACCAAAATGGTGATTTTCGAAATGGTTAAAGT 3114  
Qy 3103 AATTGGAATGCAACGCTGCGGTAGAGTACAAACAAATCAATCATCATCTGTCCTTTGTG 3162  
Db 3115 AATTGGAATGCAACGCTGCGGTAGAGTACAAACAAATCAATCATCATCTGTCCTTTGTG 3174  
Qy 3163 ATTCCAAAATCTGGATGAGCAAGTTTCGCAACAGTTTACAGTTCAACCGAAATCAAGATAT 3222  
Db 3175 ATTCCAAAATCTGGATGAGCAAGTTTCGCAACAGTTTACAGTTTCAACCGAAATCAAGATAT 3234  
Qy 3223 GTCTTACGAGTTTACTCGGAGAAAGAGGGTAGGAAATGGATATGTAAGTATCCGTTGAT 3282  
Db 3235 GTCTTACGAGTTTACTCGGAGAAAGAGGGTAGGAAATGGATATGTAAGTATCCGTTGAT 3294  
Qy 3283 GGTGGAATCAAAACAGAAACGCTTACTTTTAGTCAAGCGGATTTATGATACAAATGGAATG 3342  
Db 3295 GGTGGAATCAAAACAGAAACGCTTACTTTTAGTCAAGCGGATTTATGATACAAATGGAATG 3354  
Qy 3343 TATAATACGCAAGTGTCCAAATCAAAATGGATATTAACACAAATTAATCGGTATATACAA 3402  
Db 3355 TATAATACGCAAGTGTCCAAATCAAAATGGATATTAACACAAATTAATCGGTATATACAA 3414  
Qy 3403 GCATCGAGTACAAACCGATATAACGCAAAATAATATGTAATACGCAAGCATCGAATACA 3462  
Db 3415 GCATCGAGTACAAACCGATATAACGCAAAATAATATGTAATACGCAAGCATCGAATACA 3474  
Qy 3463 AACGGATATAACCAAAATAGTGTCAATGATCAAAACCGGCTATATCAAAACAAAGT 3522  
Db 3475 AACGGATATAACCAAAATAGTGTCAATGATCAAAACCGGCTATATCAAAACAAAGT 3534  
Qy 3523 ACATTCATCCCGTATACAGATCAAAATGTGGATTTGAGATGAGTGAAGAGGTTACATTC 3582  
Db 3535 ACATTCATCCCGTATACAGATCAAAATGTGGATTTGAGATGAGTGAAGAGGTTACATTC 3594  
Qy 3583 TATATGAAGTCTAGAAATTTGATTGTAGACGTAGATTA 3621  
Db 3595 TATATGAAGTCTAGAAATTTGATTGTAGACGTAGATTA 3633

RESULT 4

ABK87248

ID ABK87248 standard; DNA; 6613 BP.

XX

AC ABK87248;

XX



DT 07-OCT-2002 (first entry)  
 XX Bacillus thuringiensis genomic CryI218-2 DNA sequence.  
 XX  
 KW Pesticidal; spraying; dusting; broadcasing; seed coating; insect pest;  
 KW Colorado potato beetle; western corn rootworm; southern corn rootworm;  
 KW insect target range; endotoxin; CryI218; ds.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 XX WO200234774-A2.  
 XX  
 XX 02-MAY-2002.  
 XX  
 XX 24-OCT-2001; 2001WO-US45468.  
 XX  
 XX 24-OCT-2000; 2000US-242838P.  
 PR 23-OCT-2001; 2001US-0032717.  
 XX  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX  
 XX Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;  
 XX WPI; 2002-519178/55.  
 XX  
 XX New isolated pesticidal polypeptide useful for impacting insect pest  
 XX e.g. Colorado potato beetle -  
 XX  
 XX Claim 13; Page 145-147; 176pp; English.  
 XX  
 XX The present invention relates to a new pesticidal polypeptide. The  
 CC invention is useful for impacting an insect pest by applying the  
 CC the molecules of the invention to the environment of the insect pest by  
 CC spraying, dusting, broadcasing, or seed coating, where the insect pest  
 CC is selected from Colorado potato beetle, western corn rootworm or  
 CC southern corn rootworm. The invention is also useful for increasing  
 CC insect target range and for producing transgenic microorganisms and  
 CC plants that express the pesticidal polypeptide. The invention is also  
 CC useful for producing transformed plants and in transformation any organism  
 CC to produce the pesticidal polypeptide of the invention. The present  
 CC nucleic acid sequence represents the Bacillus thuringiensis CryI218-2  
 CC endotoxin genomic DNA sequence.  
 XX  
 XX SQ Sequence 6613 BP; 2289 A; 1049 C; 1306 G; 1969 T; 0 other;  
 Query Match 87.0%; Score 3151.8; DB 24; Length 6613;  
 Best Local Similarity 92.1%; Pred. No. 0;  
 Matches 3353; Conservative 0; Mismatches 262; Indels 24; Gaps 2;  
 QY 1 ATGAGTCCAAATAAATCAAAATGAATGAAATTTATAGATGCGACACCTTCTACTTCTGTA 60  
 DB 1254 ATGAGTCCAAATAAATCAAAATGAATGAAATTTATAGATGCGACACCTTCTACTTCTGTA 1313  
 QY 61 TCCAAATGATTTCAACAGATACCCCTTTTGGGAATGAGCCAAACAAATGCGCTACAAATATG 120  
 DB 1314 TCCAAATGATTTCAACAGATACCCCTTTTGGGAATGAGCCAAACAAATGCGCTACAAATATG 1373  
 QY 121 GATTATAAGATTTTAAATATGCTGGGGAATGCTAGTGAATACCCCTGGTTCACCT 180  
 DB 1374 GATTATAAGATTTTAAATATGCTGGGGAATGCTAGTGAATACCCCTGGTTCACCT 1433  
 QY 181 GAAGTACTTTGTAGCGGACAAAGATGAGCTAAGCGCGCAATGATATAGTAGTAAATTA 240  
 DB 1434 GAAGTACTTTGTAGCGGACAAAGATGAGCTAAGCGCGCAATGATATAGTAGTAAATTA 1493  
 QY 241 CTATCAGGTTTGGGGTCCCATTTGTTGGCCGATAGTGGATCTTTATCTCAACTTAT 300  
 DB 1494 CTATCAGGTTTGGGGTCCCATTTGTTGGCCGATAGTGGATCTTTATCTCAACTTAT 1553  
 QY 301 GATATTTCTGGCTTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360  
 DB 1554 GATATTTCTGGCTTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 1613  
 QY 361 GAACTCATTAATCAAAAATAGCAGAAATATGCAAGGAATAAAGCGCTTTCGGAATTAGAA 420  
 DB 1614 GAACTCATTAATCAAAAATAGCAGAAATATGCAAGGAATAAAGCGCTTTCGGAATTAGAA 1673  
 QY 421 GGATTAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480  
 DB 1674 GGATTAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1733  
 QY 481 AATGGTTCAAGAGCCTTACGAGATGTCGGAATCGATTTGAAATCCTCGATAGTTTATTT 540  
 DB 1734 AATGGTTCAAGAGCCTTACGAGATGTCGGAATCGATTTGAAATCCTCGATAGTTTATTT 1793  
 QY 541 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATTCCTTACTGTATAT 600  
 DB 1794 ACGCAATATATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCAATTCCTTACTGTATAT 1853  
 QY 601 GCAATGGCAGCCCACTTCAATTTACTGTTATTAAGAGCGGTCAATTTTGGGAGAGAA 660  
 DB 1854 ACACAGGCGAGCCCACTTCAATTTACTGTTATTAAGAGCGGTTCATTTTGGGAGAGAA 1913  
 QY 661 TGGGATGCTCAACCACTACTTAAATAACTATTATGATCGTCAATGAACTTACTGCA 720  
 DB 1914 TGGGATGCTCAACCACTACTTAAATAACTATTATGATCGTCAATGAACTTACTGCA 1973  
 QY 721 GAATATTTCTGATCACTGTGTAAAGTGTATGAAACTGGTTTAGCAAAATTTAAAGGCACG 780  
 DB 1974 GAATATTTCTGATCACTGTGTAAAGTGTATGAAACTGGTTTAGCAAAATTTAAAGGCACG 2033  
 QY 781 AGCGCTAAACCAATGGGTGACATAAACAATTCCTGAGAGAAATGACACTGCGGGTTTAA 840  
 DB 2034 AGCGCTAAACCAATGGGTGACATAAACAATTCCTGAGAGAAATGACACTGACGGTTTAA 2093  
 QY 841 GATGTTGTGCAATTTATCCCAATTTATGACACACGCTACCCCAATGGAACGAAAGCA 900  
 DB 2094 GATGTTGTGCAATTTATCCCAATTTATGACACACGCTACCCCAATGGAACGAAAGCA 2153  
 QY 901 CAACTAAACAGGAAGTATATACAGATCACTGGGCGGGTAAACGTGCTTCAATTTGT 960  
 DB 2154 CAACTAAACAGGAAGTATATACAGATCACTGGGCGGGTAAACGTGCTTCAATTTGT 2213  
 QY 961 TCCTGGTATGACAAAGCCTTTCTTTTCGAGTGTATAGAAATCATCCGTTATTCGACACCC 1020  
 DB 2214 TCCTGGTATGACAAAGCCTTTCTTTTCGAGTGTATAGAAATCATCCGTTATTCGACACCC 2273  
 QY 1021 CATGTTATTTGATTTATTAACGGGACTCACTGCTGATATACATCAAGAGCAATTTCTTCC 1080  
 DB 2274 CATGTTATTTGATTTATTAACGGGACTCACTGCTGATATACATCAAGAGCAATTTCTTCC 2333  
 QY 1081 GCTCGCTATATAAGACATTTGGGCTGCTCATCAATAAGCTACCATCGTGTCACTAGTGGGT 1140  
 DB 2334 GCTCGCTATATAAGACATTTGGGCTGCTCATCAATAAGCTACCATCGTGTCACTAGTGGGT 2393  
 QY 1141 AGTAATCTTCAACAAATGTATGGAATCAATCAAAATCTACACAGCACTAGTACCTTTGAT 1200  
 DB 2394 AATAATATAAACAAGTGTATGGAATCAATCAAAATCTACACAGCACTAGTACCTTTGAT 2453  
 QY 1201 TTTAGCAATTTATGATTTTACAGACTCTTCAAGAGGATGCACTGCTTCTGATTTGTT 1260  
 DB 2454 TTTAGCAATTTATGATTTTACAGACTCTTCAAGAGGATGCACTGCTTCTGATTTGTT 2513  
 QY 1261 TACCTCGTGTATACGTTATATTTTGGAAATGCGAGAGTGTGCTTTTCACTGGTAAAC 1320  
 DB 2514 TTTCTCGTGTATACGTTATATTTTGGAAATGCGAGAGTGTGCTTTTCACTGGTAAAC 2573  
 QY 1321 CAAATGAATAATACAGAAAGCGTTAAAGTATATAATCCAGTTTCCAAAGATATTATAGCG 1380  
 DB 2574 CAAATGAATAATACAGAAAGCGTTAAAGTATATAATCCAGTTTCCAAAGATATTATAGCG 2633  
 QY 1381 AGTACAAGNGATTCGGAATTTAGAAATTTACTCCAGAACTTCAGATCAACCAATTTATGAG 1440  
 DB 2634 GGGACAAGAGATTCGGAATTTAGAAATTTACTCCAGAACTTCAGATCAACCAATTTATGAG 2693  
 QY 1441 TCATATAGCCATAGATTATGTCTATATCAAGTATTTCCGCGAGCGGTAACTACCGGA 1500

Db 2694 TCATATAGCCATAGATTTATGTCTATATCAAGATATTCGCGGACGGTTCACATACCGGA 2753  
Qy |||||  
Db 1501 TTAGTACCTGTATTTCTTGGACACATCGAAGTGCAGATTTAAACAATACATATATTC 1560  
Qy |||||  
Db 2754 TTAGTACCTGTATTTCTTGGACACATCGAAGTGCAGATTTAAACAATAGCAGTTCATTC 2813  
Qy |||||  
Db 1561 GATAAAATCACTCAAAATCCGGCGGTAAATGTGGGATAAATTTACCGTTTGT----- 1613  
Qy |||||  
Db 2814 GATAAAATTTACTCAGATTCGGGTCTGTAAGGTTTCTGATTTGGCTCCCTCTATAACAGGA 2873  
Qy |||||  
Qy 1614 -----TCCAGTGTAAAGACACAGACATACAGGAGGATTTATTTACAGTAT 1662  
Db 2874 GGGCCAAATTAATACCGTTGTATCGGCTCTCGATTTACAGGGGGGGGATAATANAAGTA 2933  
Qy |||||  
Qy 1663 AATAGAGTACTGGTTCGTAGGAACTTTATTTCTAGCTCGATGCTATGCTAGCTAGCTAGGAA 1722  
Db 2934 ATAAGAAATGGAGTAATATATATACATATCGGTGTTAAATTTTACAGACATTAACAAAGAA 2993  
Qy |||||  
Qy 1723 AAAGCAGGGAATATCGTGTAAAGACTGAGATATGCTACTGATGCGATATTTGTATTCAT 1782  
Db 2994 TATAGTATGAGGATTCGGTATGCTTCGGCTAATTAATTAATTAATTAATTAATTAATTAAT 3053  
Qy |||||  
Qy 1783 GTAACGATGCTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 1842  
Db 3054 GAAAGAAACGTTAAATCTCAGCTCAAAAAAATCTATGAATAGAGGTGAAGCTTTAAACATAT 3113  
Qy |||||  
Qy 1843 AAAATCTTTAAAGTTGCAGATGCTATCAACAATTAATTTAGCACAGATAGTTCGCTA 1902  
Db 3114 AATAAATTTAATATGCGACTTTGCCCCCTATTAATTTTACGACAAACCGAACCCTTTTCAT 3173  
Qy |||||  
Qy 1903 GCATTTGAAACATAATTTAGGTGAAGACCTTAATTTCAACATATCTGGTATAGTTTACGTT 1962  
Db 3174 ACTCTAGGGCTATATTTGAAGCGGAAGACTTTCTTGGAT-----TGAAGCTTATATA 3227  
Qy |||||  
Qy 1963 GACCAATCGAATTCATCCAGTAGATGAGACATATGAAGCGGAAACAAGATTTAGAAGCA 2022  
Db 3228 GACCAATCGAATTTATCCAGTAGATGAGACATATGAAGCGGAAACAAGATTTAGAAGCA 3287  
Qy |||||  
Qy 2023 GCGAAGAAAGCAGTGAATGCTTTTTCGAAATACAAAGATAGGCTTACGACCGGCGTA 2082  
Db 3288 GCGAAGAAAGCAGTGAATGCTTTTTCGAAATACAAAGATAGGCTTACGACCGGCGTA 3347  
Qy |||||  
Qy 2083 ACGGATTTAGAGTGAATCAAGCGGCAAACTTAGTGGAAATGCTATCGGATGATTTGTAT 2142  
Db 3348 ACGGATTTAGAGTGAATCAAGCGGCAAACTTAGTGGAAATGCTATCGGATGATTTGTAT 3407  
Qy |||||  
Qy 2143 CCAATGAAAAACGATTTGTATTTGATGAGTGAGAGGCAAAACGCTCTCAGTGAGGCA 2202  
Db 3408 CCAATGAAAAACGATTTGTATTTGATGAGTGAGAGGCAAAACGCTCTCAGTGAGGCA 3467  
Qy |||||  
Qy 2203 CGTAATTTGCTTCAAGATCCAGATTTTCCAGAGATTAATGGAGAAATGCTGCGACGGCA 2262  
Db 3468 CGTAATTTGCTTCAAGATCCAGATTTTCCAGAGATTAATGGAGAAATGCTGCGACGGCA 3527  
Qy |||||  
Qy 2263 AGTACGGGAATTTGAGTTATAGAGGGGATGCTTTATTTCAAGGGGCTTATCTACGCCCTA 2322  
Db 3528 AGTACGGGAATTTGAGTTATAGAGGGGATGCTTTATTTCAAGGGGCTTATCTACGCCCTA 3587  
Qy |||||  
Qy 2323 CCAGTGGCAGAGAAATAGATACGGAACGATTCGAACGATCTGATCAAAAAGTAGAG 2382  
Db 3588 CCAGTGGCAGAGAAATAGATACGGAACGATTCGAACGATCTGATCAAAAAGTAGAG 3647  
Qy |||||  
Qy 2383 GAAGGTATTTAAACCATACACAGATATAGTTGAGAGGTTTGTCCGAGCAGTCAA 2442  
Db 3648 GAAGGTATTTAAACCATACACAGATATAGTTGAGAGGTTTGTCCGAGCAGTCAA 3707  
Qy |||||  
Qy 2443 GGAATGGAATTTTCAAAATTCGTCATCAAAACGAACTGTAATAAATGTACCGGAT 2502  
Db 3708 GGAATGGAATTTTCAAAATTCGTCATCAAAACGAACTGTAATAAATGTACCGGAT 3767  
Qy |||||  
Qy 2503 GAATTTGCTGCCAGATGATCTCTGTTAACTCGGATGGTAGTATCAATCGATGCGACGAA 2562  
Db |||||

Db 3768 GAATTTGCTGCCAGATGATCTCTGTTAACTCGGATGGTAGTATCAATCGATGCGACGAA 3827  
Qy |||||  
Qy 2563 CAAAAGTATGCAATAGCCGTTTTCAGAGTGAAGAAACCGTTCTGGGTGAAGCGCATGAGTTC 2622  
Db 3828 CAAAAGTATGCAATAGCCGTTTTCAGAGTGAAGAAACCGTTCTGGGTGAAGCGCATGAGTTC 3887  
Qy |||||  
Qy 2623 TCTATTTCTTATTGATACAGGTGAAATTCGATTAACAATGAAAAATGCGAGGAATATGGGTGGA 2682  
Db 3888 TCTATTTCTTATTGATACAGGTGAAATTCGATTAACAATGAAAAATGCGAGGAATATGGGTGGA 3947  
Qy |||||  
Qy 2683 TTTAAGATTTACGACCCGACAGGAGATTCGCAACACTCGGAAACCTAGAAATTTGGTTCGAAGAG 2742  
Db 3948 TTTAAGATTTACGACCCGACAGGAGATTCGCAACACTCGGAAACCTAGAAATTTGGTTCGAAGAG 4007  
Qy |||||  
Qy 2743 GGACCTTTTATCAGGAGACGCTTTAGAAACGTTTGAAGAGAGAAACAACAGTGGAGATTT 2802  
Db 4008 GGACCTTTTATCAGGAGACGCTTTAGAAACGTTTGAAGAGAGAAACAACAGTGGAGATTT 4067  
Qy |||||  
Qy 2803 CAAATGACAAAGAGACGTTGAAGAAACAGATAGAGGATATATGGCATCGAAAAACAAGCGGTA 2862  
Db 4068 CAAATGACAAAGAGACGTTGAAGAAACAGATAGAGGATATATGGCATCGAAAAACAAGCGGTA 4127  
Qy |||||  
Qy 2863 GATCGTTTATATGCGGATTTATCAGGATCAGCAACTGAAATCTCTGATGTAGAGATTTACAGAT 2922  
Db 4128 GATCGTTTATATGCGGATTTATCAGGATCAGCAACTGAAATCTCTGATGTAGAGATTTACAGAT 4187  
Qy |||||  
Qy 2923 CTTTACTGGGGCCCAAGATCTGATACAGTCCATTTCTTACGTTATATAACGAAATGTTCCCA 2982  
Db 4188 CTTTACTGGGGCCCAAGATCTGATACAGTCCATTTCTTACGTTATATAACGAAATGTTCCCA 4247  
Qy |||||  
Qy 2983 GAAATACCAAGGATGAACTTATACGAAGTTTACAGAAATTAACAGATCGACTCCAAACAAGCG 3042  
Db 4248 GAAATACCAAGGATGAACTTATACGAAGTTTACAGAAATTAACAGATCGACTCCAAACAAGCG 4307  
Qy |||||  
Qy 3043 TGGAGTTTGTATGATCAGGAAATGCCATACCAATGTTGATTTTCGAAATCGGTTAAATG 3102  
Db 4308 TGGAGTTTGTATGATCAGGAAATGCCATACCAATGTTGATTTTCGAAATCGGTTAAATG 4367  
Qy |||||  
Qy 3103 AATTGGAATGCAACCCCTGGCGTAGAAGTACAAACAAATCAATCATACATCTCTGCTTGTG 3162  
Db 4368 AATTGGAATGCAACCCCTGGCGTAGAAGTACAAACAAATCAATCATACATCTCTGCTTGTG 4427  
Qy |||||  
Qy 3163 AYTCCAAATCGGATGAGCAAGTTTCGCAACAGTTTACAGTTTCAACCGGAATCAAGATAT 3222  
Db 4428 AYTCCAAATCGGATGAGCAAGTTTCGCAACAGTTTACAGTTTCAACCGGAATCAAGATAT 4487  
Qy |||||  
Qy 3223 GTGTTACGAGTTTACGCGAGAAAGAGGGGTAGGAATGGAATGGAATGTAAGTATCCGTGAT 3282  
Db 4488 GTGTTACGAGTTTACGCGAGAAAGAGGGGTAGGAATGGAATGGAATGTAAGTATCCGTGAT 4547  
Qy |||||  
Qy 3283 GGTGGAATTCAAACAGAAACGCTTACTTTTGTAGTCAAGCGATTATGATCAAAATGGAATG 3342  
Db 4548 GGTGGAATTCAAACAGAAACGCTTACTTTTGTAGTCAAGCGATTATGATCAAAATGGAATG 4607  
Qy |||||  
Qy 3343 TATAATACGAAGTGTCCAAATCAAAATGGAATATAACAAATAATGCGGATTAATACACAA 3402  
Db 4608 TATAATACGAAGTGTCCAAATCAAAATGGAATATAACAAATAATGCGGATTAATACACAA 4667  
Qy |||||  
Qy 3403 GCATCGAGTACAAACGGAATATAACGCAATATATGTAATAACGCAAGATCGGAATACA 3462  
Db 4668 GCATCGAGTACAAACGGAATATAACGCAATATATGTAATAACGCAAGATCGGAATACA 4727  
Qy |||||  
Qy 3463 AACGATATACAAATAGTGTGTACATGATCAACCGGCTATATCAAAACAGAGT 3522  
Db 4728 AACGATATACAAATAGTGTGTACATGATCAACCGGCTATATCAAAACAGAGT 4787  
Qy |||||  
Qy 3523 ACATTCATCCCGTATACAGATCAAAATGTTGATGAGTGAAGTGAAGTGAAGTGAAGTGA 3582  
Db 4788 ACATTCATCCCGTATACAGATCAAAATGTTGATGAGTGAAGTGAAGTGAAGTGAAGTGA 4847  
Qy |||||  
Qy 3583 TATATAGAAAGTGTAGAAATTTGATTTAGACGTTAGAGTAA 3621  
Db 4848 TATATAGAAAGTGTAGAAATTTGATTTAGACGTTAGAGTAA 4886

## RESULT 5

AAT43221  
ID AAT43221 standard; DNA; 3507 BP.

XX AC AAT43221;

XX DT 28-JAN-1997 (first entry)

XX DE Antiscarab pest toxin 50C(b) coding sequence.

XX KW Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae; pest control;  
XX KW larval stage insect; grain; tuberous crop; white grub; chafer grub;  
XX KW cyclocephala; popillia; ds.

XX OS Bacillus thuringiensis strain kumamotoensis.

XX PN US554534-A.

XX PD 10-SEP-1996.

XX PF 30-SEP-1994; 94US-0315468.

XX PR 01-FEB-1993; 93US-0014941.

XX PR 16-DEC-1991; 91US-0808316.

XX PR 30-JAN-1992; 92US-0828430.

XX PR 30-SEP-1994; 94US-0315468.

XX PA (MYCO) MYCOGEN CORP.

XX PI Foncerrada L, Michaels TE, Narva KE;

XX DR WPI; 1996-424659/42.

XX DR P-PSDB; AAW06417.

XX PT New nucleic acid encoding B.thuringiensis toxin active against

XX PT scarab(s) - also related toxin and transformed microbes, effective

XX PT against adult pests and their larvae

XX PS Claim 2; Column 27-30; 24pp; English.

XX CC AAT43221-T43223 represent the coding sequences for toxins that are  
XX CC active against scarab pests. This sequence was isolated from the  
XX CC Bacillus thuringiensis strain kumamotoensis. Insects in the family  
XX CC Scarabaeidae constitute a serious pest control problem, especially when  
XX CC destructive larval stage insects infest high value turf found in golf  
XX CC courses, playing fields and lawns. The larvae of many species also  
XX CC attack grains, tuberous crops, and ornamentals. The larvae are known as  
XX CC white grubs, or chafer grubs, and can be found in decaying organic  
XX CC matter, or in the soil where they consume plant roots. In Europe and the  
XX CC U.S. populations of these larvae and adults have developed resistance to  
XX CC chemical insecticides such as the organochlorines and DDT. The toxins  
XX CC encoded by these sequences, and intact cells that are capable of  
XX CC expressing the proteins, can be used to control many pests of the family  
XX CC scarabaeidae, such as species of Cyclocephala, and Popillia. The toxins  
XX CC are active against larvae (present in soil) and against adults.

XX SQ Sequence 3507 BP; 1256 A; 576 C; 732 G; 943 T; 0 other;

Query Match 70.8%; Score 2565.2; DB 17; Length 3507;

Best Local Similarity 85.1%; Pred. No. 0;

Matches 2906; Conservative 0; Mismatches 493; Indels 15; Gaps 3;

Qy 1 ATGAGTCCAAATTAATCAAAATGAATATGAATATATAGATGCGACACCTTCTACTCTGTA 60

Db 1 ATGAGTCCAAATTAATCAAAATGAATATGAATATATAGATGCGACACCTTCTACTCTGTA 60

Qy 61 TCCAAATGATTTCAACAGATACCCCTTTTGGGAATGAGCCAAACAAATGCGCTACAAATATG 120

Db 61 TCCAAATGATTTCAACAGATACCCCTTTTGGGAATGAGCCAAACAAATGCGCTACAAATATG 120

Qy 121 GATTATAGATTAATTAATAATGTCGCGGGAATGCTAGTGAATACCCCTGGTTCACT 180

Db 121 GATTATAGATTAATTAATAATGTCGCGGGAATGCTAGTGAATACCCCTGGTTCACT 180

Qy 181 GAAGTACTTTGTAGCGGCAAGATGCGAGCTAAGCGCGCAATGATATAGTAGTAAATTA 240

Db 181 GAGGTATTTCTAAGCGAGCAAGATGCGAGCTAAGCGCGCAATGATATAGTAGTAAATTA 240

Qy 241 CTATCAGGTTTGGGGTCCCATTTGTTGGGCGATAGTAGTGTCTTTATCTCAACTTATT 300

Db 241 CTRACAGGTTTGGGGTCCCATTTGTTGGGCGATAGTAGTGTCTTTATCTCAACTTATT 300

Qy 301 GATATTTCTGTGCGCTTACGGGGAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360

Db 301 GATATTTCTGTGCGCTTCAAAACAAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360

Qy 361 GAATCTAATTAACAAAATAGCAGATATGCAAGGATTAAGCGCTTTCGGAATTAGAA 420

Db 361 GAATCTAATTAACAAAATAGCAGATATGCAAGGATTAAGCGCTTTCGGAATTAGAA 420

Qy 421 GGATTAGGTAATTAATTAACCAATTAATCTAATGCGCTTGAAGAAATGGAAGAAATCCA 480

Db 421 GGGTAGGGAATTAATTAACCAATTAATCTAATGCGCTTGAAGAAATGGAAGAAATCCA 480

Qy 481 AATGGTTCAAGAGCGCTTACGAGATGTCGAAATCGATTTGAAATCCTGGATAGTTTAT 540

Db 481 AATGGTTCAAGAGCGCTTACGAGATGTCGAAATCGATTTGAAATCCTGGATAGTTTAT 540

Qy 541 AGCAATATATGCGCATCTTTTGTAGAGTGACAAATTTTGAAGTACCAATTCCTACTGTAT 600

Db 541 AGCAATATATGCGCATCTTTTGTAGAGTGACAAATTTTGAAGTACCAATTCCTACTGTAT 600

Qy 601 GCAATGGCAGCCCAACCTTCATTTACTGTTTAAAGGAGCGGTCAATTTTGGGAAGAA 660

Db 601 GCAATGGCAGCCCAACCTTCATTTACTGTTTAAAGGAGCGGTCAATTTTGGGAAGAA 660

Qy 661 TGGGATGCTCAACCACTACTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 720

Db 661 TGGGATGCTCAACCACTACTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 720

Qy 721 GAATATTCGTACTGTTGTAAGTGTATGAACTGGTTAGCAAAATTAAGAGCAGC 780

Db 721 GAATATTCGTACTGTTGTAAGTGTATGAACTGGTTAGCAAAATTAAGAGCAGC 780

Qy 781 AGCGCTAAACAAATGGTTGACTATTAACCAATTCGTTAGAGAAATGACACTGCGGTTTA 840

Db 781 AGCGCTAAACAAATGGTTGACTATTAACCAATTCGTTAGAGAAATGACACTGCGGTTTA 840

Qy 841 GATGTTGTTGCAATTAATCCCAATTAATGACACACGACGATCCCAATGGAACGAAAGCA 900

Db 841 GATGTTGTTGCAATTAATCCCAATTAATGACACACGACGATCCCAATGGAACGAAAGCA 900

Qy 901 CAACTAACAGGAAGTATATACAGATCCACTGGGCGGTTAAACGTGCTTCAATTTGT 960

Db 901 CAGCTTACAGGAAGTATATACAGATCCACTGGGCGGTTAGATGTCCTTAATTTTGC 960

Qy 961 TCCTGATGACAAAGCAGCTTCTTTCCGAGTGTAGATCATCCGTTATTCGACACCC 1020

Db 961 TCCTGATGACAAAGCAGCTTCTTTCCGAGTGTAGATCATCCGTTATTCGACACCC 1020

Qy 1021 CATGTATTTGATTAATTAACCGGACTCAAGTGTATATACCAATCAAGAAAGCAATTTCT 1080

Db 1021 CATGTATTTGATTAATTAACCGGACTCAAGTGTATATACCAATCAAGAAAGCAATTTCT 1080

Qy 1081 GCTCGCTATATAAGACATTTGGGCTGGTCAATCAATTAAGTACCATCGTGTAGTAGGGT 1140

Db 1081 GATCGTTATATGAGATATTTGGGCTGGTCAATCAATTAAGTACCATCGTGTAGTAGGGT 1140

Qy 1141 AGTATCTTCAACAAATGATGGAATTAATCAAAATCTACACAGCACTAGTACTTTGAT 1200

Db 1141 AGTATCTTCAACAAATGATGGAATTAATCAAAATCTACACAGCACTAGTACTTTGAT 1200

Qy 1201 TTTTACGAATTAATTAATTAACAGACTTATCAAGAGTCTATCAAGAGTACAGTACTCTCT 1260

Db 1201 TTACGAATACGATATTTTCAAGACTTTATCAAAATGGTGCAGTACTCCTTGATATAGTT 1260  
Qy 1261 TACCTCTGGTTATACGTATATATTTTTTGGAAATGCCAGAGAGTGCAGTTTTTTCATGGTAAAC 1320  
Db 1261 TACCTCTGGTTATACGTATATATTTTTTGGAAATGCCAGAGAGTGCAGTTTTTTCATGGTAAAT 1320  
Qy 1321 CAATTTGAATTAATACCAAGAAAGCGTTTAAAGTATAATCCAGTTTCCAAAGATATATATAGCG 1380  
Db 1321 CAATTTGAATTAATACCAAGAAAGCGTTTAAAGTATAATCCAGTTTCCAAAGATATATATAGAT 1380  
Qy 1381 AGTACAGAGATTCGGAATTAGAATTTACCTCCGAAACTTCAGATCAACCAATATATAGAG 1440  
Db 1381 CGACAGAGATTCGGAATTAGAATTTACCTCCGAAACTTCAGATCAACCAATATATAGAG 1440  
Qy 1441 TCATATAGCATATAGTATATGTCATATCAAGTATTTCCGCGAGCGGTAACTACCTACCGGA 1500  
Db 1441 TCATATAGCATATAGTATATGTCATATCAAGTATTTCCGCGAGCGGTAACTACCTACCGGA 1500  
Qy 1501 TTAGTACCTGTATTTTCTTGGACACATCGAAGTGCAGATTTTAAACAAATACAATATATCA 1560  
Db 1498 TATGTACCTGTATTTTCTTGGACACATCGAAGTGCAGATTTTAAACAAATACAATATATCA 1557  
Qy 1561 GATAAATACATCAAAATCCGCGCGTTAAATGTTGGGATAATTTACCGTTTGTTCAGTG 1620  
Db 1558 GCGGAATCACCCNAATACAGGGGCAAGTCTAGCACCATAGGCGAAGATACTATATA 1617  
Qy 1621 GTAAAGGACAGGACATACAGAGGGGATTTATACAGTATATAGAGTACTGTTCT 1680  
Db 1618 ATAAAGGGCGTGTATACAGGGGAGACTTAGTGCGTTTAAAGGACCGCATCGGAAT 1677  
Qy 1681 GPAGGAACCTTATTTCTAGCTCGATGCGCTAGCAATAGCAATAGAAAGACGAGGAATATCGT 1740  
Db 1678 TGTGAGTTTCAGATGATCTTCCAGAGTCTCAACGATTCGGTATTCGGATTCGTTACGCT 1737  
Qy 1741 GTAAGCTGAGATATGCTACTGATGACAGATATTTGATGTCATGTAACGATGCTCAGAT 1800  
Db 1738 TCTAAATGAACCTAGTTATATATAGTTTATACGGAATTAACCAAGCGGAATCTTAAATTC 1797  
Qy 1801 CAGATGCCAAAACAAATGAACCCAGGTGAGGATCTGACATCTAAAACCTTTTAAAGTTGCA 1860  
Db 1798 AACAGACATATCTTAATAAAATGAATGATTTAACAATATATGATTTCAATATATA 1857  
Qy 1861 GATGCTATCAACACATTAATTTAGCAACAGATAGTTTCGTCAGATTTGAAACATATATTA 1920  
Db 1858 GAATATC---CAAGAGTCAATTCAGTAATGCTTCTTCAACATACAGAGTTATCTATA 1914  
Qy 1921 GGTGAAGCCCTTAATCAACATATCTGCTATAGTTTACGTTGACCGAATCGAATTCATC 1980  
Db 1915 GGTATACAAACGAATACAAATTTATTTATTTA-----GACCGAATCGAATTCATC 1965  
Qy 1981 CCAGTAGATGACATATCAAGCGGAACAAGATTTTAGAGCAGCGGAAGCAAGTGAAT 2040  
Db 1966 CCAGTAGATGACATATAGCGGGAACCGGATTTAGAGCGGCAAGAAAGCAGTGAAT 2025  
Qy 2041 GCCTTTGTTTACGAATACAAAGATGCTTTACGACCAAGCGGTAAACGATATGAAGTGAAT 2100  
Db 2026 GCCTTTGTTTACGAATACAAAGATGCTTTACGACCAAGGTAAACGATATGAAGTGAAT 2085  
Qy 2101 CAAGCGGCAAACTTAGTGAATGCCTATCGGATGATTTGATTCAAATGAAACCAAGTTG 2160  
Db 2086 CAAGCGGCAAACTTAGTGAATGCCTATCGGATGATTTGATTCAAATGAAACCAAGTTG 2145  
Qy 2161 TTATTTGATGCTAGAGAGGCAAAACCCCTCAGTGCAGCGAGTAAATTTGCTTCAAGT 2220  
Db 2146 TTATTTGATGCTAGAGAGGCAAAACCGCTTAGCGAGCGAGTAAATTTGCTTCAAGT 2205  
Qy 2221 CCAGATTTCCAGAGATTAATGGAGAAATGCTGCGAGCGAGTAAATTTGAGGTT 2280  
Db 2206 CCAGATTTCCAGAGATTAATGGAGAAATGCTGCGAGCGAGTAAATTTGAGGTT 2265  
Qy 2281 ATAGAGGGGATGCTTTATTTCAAGGGCGTTATCTACGCTACAGGTGCGAGAGAAATA 2340  
Db 2266 ATAGAGGGGATGCTTTATTTCAAGGGCGTTATCTACGCTACAGGTGCGAGAGAAATA 2325

Qy 2341 GATACGGAACGATATCCAAACGATCTGTATCAAAAGTAGAGGAAGGTGTATTTAAACCA 2400  
Db 2326 GATACGGAACGATATCCAAACGATCTGTATCAAAAGTAGAGGAAGGTGTATTTAAACCA 2385  
Qy 2401 TACACAAGATATAGATTCAGAGGGTTTTCGGAAGCAGTCAAGGATTTGGAATTTTCA 2460  
Db 2386 TACACAAGATATAGATTCAGAGGGTTTTCGGAAGCAGTCAAGGATTTGGAATTTTATACG 2445  
Qy 2461 ATTCTGTCATCAACCAACCGAATTCGGAATTTTACCGGATGATTTGCTGCCAGATGTA 2520  
Db 2446 ATTCTGTCATCAACCAACCGAATTCGGAATTTTACCGGATGATTTTACCGGATGTA 2505  
Qy 2521 TCTCTCTGTTAACTCCGATGCTAGTATCAATCGATCGAGCAACAAAGATGTTGAATAGC 2580  
Db 2506 CTTCTCTGTTAACTAGATGCTAGTATCAATCGATCGAGCAACAAAGATGTTGAATAGT 2565  
Qy 2581 CTTTTAGAGTAGAATAACCGTTCTCGTGAAGCGCATGTTCTTATTCCTATTTGATACA 2640  
Db 2566 CTTTTAGAGTAGAATAACCGTTCTCGTGAAGCGCATGTTCTTATTCCTATTCGATACA 2625  
Qy 2641 GGTGAATTCGATTAACAATGAAATCGAGAAATCGGTTTGAATTTTAAAGATTCAGGACCCA 2700  
Db 2626 GGAGAGCTGGATTAACAATGAAATCGAGAAATCGGTTTGAATTTTAAAGATTCAGGACCCA 2685  
Qy 2701 GAGGATATGCAACACTCGGAAACCTAGAAATTTGGTTCGAAGAGGACCTTTTATCAGGAGAC 2760  
Db 2686 GAGGATATGCAACACTCGGAAATTTGGAAATCTTGAATTTGGTTCGAAGAGGACCTTTTGCAGGAGAC 2745  
Qy 2761 GCATTTAGAACGCTTCCAAAGAGAGAAACAAACAGTGGAGATTTCAAATGACAGAGACGT 2820  
Db 2746 GCATTTAGAACGCTTCCAAAGAGAGAAACAAACAGTGGAGATTTCAAATGACAGAGACGT 2805  
Qy 2821 GAAGAAACAGATAGAGTATATGTCATCGAACAAGCGGTAGATCGTTTATATCCGAT 2880  
Db 2806 GAAGAAACAGATAGAGTATATGTCATCGAACAAGCGGTAGATCGTTTATATCCGAT 2865  
Qy 2881 TATCAGGATCAGCAACTGAACTCTGATGTAGAGATTTACAGATCTTACTCGGCGCCCAAGAT 2940  
Db 2866 TATCAGGATCAGCAACTGAACTCTGATGTAGAGATTTACAGATCTTACTCGGCGCTCAGAT 2925  
Qy 2941 CTGATACAGTCCATCTCTTACGTATATATACGAAATGTTTCCAGAAATACCAAGGATGAAC 3000  
Db 2926 CTAATACAGTCCATCTCTTACGTATATATACGAAATGTTTCCAGAAATACCAAGGATGAAC 2985  
Qy 3001 TATACAGAGTTTACAGAAATTAACAGATCGATCCCAACAGCGTGGAGTTTGTATGATCAG 3060  
Db 2986 TATACAGAGTTTACAGAGTTTAAACAGATCGATCCCAACAGCGTGGAGTTTGTATGATCAA 3045  
Qy 3061 CGAAATGCCATACCAAAATGCTGATTTTCGAAATGGTTAAGTAAATTTGGAATTCGAACGCT 3120  
Db 3046 CGAAATGCCATACCAAAATGCTGATTTTCGAAATGGTTAAGTAAATTTGGAATTCGAACATCT 3105  
Qy 3121 GCGGTAGAGTACAAACAAATCAATCATCTGCTCTTGTGATTTCCAACTGGGATGAG 3180  
Db 3106 GGTGTGAATGTACAAACAAATCAATCATCTGCTCTTGTGATTTCCAACTGGGATGAG 3165  
Qy 3181 CAAAGTTTCGCAACAGTTTACAGTTCAAACGATCAAGATATGTTTACGAGTTACTGCG 3240  
Db 3166 CAAAGTTTCGCAACAGTTTACAGTTCAAACGATCAAGATATGTTTACGAGTTACTGCG 3225  
Qy 3241 AGAAAGAGGGGTAGGAAATGGATATGTAAGTATTCGCTGATGGTGAATTAACACAGAA 3300  
Db 3226 AGAAAGAGGGGTAGGAAATGGATATGTAAGTATTCGCTGATGGTGAATTAACACAGAA 3285  
Qy 3301 ACGCTTACTTTTGTGCAAGCGATTTATGATACAAATGGAATGTATTAATACGCAAGTGTCC 3360  
Db 3286 ACGCTTACTTTTGTGCAAGCGATTTATGATACAAATGGAATGTATTAATACGCAAGTGTCC 3345  
Qy 3361 AATACAAATGGATATTAACAAATATGCGTATATATACAAAGCATCGAGTACA 3414  
Db 3346 AATACAAAGCGATATAACAAATATGTTGTATCATGATCAAAACCGGCTATATCA 3399

## RESULT 6

ABK87241  
 ID ABK87241 standard; DNA; 2010 BP.  
 XX AC ABK87241;  
 XX DT 07-OCT-2002 (first entry)  
 XX DE Bacillus thuringiensis Cry1218-1A truncated gene sequence.  
 XX KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;  
 XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;  
 XX KW insect target range; endotoxin; Cry1218; gene; ds.  
 XX OS Bacillus thuringiensis.  
 XX PN W0200234774-A2.  
 XX PD 02-MAY-2002.  
 XX PF 24-OCT-2001; 2001WO-US45468.  
 XX PR 24-OCT-2000; 2000US-242838P.  
 XX PR 23-OCT-2001; 2001US-0032717.  
 XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;  
 XX DR WPI; 2002-519178/55.  
 XX DR P-PSDB; AAU99262.  
 XX PT New isolated pesticidal polypeptide useful for impacting insect pest  
 XX PT e.g. Colorado potato Beetle -  
 XX PS Claim 1; Page 123-125; 176pp; English.  
 XX CC The present invention relates to a new pesticidal polypeptide. The  
 CC invention is useful for impacting an insect pest by applying the  
 CC the molecules of the invention to the environment of the insect pest by  
 CC spraying, dusting, broadcasting, or seed coating, where the insect pest  
 CC is selected from Colorado potato beetle, western corn rootworm or  
 CC southern corn rootworm. The invention is also useful for increasing  
 CC insect target range and for producing transgenic microorganisms and  
 CC plants that express the pesticidal polypeptide. The invention is also  
 CC useful for producing transformed plants and in transforming any organism  
 CC to produce the pesticidal polypeptide of the invention. The present  
 CC nucleic acid sequence encodes a Bacillus thuringiensis wild-type  
 CC Cry1218 endotoxin protein.  
 XX SQ Sequence 2010 BP; 690 A; 348 C; 394 G; 578 T; 0 other;

Query Match 55.5%; Score 2008.4; DB 24; Length 2010;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2009; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |      |             |          |        |         |        |         |        |         |       |      |
|----|------|-------------|----------|--------|---------|--------|---------|--------|---------|-------|------|
| QY | 241  | CTATCAGGTTT | AGGGTCC  | CAATTT | GTGGCCG | AGTAGT | AGTCTTT | TATAC  | CAACTT  | TATT  | 300  |
| DB | 241  | CTATCAGGTTT | AGGGTCC  | CAATTT | GTGGCCG | AGTAGT | AGTCTTT | TATAC  | CAACTT  | TATT  | 300  |
| QY | 301  | GATATTTCT   | GTGGCTTC | CAGGG  | AAAGAGT | CAATGG | AAATTTT | TATGG  | ACAGT   | AGAA  | 360  |
| DB | 301  | GATATTTCT   | GTGGCTTC | CAGGG  | AAAGAGT | CAATGG | AAATTTT | TATGG  | ACAGT   | AGAA  | 360  |
| QY | 361  | GAATCTCA    | TAAATCA  | AAAAAT | TAGCAG  | AATATG | CAAGG   | ATAA   | AGCGCTT | TCGGA | 420  |
| DB | 361  | GAATCTCA    | TAAATCA  | AAAAAT | TAGCAG  | AATATG | CAAGG   | ATAA   | AGCGCTT | TCGGA | 420  |
| QY | 421  | GGATTAGT    | TAATTA   | TACCA  | ATTATAT | CTA    | CTGCG   | CTTGA  | AGAA    | TTGGA | 480  |
| DB | 421  | GGATTAGT    | TAATTA   | TACCA  | ATTATAT | CTA    | CTGCG   | CTTGA  | AGAA    | TTGGA | 480  |
| QY | 481  | ANTGGTT     | CAAGG    | CTTAC  | GAGATG  | TGCG   | GAATG   | CAATTC | GAATTC  | CTGAT | 540  |
| DB | 481  | ANTGGTT     | CAAGG    | CTTAC  | GAGATG  | TGCG   | GAATG   | CAATTC | GAATTC  | CTGAT | 540  |
| QY | 541  | ACGCAAT     | TATATG   | CCATCT | TTTAG   | AGTGA  | CAAAAT  | TTTGA  | AGTAC   | CAAT  | 600  |
| DB | 541  | ACGCAAT     | TATATG   | CCATCT | TTTAG   | AGTGA  | CAAAAT  | TTTGA  | AGTAC   | CAAT  | 600  |
| QY | 601  | GCAATG      | CAGC     | CAAC   | CTTCA   | TTTAC  | TCTG    | TATTA  | AAAG    | CACG  | 660  |
| DB | 601  | GCAATG      | CAGC     | CAAC   | CTTCA   | TTTAC  | TCTG    | TATTA  | AAAG    | CACG  | 660  |
| QY | 661  | TGGGAT      | GTTCA    | CAACT  | ACTAT   | TATTA  | TAAT    | TAAT   | TATG    | ATG   | 720  |
| DB | 661  | TGGGAT      | GTTCA    | CAACT  | ACTAT   | TATTA  | TAAT    | TAAT   | TATG    | ATG   | 720  |
| QY | 721  | GAATATT     | CTGAT    | CACTG  | TAAAG   | TGTAT  | GAAAT   | CTGTT  | TAG     | CAAA  | 780  |
| DB | 721  | GAATATT     | CTGAT    | CACTG  | TAAAG   | TGTAT  | GAAAT   | CTGTT  | TAG     | CAAA  | 780  |
| QY | 781  | AGCGCT      | AAACA    | ATGG   | GTG     | ACTATA | TAACA   | CAAT   | TCCG    | TAG   | 840  |
| DB | 781  | AGCGCT      | AAACA    | ATGG   | GTG     | ACTATA | TAACA   | CAAT   | TCCG    | TAG   | 840  |
| QY | 841  | GATGTT      | GTG      | CAAT   | TAT     | TCCCA  | ATTAT   | GAC    | CACG    | CACT  | 900  |
| DB | 841  | GATGTT      | GTG      | CAAT   | TAT     | TCCCA  | ATTAT   | GAC    | CACG    | CACT  | 900  |
| QY | 901  | CAACTA      | CAAG     | GAAT   | TATAC   | AGAT   | CCACT   | GCG    | CGGT    | TAAC  | 960  |
| DB | 901  | CAACTA      | CAAG     | GAAT   | TATAC   | AGAT   | CCACT   | GCG    | CGGT    | TAAC  | 960  |
| QY | 961  | TCCTG       | GTATG    | CAAA   | GCA     | CCCTT  | CTT     | CGG    | AGT     | GTAG  | 1020 |
| DB | 961  | TCCTG       | GTATG    | CAAA   | GCA     | CCCTT  | CTT     | CGG    | AGT     | GTAG  | 1020 |
| QY | 1021 | CATG        | TATTT    | GAAT   | TATA    | TAA    | CGG     | GA     | CTCA    | CACT  | 1080 |
| DB | 1021 | CATG        | TATTT    | GAAT   | TATA    | TAA    | CGG     | GA     | CTCA    | CACT  | 1080 |
| QY | 1081 | GCTCG       | TATTA    | TAAC   | ATG     | CGG    | CTG     | CTCA   | CAAT    | AGT   | 1140 |
| DB | 1081 | GCTCG       | TATTA    | TAAC   | ATG     | CGG    | CTG     | CTCA   | CAAT    | AGT   | 1140 |
| QY | 1141 | AGTAAT      | CTTCA    | CAAA   | TATG    | TAA    | CTAA    | ATCT   | CA      | CAG   | 1200 |
| DB | 1141 | AGTAAT      | CTTCA    | CAAA   | TATG    | TAA    | CTAA    | ATCT   | CA      | CAG   | 1200 |
| QY | 1201 | TTTAC       | GAAAT    | TATG   | ATTA    | CA     | AGCT    | CTAT   | CA      | AGG   | 1260 |
| DB | 1201 | TTTAC       | GAAAT    | TATG   | ATTA    | CA     | AGCT    | CTAT   | CA      | AGG   | 1260 |
| QY | 1261 | TACCT       | CGT      | TATG   | ATTA    | TAT    | TTT     | GG     | ATG     | CG    | 1320 |
| DB | 1261 | TACCT       | CGT      | TATG   | ATTA    | TAT    | TTT     | GG     | ATG     | CG    | 1320 |
| QY | 1321 | CAAT        | TGA      | ATTA   | TAC     | GAA    | AG      | CGT    | TAA     | AGT   | 1380 |

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|----|------|--|------|
| Db | 1321 | CAATTTGAATATATACCGAAGAAGCGTTAAAGTATAATCCAGTTTCCAAAGATATTATAGCG   | 1380 |
| Qy | 1381 | AGTACAAGAGATTTCGGAAATTGAAATTACCTCCAGAAACTTCAGATCAACCAAAATATGAG   | 1440 |
| Db | 1381 | AGTACAAGAGATTTCGGAAATTGAAATTACCTCCAGAAACTTCAGATCAACCAAAATATGAG   | 1440 |
| Qy | 1441 | TCATATAGCCATAGATATTATGTCAATATCACAGTATTTCCCGCGACGGGTAACTACCGGA    | 1500 |
| Db | 1441 | TCATATAGCCATAGATATTATGTCAATATCACAGTATTTCCCGCGACGGGTAACTACCGGA    | 1500 |
| Qy | 1501 | TTAGTACCTGTATTTTCTTTGGACACATCGAAGTGCAGATTTTAAACAATACAATATATTC    | 1560 |
| Db | 1501 | TTAGTACCTGTATTTTCTTTGGACACATCGAAGTGCAGATTTTAAACAATACAATATATTC    | 1560 |
| Qy | 1561 | GATAAAATCACTCAAATTCGCGCCGTTAAATGTGGGATAATTTACCGTTTGTTCAGATG      | 1620 |
| Db | 1561 | GATAAAATCACTCAAATTCGCGCCGTTAAATGTGGGATAATTTACCGTTTGTTCAGATG      | 1620 |
| Qy | 1621 | GTTAAAGACCAGGACATACAGAGGGGATTTTATTCAGTATAATAGAAGTACTGTTCT        | 1680 |
| Db | 1621 | GTTAAAGACCAGGACATACAGAGGGGATTTTATTCAGTATAATAGAAGTACTGTTCT        | 1680 |
| Qy | 1681 | GTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATTAGAAAAAGCAGGGAAATATCGT     | 1740 |
| Db | 1681 | GTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATTAGAAAAAGCAGGGAAATATCGT     | 1740 |
| Qy | 1741 | GTAAGACTGAGATATGCTACTGATGCAGATATTTGTTATTCATGTAAACGATGCTCAGATT    | 1800 |
| Db | 1741 | GTAAGACTGAGATATGCTACTGATGCAGATATTTGTTATTCATGTAAACGATGCTCAGATT    | 1800 |
| Qy | 1801 | CAGATGCCAAAAAACAATGAAACCCAGGTGAGATCTGACATCTAAAAACTTTTAAAGTTGCA   | 1860 |
| Db | 1801 | CAGATGCCAAAAAACAATGAAACCCAGGTGAGATCTGACATCTAAAAACTTTTAAAGTTGCA   | 1860 |
| Qy | 1861 | GATGCTATCAACAACATTTAAATTTTGGCAACAGATAGTTTCGCTAGCATTTGAAACATATTTA | 1920 |
| Db | 1861 | GATGCTATCAACAACATTTAAATTTTGGCAACAGATAGTTTCGCTAGCATTTGAAACATATTTA | 1920 |
| Qy | 1921 | GGTGAAGACCCCTAAATTCAACTATCTGCTATAGTTTACGTTTGACCGAATTCGAATTCATC   | 1980 |
| Db | 1921 | GGTGAAGACCCCTAAATTCAACTATCTGCTATAGTTTACGTTTGACCGAATTCGAATTCATC   | 1980 |
| Qy | 1981 | CCAGTAGATGAGACATATGAAAGCGGAACAA                                  | 2010 |
| Db | 1981 | CCAGTAGATGAGACATATGAAAGCGGAATTA                                  | 2010 |

**SECRET**

## RESULT 7

ABK87236

ID ABK87236



AC ABK87236:

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1657/5094

07-OCT-2003 15:04:00

07-OCT-2002 (11st entry)

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DE Bacillus thuringiensis Cry

100

KW Pesticidal: spraying: dust:

Colorado potato beetle: we

**NY** NY  
insect treatment orders; we  
colorado potato beetle; we

KW insect target range; endot

(DUPO ) DU PONT DE NEMOURS & CO E I.  
Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;  
WPI: 2002-519178/55.  
P-PSDB: AAU99257.  
New isolated pesticidal polypeptide useful for impacting insect pest  
e.g. Colorado potato beetle -  
Claim 1; Page 106-108; 176pp; English.  
The present invention relates to a new pesticidal polypeptide. The  
invention is useful for impacting an insect pest by applying the  
molecules of the invention to the environment of the insect pest by  
spraying, dusting, broadcasting, or seed coating, where the insect pest  
is selected from Colorado potato beetle, western corn rootworm or  
southern corn rootworm. The invention is also useful for increasing  
insect target range and for producing transgenic microorganisms and  
plants that express the pesticidal polypeptide. The invention is also  
useful for producing transformed plants and in transforming any organism  
to produce the pesticidal polypeptide of the invention. The present  
nucleic acid sequence encodes a *Bacillus thuringiensis* wild-type  
Cry1218 endotoxin protein.  
Sequence 2003 BP: 686 A; 348 C; 392 G; 577 T; 0 other;

|                            |         |              |        |              |
|----------------------------|---------|--------------|--------|--------------|
| Query Match                | 55.3%;  | Score 2003;  | DB 24; | Length 2003; |
| Best Local Similarity      | 100.0%; | Pred. No. 0; |        |              |
| Matches 2003: Conservative | 0;      | Mismatches   | 0;     | Indels 0;    |
| Matches 2003: Gaps         | 0;      |              |        |              |

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|----|-----|--|-----|
| Qy | 1   | ATGAGTCCAAATATCAAAATGAATATGAATATATAGATGGACACCTTCTACTCTCGTA     | 60  |
| Db | 1   | ATGAGTCCAAATATCAAAATGAATATGAATATATAGATGGACACCTTCTACTCTCGTA     | 60  |
| Qy | 61  | TCCAATGATTTCTAACAGATACCCCTTTTGGCAATGAGCCAAACAAATGGCTACAAAAATG  | 120 |
| Db | 61  | TCCAATGATTTCTAACAGATACCCCTTTTGGCAATGAGCCAAACAAATGGCTACAAAAATG  | 120 |
| Qy | 121 | GATTATTAAGANTTATTTAAAAATGCTGCGGGAAATCTAGTGAATACCTTGGTTACCT     | 180 |
| Db | 121 | GATTATTAAGANTTATTTAAAAATGCTGCGGGAAATCTAGTGAATACCTTGGTTACCT     | 180 |
| Qy | 181 | GAACTACTTGTGTAGCGACAAGATGCAGCTAAGGCCCAATTGATATAGTAGGTAATA      | 240 |
| Db | 181 | GAACTACTTGTGTAGCGACAAGATGCAGCTAAGGCCCAATTGATATAGTAGGTAATA      | 240 |
| Qy | 241 | CTATCAGGTTTAGGGGTCCCAATTTGTTGGGCCGATAGTGAGTCTTTATATCTCAACTTATT | 300 |
| Db | 241 | CTATCAGGTTTAGGGGTCCCAATTTGTTGGGCCGATAGTGAGTCTTTATATCTCAACTTATT | 300 |
| Qy | 301 | GATATCTGTGGCCTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAAACAGTAGAA     | 360 |
| Db | 301 | GATATCTGTGGCCTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAAACAGTAGAA     | 360 |
| Qy | 361 | GAACTCATTAATCAAAAAATAGCAGAAATATGCAAGGAATAAAGCGCTTTCGGAATTAGAA  | 420 |
| Db | 361 | GAACTCATTAATCAAAAAATAGCAGAAATATGCAAGGAATAAAGCGCTTTCGGAATTAGAA  | 420 |
| Qy | 421 | GGATTAGTAATAATTACCAATTATATCTAACTCGCTTGAAGAAATCGGAAGAAAATCCA    | 480 |
| Db | 421 | GGATTAGTAATAATAACCAATTATATCTAACTCGCTTGAAGAAATCGGAAGAAAATCCA    | 480 |
| Qy | 481 | AATGGTTCAAGAGCCTTTACGAGATGTCGAAATCGATTTGAAATCCTGGATGTTTATT     | 540 |
| Db | 481 | AATGGTTCAAGAGCCTTTACGAGATGTCGAAATCGATTTGAAATCCTGGATGTTTATT     | 540 |
| Qy | 541 | ACGCAATATAGCCATCTTTTAGGTGACAAATTTTGAAGTACCAATTCCTTACTGTATAT    | 600 |
| Db | 541 | ACGCAATATATGCCATCTTTTAGGTGACAAATTTTGAAGTACCAATTCCTTACTGTATAT   | 600 |
| Qy | 601 | GCAATGGCAGCCAACTTTCATTTACTGTTATTAAGGACCGCTCAATTTTTTGGAGAGAAGAA | 660 |

Db 601 GCAATGGCAGCAACCTTCATTCTTCTGTTTAAAGGACGCGTCAATTTTGGAGAAGAA 660  
Qy 661 TGGGATGTCACAACTACTATTAATACTATTATGATCGTCAAAATGAACCTTACTGCA 720  
Db 661 TGGGATGTCACAACTACTATTAATACTATTATGATCGTCAAAATGAACCTTACTGCA 720  
Qy 721 GAATATTTCTGATCAGTGTGTAAGTGTGATGAACCTGTTTGTAGCAAAATTTAAAGGCACG 780  
Db 721 GAATATTTCTGATCAGTGTGTAAGTGTGATGAACCTGTTTGTAGCAAAATTTAAAGGCACG 780  
Qy 781 AGCGTAAACAATGGTGTGATCAATCAAAATTCCTGAGAGAAATGACACTGGCGGTTTTTA 840  
Db 781 AGCGTAAACAATGGTGTGATCAATCAAAATTCCTGAGAGAAATGACACTGGCGGTTTTTA 840  
Qy 841 GATGTTGTTGCAATTTTCCCAAATTTATGACACGACGCTACCCATGGAAGCA 900  
Db 841 GATGTTGTTGCAATTTTCCCAAATTTATGACACGACGCTACCCATGGAAGCA 900  
Qy 901 CAACTAAAGGGAAGTATATACAGATCCACTGGGCGCGGTAAACCGTCTTCAATTTGGT 960  
Db 901 CAACTAAAGGGAAGTATATACAGATCCACTGGGCGCGGTAAACCGTCTTCAATTTGGT 960  
Qy 961 TCCTGGTATGCAAGCACCTTCTTTCGGAGTGATGATCATCCGTTTATTCGACCACCC 1020  
Db 961 TCCTGGTATGCAAGCACCTTCTTTCGGAGTGATGATCATCCGTTTATTCGACCACCC 1020  
Qy 1021 CATGTTATTTGATTATATAACGGGACTCAGAGTGTATACAAATCAAGAGCATTTCTTCC 1080  
Db 1021 CATGTTATTTGATTATATAACGGGACTCAGAGTGTATACAAATCAAGAGCATTTCTTCC 1080  
Qy 1081 GCTCGCTATATAAGACATTTGGGCTGCTCATCAAAATGATACCATCGTGTAGTGGGT 1140  
Db 1081 GCTCGCTATATAAGACATTTGGGCTGCTCATCAAAATGATACCATCGTGTAGTGGGT 1140  
Qy 1141 AGTAATCTTCAACAAATGATGGAACCTATCAAAATCTACAGACACTAGTACCTTTGAT 1200  
Db 1141 AGTAATCTTCAACAAATGATGGAACCTATCAAAATCTACAGACACTAGTACCTTTGAT 1200  
Qy 1201 TTTACGAATTTATGATATTTTACAGACTCTATCAAGAGTGACGACTCTCTTGTATTTGT 1260  
Db 1201 TTTACGAATTTATGATATTTTACAGACTCTATCAAGAGTGACGACTCTCTTGTATTTGT 1260  
Qy 1261 TACCTCGTTATACGATATATTTTGGAAATCCAGAAAGTCAGTGTTCATGTTGTAAC 1320  
Db 1261 TACCTCGTTATACGATATATTTTGGAAATCCAGAAAGTCAGTGTTCATGTTGTAAC 1320  
Qy 1321 CAATTTGAATTAACAGAAAGCGTTAAAGTATTAATCCAGTTTCCAAAGATATATAGCG 1380  
Db 1321 CAATTTGAATTAACAGAAAGCGTTAAAGTATTAATCCAGTTTCCAAAGATATATAGCG 1380  
Qy 1381 AGTACAGAGATTCGGAATTTAGAAATTTACCTCCAGAAACTTCAGATCAACCAAAATATAG 1440  
Db 1381 AGTACAGAGATTCGGAATTTAGAAATTTACCTCCAGAAACTTCAGATCAACCAAAATATAG 1440  
Qy 1441 TCATATAGCCATAGATTTATGTCATATACAAAGTATTTCCGCGAGCGGTAACTACCGGA 1500  
Db 1441 TCATATAGCCATAGATTTATGTCATATACAAAGTATTTCCGCGAGCGGTAACTACCGGA 1500  
Qy 1501 TTAGTACCTGTTATTTCTGGACACATCGAAGTGCAGATTTAAACAATACAAATATATCA 1560  
Db 1501 TTAGTACCTGTTATTTCTGGACACATCGAAGTGCAGATTTAAACAATACAAATATATCA 1560  
Qy 1561 GATAAATCACTCAAAATTCGCGCGGTAAATGTTGGATTAATTTACGTTTGTTCAGTG 1620  
Db 1561 GATAAATCACTCAAAATTCGCGCGGTAAATGTTGGATTAATTTACGTTTGTTCAGTG 1620  
Qy 1621 GTAAAGGACCCAGGACATACAGAGGGGATTTATTACGATATATAGAGTACTGGTTCT 1680  
Db 1621 GTAAAGGACCCAGGACATACAGAGGGGATTTATTACGATATATAGAGTACTGGTTCT 1680  
Qy 1681 GTAGGAACCTTATTTCTAGCTCGATATGGCTAGCAATTTAGAAAAGCAGGAAATATCGT 1740  
Db 1681 GTAGGAACCTTATTTCTAGCTCGATATGGCTAGCAATTTAGAAAAGCAGGAAATATCGT 1740

Qy 1741 GTAAGACTCAGATATGCTACTGATGCAGATATTTGTTATGCTGTAAGAGTCTCAGATT 1800  
Db 1741 GTAAGACTCAGATATGCTACTGATGCAGATATTTGTTATGCTGTAAGAGTCTCAGATT 1800  
Qy 1801 CAGATGCCAAAACAAATGAACCCAGGTGAGGATCTGACATCTTAAACCTTTTAAAGTTGCA 1860  
Db 1801 CAGATGCCAAAACAAATGAACCCAGGTGAGGATCTGACATCTTAAACCTTTTAAAGTTGCA 1860  
Qy 1861 GATGCTATCACAAACATTAATTTAGCAACAGATAGTTCGCTAGCATTTGAAACATATTTA 1920  
Db 1861 GATGCTATCACAAACATTAATTTAGCAACAGATAGTTCGCTAGCATTTGAAACATATTTA 1920  
Qy 1921 GGTGAAGACCCCTAAATTTCAACATTTATCTGTATAGTTCGTTGACCGAATCGAATTCATC 1980  
Db 1921 GGTGAAGACCCCTAAATTTCAACATTTATCTGTATAGTTCGTTGACCGAATCGAATTCATC 1980  
Qy 1981 CCAGTAGATGAGACATATGAAGC 2003  
Db 1981 CCAGTAGATGAGACATATGAAGC 2003

## RESULT 8

ABK87245

ID ABK87245 standard; DNA; 2013 BP.

XX AC ABK87245;

XX DT 07-OCT-2002 (first entry)

XX DE *Bacillus thuringiensis* LKMS.R1218-1 mutant gene sequence.

XX KW Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;  
XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;  
XX KW insect target range; endotoxin; Cry1218; gene; mutant; ds.

XX OS *Bacillus thuringiensis*.

XX PN WO200234774-A2.

XX PD 02-MAY-2002.

XX PF 24-OCT-2001; 2001WO-US45468.

XX PR 24-OCT-2000; 2000US-242838P.

XX PR 23-OCT-2001; 2001US-0032717.

XX PA (DUPO ) DU PONT DE NEMOURS &amp; CO E I.

XX PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LB;

XX DR WPI: 2002-519178/55.

XX DR P-PSDB; AAU99266.

XX PT New isolated pesticidal polypeptide useful for impacting insect pest  
XX PT e.g. Colorado potato beetle -

XX PS Claim 23; Page 139-142; 176pp; English.

XX CC The present invention relates to a new pesticidal polypeptide. The  
XX CC invention is useful for impacting an insect pest by applying the  
XX CC the molecules of the invention to the environment of the insect pest by  
XX CC spraying, dusting, broadcasting, or seed coating, where the insect pest  
XX CC is selected from Colorado potato beetle, western corn rootworm or  
XX CC southern corn rootworm. The invention is also useful for increasing  
XX CC insect target range and for producing transgenic microorganisms and  
XX CC plants that express the pesticidal polypeptide. The invention is also  
XX CC useful for producing transformed plants and in transforming any organism  
XX CC to produce the pesticidal polypeptide of the invention. The present  
XX CC nucleic acid sequence encodes a *Bacillus thuringiensis* mutant Cry1218  
XX CC endotoxin protein.

XX SQ Sequence 2013 BP; 692 A; 348 C; 393 G; 580 T; 0 other;



|                       |     |   |               |            |              |
|-----------------------|-----|---|---------------|------------|--------------|
| Query Match           |     | 54.9%;  | Score 1987.4; | DB 24;     | Length 2013; |
| Best Local Similarity |     | 99.6%;  | Pred. No. 0;  |            |              |
| Matches 2004;         |     | Conservative  | 0;            | Mismatches | 6;           |
|                       |     |   |               | Indels     | 3;           |
|                       |     |   |               | Gaps       | 1;           |
| Qy                    | 1   | ATGAGTCCAAATTAATCAAAATGAATGAAATGAAATATATAGATGCGACACCTTCTACTTCTGTA | 60            |            |              |
| Db                    | 1   | ATGAGTCCAAATTAATCAAAATGAATGAAATATATAGATGCGACACCTTCTACTTCTGTA      | 60            |            |              |
| Qy                    | 61  | TCCAATGATTTCTAAACAGATACCTTTTGGGAATGAGCCAAACAAATGCGCTACAAATATG     | 120           |            |              |
| Db                    | 61  | TCCAATGATTTCTAAACAGATACCTTTTGGGAATGAGCCAAACAAATGCGCTACAAATATG     | 120           |            |              |
| Qy                    | 121 | GATTATAAGATTAATTTAAATATGCTCGGGGAAATGCTAGTGAATACCTCGTTCACCT        | 180           |            |              |
| Db                    | 121 | GATTATAAGATTAATTTAAATATGCTCGGGGAAATGCTAGTGAATACCTCGTTCACCT        | 180           |            |              |
| Qy                    | 181 | GAACTACTTTAGCGGACAGATGACATGAGCGGAAATGCTAGTGAATACCTCGTTCACCT       | 240           |            |              |
| Db                    | 181 | GAACTACTTTAGCGGACAGATGACATGAGCGGAAATGCTAGTGAATACCTCGTTCACCT       | 240           |            |              |
| Qy                    | 241 | CTATCAGGTTTATAGGCTCCCATTTGTTGGCCGATAGTGAATACCTCGTTCACCT           | 300           |            |              |
| Db                    | 241 | CTATCAGGTTTATAGGCTCCCATTTGTTGGCCGATAGTGAATACCTCGTTCACCT           | 300           |            |              |
| Qy                    | 301 | GATATTTCTGTGCGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAGATGAGAA     | 360           |            |              |
| Db                    | 301 | GATATTTCTGTGCGCTTCAGGGGAAAGAGTCAATGGGAAATTTTATGGAAACAGATGAGAA     | 360           |            |              |
| Qy                    | 361 | GAACTCAATTAATCAAAATATGACAGAAATGCAAGGAATAAAGCGCTTTCCGGAATTAGAA     | 420           |            |              |
| Db                    | 361 | GAACTCAATTAATCAAAATATGACAGAAATGCAAGGAATAAAGCGCTTTCCGGAATTAGAA     | 420           |            |              |
| Qy                    | 421 | GGATTAGTGAATTAATCAATATATATCTAACTGCGCTTGAAGATGGGAAGAAATCC-         | 479           |            |              |
| Db                    | 421 | GGATTAGTGAATTAATCAATATATATCTAACTGCGCTTGAAGATGGGAAGAAATCC          | 480           |            |              |
| Qy                    | 480 | - - AAATGGTTTCAAGAGCCTTACAGATGTCGAAATCGAATTTGAAATCTGTGATGTTTA     | 537           |            |              |
| Db                    | 481 | TTAAATGCTCTAGAGCCTTACAGATGTCGAAATCGAATTTGAAATCTGTGATGTTTA         | 540           |            |              |
| Qy                    | 538 | TTTACGCAATATATGCAATCTTTTATAGATGACAAATTTTGAAGTACCAATTCCTTACTGTA    | 597           |            |              |
| Db                    | 541 | TTTACGCAATATATGCAATCTTTTATAGATGACAAATTTTGAAGTACCAATTCCTTACTGTA    | 600           |            |              |
| Qy                    | 598 | TATGCAATGGCAGCCACCTTCAATTTACTGTTATTAAGGACGCTCAATTTTGGAGAA         | 657           |            |              |
| Db                    | 601 | TATGCAATGGCAGCCACCTTCAATTTACTGTTATTAAGGACGCTCAATTTTGGAGAA         | 660           |            |              |
| Qy                    | 658 | GAACTGGGATGTCACAACTACTATTAATACTATTATGATCGTCAAAATGAACTTACT         | 717           |            |              |
| Db                    | 661 | GAACTGGGATGTCACAACTACTATTAATACTATTATGATCGTCAAAATGAACTTACT         | 720           |            |              |
| Qy                    | 718 | GCAGAAATTTCTGATCAGTGTGTAAGTGTATGAACTGTTTACGAAATTTAAAGGC           | 777           |            |              |
| Db                    | 721 | GCAGAAATTTCTGATCAGTGTGTAAGTGTATGAACTGTTTACGAAATTTAAAGGC           | 780           |            |              |
| Qy                    | 778 | ACGAGCGCTAAACAAATGGTGTGATTAACCAATTCGCTAGAGAAATGACATGGCGGTT        | 837           |            |              |
| Db                    | 781 | ACGAGCGCTAAACAAATGGTGTGATTAACCAATTCGCTAGAGAAATGACATGGCGGTT        | 840           |            |              |
| Qy                    | 838 | TTAGATGTTGTTGCAATTTTCCCAATTTATGACACGCACTGCTCCCAATGGAAACGAA        | 897           |            |              |
| Db                    | 841 | TTAGATGTTGTTGCAATTTTCCCAATTTATGACACGCACTGCTCCCAATGGAAACGAA        | 900           |            |              |
| Qy                    | 898 | GCAACAACTAAACAGGAAGTATATACAGATCCACTGGCGCGTAAACGCTGCTCAAT          | 957           |            |              |
| Db                    | 901 | GCAACAACTAAACAGGAAGTATATACAGATCCACTGGCGCGTAAACGCTGCTCAAT          | 960           |            |              |
| Qy                    | 958 | GGTTCTGTTATGACAAAGCACTTTCTTTGGAGTGTAGAAATCATCCGTTATTCGACCA        | 1017          |            |              |
| Db                    | 961 | GGTTCTGTTATGACAAAGCACTTTCTTTGGAGTGTAGAAATCATCCGTTATTCGACCA        | 1020          |            |              |

RESULT 9  
ABK87239  
ID ABK87239 standard; DNA; 2022 BP.  
XX

|    |      |   |      |
|----|------|---|------|
| Qy | 1018 | CCCCATGATTATTGATTATATATAACGGGACTCAAGTGTTATACAAATCAAGAGCAATTTCT    | 1077 |
| Db | 1021 | CCCCATGATTATTGATTATATATAACGGGACTCAAGTGTTATACAAATCAAGAGCAATTTCT    | 1080 |
| Qy | 1078 | TCCGCTCCGTATATAAGACATTTGGCTGGTCAATCAAAATAGCTACATCGTCTCAGTAGG      | 1137 |
| Db | 1081 | TCCGCTCCGTATATAAGACATTTGGCTGGTCAATCAAAATAGCTACATCGTCTCAGTAGG      | 1140 |
| Qy | 1138 | GGTAGTAATCTTCAACAAATGATGGAATTAATCAAAATCTACACAGCACTAGTACCTTT       | 1197 |
| Db | 1141 | GGTAGTAATCTTCAACAAATGATGGAATTAATCAAAATCTACACAGCACTAGTACCTTT       | 1200 |
| Qy | 1198 | GATTTTACGAATTAATGATTAATTTCAAGACTCTATCAAAAGGATGCACTCTCTGATAT       | 1257 |
| Db | 1201 | GATTTTACGAATTAATGATTAATTTCAAGACTCTATCAAAAGGATGCACTCTCTGATAT       | 1260 |
| Qy | 1258 | GTTTACCTCGTATACGTATATATTTTTTGGAAATGCCAGAAGTCGAGTTTTTCATGGTA       | 1317 |
| Db | 1261 | GTTTACCTCGTATACGTATATATTTTTTGGAAATGCCAGAAGTCGAGTTTTTCATGGTA       | 1320 |
| Qy | 1318 | AACCAATTTGAATTAATACCCAGAAAGAGCTTTAAAGTATTAATCCAGTTTTCCAAAGATATATA | 1377 |
| Db | 1321 | AACCAATTTGAATTAATACCCAGAAAGAGCTTTAAAGTATTAATCCAGTTTTCCAAAGATATATA | 1380 |
| Qy | 1378 | GGAGTACAAAGAGATTCCGAAATTAGAATTTACCTCCAGAAACTTCAGATCAACCAAAATAT    | 1437 |
| Db | 1381 | GGAGTACAAAGAGATTCCGAAATTAGAATTTACCTCCAGAAACTTCAGATCAACCAAAATAT    | 1440 |
| Qy | 1438 | GAGTCATATAGCCATAGATTAATGTCATATCAAGATATTTCCGCGACGGGTAACTACTACC     | 1497 |
| Db | 1441 | GAGTCATATAGCCATAGATTAATGTCATATCAAGATATTTCCGCGACGGGTAACTACTACC     | 1500 |
| Qy | 1498 | GGATTAGTACCTGTATTTCTTGGACACATCGAAGTCGAGATTTAAACCAATACATATAT       | 1557 |
| Db | 1501 | GGATTAGTACCTGTATTTCTTGGACACATCGAAGTCGAGATTTAAACCAATACATATAT       | 1560 |
| Qy | 1558 | TCAGATAAAATCACTCAAAATCCGGCCGTTAAATGTTGGGATAATTTACCGTTTGTTCOA      | 1617 |
| Db | 1561 | TCAGATAAAATCACTCAAAATCCGGCCGTTAAATGTTGGGATAATTTACCGTTTGTTCOA      | 1620 |
| Qy | 1618 | GTGGTAAAGGACCAAGGACATACAGAGGGGATTTATTAAGTATAATAGAAAGTACTGGT       | 1677 |
| Db | 1621 | GTGGTAAAGGACCAAGGACATACAGAGGGGATTTATTAAGTATAATAGAAAGTACTGGT       | 1680 |
| Qy | 1678 | TCTGTAGGAAACCTTATTTCTAGCTCGATATGCGCTAGCAATTTAGAAAAGCAGGGAATAT     | 1737 |
| Db | 1681 | TCTGTAGGAAACCTTATTTCTAGCTCGATATGCGCTAGCAATTTAGAAAAGCAGGGAATAT     | 1740 |
| Qy | 1738 | CGTGTAAAGCTGAGATATGCTACTGATGAGATATTTGATTTGATGTAACGATGCTCAG        | 1797 |
| Db | 1741 | CGTGTAAAGCTGAGATATGCTACTGATGAGATATTTGATTTGATGTAACGATGCTCAG        | 1800 |
| Qy | 1798 | ATTAGATGCCAAAAACAATGAACCCAGGTAGGATCTGACATCTAAAACTTTTAAAGTT        | 1857 |
| Db | 1801 | ATTAGATGCCAAAAACAATGAACCCAGGTAGGATCTGACATCTAAAACTTTTAAAGTT        | 1860 |
| Qy | 1858 | GCAGATGCTATCAACCAATTAATTTAGCAACAGATAGTTCCGCTAGCATTTGAAACATAAT     | 1917 |
| Db | 1861 | GCAGATGCTATCAACCAATTAATTTAGCAACAGATAGTTCCGCTAGCATTTGAAACATAAT     | 1920 |
| Qy | 1918 | TTAGGTGAAGACCCCTTAATTTCAACATTTCTGTTAGTTTACGTTGACCGAATCGAATTC      | 1977 |
| Db | 1921 | TTAGGTGAAGACCCCTTAATTTCAACATTTCTGTTAGTTTACGTTGACCGAATCGAATTC      | 1980 |
| Qy | 1978 | ATCCCAGTAGATGAGACATATGAAGCGGAACAA                                 | 2010 |
| Db | 1981 | ATCCCAGTAGATGAGACATATGAAGCGGAATAA                                 | 2013 |

AC ABK87239;  
XX 07-OCT-2002 (first entry)  
XX Bacillus thuringiensis NSRG.N1218-1 mutant gene sequence.  
DE Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;  
XX Colorado potato beetle; western corn rootworm; southern corn rootworm;  
KW insect target range; endotoxin; Cry1218; gene; mutant; ds.  
XX Bacillus thuringiensis.  
OS Synthetic.  
XX WO200234774-A2.  
XX 02-MAY-2002.  
XX 24-OCT-2001; 2001WO-US45468.  
XX 24-OCT-2000; 2000US-242838P.  
XX 23-OCT-2001; 2001US-0032717.  
XX (DUPO) DU PONT DE NEMOURS & CO E I.  
PA Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;  
XX WPI; 2002-519178/55.  
XX P-PSDB; AU99260.  
XX New isolated pesticidal polypeptide useful for impacting insect pest  
XX e.g. Colorado potato beetle -  
XX Claim 23; Page 118-121; 176pp; English.  
XX The present invention relates to a new pesticidal polypeptide. The  
XX invention is useful for impacting an insect pest by applying the  
XX the molecules of the invention to the environment of the insect pest by  
XX spraying, dusting, broadcasting, or seed coating, where the insect pest  
XX is selected from Colorado potato beetle, western corn rootworm or  
XX southern corn rootworm. The invention is also useful for increasing  
XX insect target range and for producing transgenic microorganisms and  
XX plants that express the pesticidal polypeptide. The invention is also  
XX useful for producing transformed plants and in transforming any organism  
XX to produce the pesticidal polypeptide of the invention. The present  
XX nucleic acid sequence encodes a Bacillus thuringiensis mutant Cry1218  
XX endotoxin protein.  
XX Sequence 2022 BP; 692 A; 351 C; 398 G; 581 T; 0 other;  
SQ Query Match 54.9%; Score 1986.4; DB 24; Length 2022;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 2009; Conservative 0; Mismatches 1; Indels 12; Gaps 1;  
QY 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATCGGACACCTTCTACTCTGTA 60  
DB 1 ATGAGTCCAAATATCAAAATGAATATGAATATATAGATCGGACACCTTCTACTCTGTA 60  
QY 61 TCCAAATGATCTAACAGATACCTTTTGGCAATGAGGCCAACAAATGCGCTACAAATATG 120  
DB 61 TCCAAATGATCTAACAGATACCTTTTGGCAATGAGGCCAACAAATGCGCTACAAATATG 120  
QY 121 GATTATAAAGATTATTTAAATAATGCTGCGGAAATGCTAGTGAATACCTGGTTCACCT 180  
DB 121 GATTATAAAGATTATTTAAATAATGCTGCGGAAATGCTAGTGAATACCTGGTTCACCT 180  
QY 181 GAAGTACTTTGTTAGCGGACGAAGATGAGCTAAGCCGCAATGATATAGTAAATTA 240  
DB 181 GAAGTACTTTGTTAGCGGACGAAGATGAGCTAAGCCGCAATGATATAGTAAATTA 240  
QY 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTACTTTATCTCAACTTATT 300  
DB 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTACTTTATCTCAACTTATT 300

QY 301 GATATTTCTGTGGCCTTCAGGGGAAAAGAGTCAATGGGAAAATTTTTATGAAACAAGTAGAA 360  
DB 301 GATATTTCTGTGGCCTTCAGGGGAAAAGAGTCAATGGGAAAATTTTTATGAAACAAGTAGAA 360  
QY 361 GAACCTCATTAATCAAAAATAGCAGCAATATGCAAGCAATAAAGCGCTTTCCGAATTAGAA 420  
DB 361 GAACCTCATTAATCAAAAATAGCAGCAATATGCAAGCAATAAAGCGCTTTCCGAATTAGAA 420  
QY 421 CGATTAGGTAAATTAATCAAAATATATCTAACTGCGCTTTGAAGAATGGGAAGAATATCA 480  
DB 421 CGATTAGGTAAATTAATCAAAATATATCTAACTGCGCTTTGAAGAATGGGAAGAATATCA 480  
QY 481 AATGTTCAAGA-----GCCTTACGAGATGTCGAAATCGATTTGAAATCCTG 528  
DB 481 AATGTTCAAGAATGTTCCCGGCGCTTACGAGATGTCGAAATCGATTTGAAATCCTG 540  
QY 529 GATAGTTTATTTACGCAATATATGCAATCTTTTAGAGTGACAAATTTTGAAGTACCATTC 588  
DB 541 GATAGTTTATTTACGCAATATATGCAATCTTTTAGAGTGACAAATTTTGAAGTACCATTC 600  
QY 589 CTCTACTGTATATGCAATGGCAGCCCAACCTTCATTTTACTGTTTAAAGGACGCGTCAATT 648  
DB 601 CTCTACTGTATATGCAATGGCAGCCCAACCTTCATTTTACTGTTTAAAGGACGCGTCAATT 660  
QY 649 TTTGGAGAAGAAATGGGATGGTCAACAACTACTATTAATAACTATTTATGATCGTCAAAATG 708  
DB 661 TTTGGAGAAGAAATGGGATGGTCAACAACTACTATTAATAACTATTTATGATCGTCAAAATG 720  
QY 709 AAACCTTACTGCAAGATATTTCTGATCACTGTGTAAAGTGTATGAAACTGTTTGGCAAAA 768  
DB 721 AAACCTTACTGCAAGATATTTCTGATCACTGTGTAAAGTGTATGAAACTGTTTGGCAAAA 780  
QY 769 TTTAAAAGGCACGAGCGCTAAACAAATGGGTTGACTATAACCAATTCGTTAGAGAAATGACA 828  
DB 781 TTTAAAAGGCACGAGCGCTAAACAAATGGGTTGACTATAACCAATTCGTTAGAGAAATGACA 840  
QY 829 CTGGCGGTTTTAGATGTTGTTGCTATTTCCCAATTTATGACACACGACGACGACGACGACG 888  
DB 841 CTGGCGGTTTTAGATGTTGTTGCTATTTCCCAATTTATGACACACGACGACGACGACGACG 900  
QY 889 GAAACGAAAGCAACTAAACAGGGAAGTATATACAGATCCACTGGGCGGCGGTTAAACGTTG 948  
DB 901 GAAACGAAAGCAACTAAACAGGGAAGTATATACAGATCCACTGGGCGGCGGTTAAACGTTG 960  
QY 949 TCTTCAATTTGTTCTCTGTTGATGACAAAGCACCTTCTTTCCGAGTGTAGTAATCATCGTT 1008  
DB 961 TCTTCAATTTGTTCTCTGTTGATGACAAAGCACCTTCTTTCCGAGTGTAGTAATCATCGTT 1020  
QY 1009 ATTGCAACCCCATGTTATTTGATTATATAACGGGACTCACAGTGTATACAAATCAAGA 1068  
DB 1021 ATTGCAACCCCATGTTATTTGATTATATAACGGGACTCACAGTGTATACAAATCAAGA 1080  
QY 1069 AGCATTTCTTCGCTCGCTATATAGACATTTGGGCTGTCATCAATAAGTACCATCGT 1128  
DB 1081 AGCATTTCTTCGCTCGCTATATAGACATTTGGGCTGTCATCAATAAGTACCATCGT 1140  
QY 1129 GTTCAGTAGGGTAGTAATCTTCAACAAATGATGGAATTAACCAATCTACACAGCACT 1188  
DB 1141 GTTCAGTAGGGTAGTAATCTTCAACAAATGATGGAATTAACCAATCTACACAGCACT 1200  
QY 1189 AGTACCTTTGATTTTACGAATTTATGATATTTTACAGACTCTATCAAGGATGAGTACTC 1248  
DB 1201 AGTACCTTTGATTTTACGAATTTATGATATTTTACAGACTCTATCAAGGATGAGTACTC 1260  
QY 1249 CTGTATTTGTTTACCTGTTTATAGTATATTTTGGAAATGCCAAGTCCGAGTCTT 1308  
DB 1261 CTGTATTTGTTTACCTGTTTATAGTATATTTTGGAAATGCCAAGTCCGAGTCTT 1320  
QY 1309 TTTCAATGTTAAACCAATTTGAATTAATCCAGAAAGCGTTAAAGTATATCCAGTTTCCAA 1368  
DB 1321 TTTCAATGTTAAACCAATTTGAATTAATCCAGAAAGCGTTAAAGTATATCCAGTTTCCAA 1380  
QY 1369 GATATTATAGCGAGTACAAGAGATTTCGGAATTAGAAATTACCTCCAGAACTTCAGATCAA 1428

Db 1381 GATATATTACGAGTACAGAGATTCGGAATTAGATTTACCTCCAGAACTTCAGATCAA 1440  
QY 1429 CCAAAATTATGAGTCATATAGCCATAGATTATGTCTCATATCACAAGTATTCCCGCAGCGGT 1488  
Db 1441 CCAATTTAGTCATATAGCCATAGATTATGTCTCATATCACAAGTATTCCCGCAGCGGT 1500  
QY 1489 AACACTACCGGATTAGTACCTGTATTTCTTTGGACACATCGAAGTCGAGATTTAAACAAT 1548  
Db 1501 AACACTACCGGATTAGTACCTGTATTTCTTTGGACACATCGAAGTCGAGATTTAAACAAT 1560  
QY 1549 ACAATATATTAGATAAAATCACTCAAAATTCGGCCGGTTAAATGTTGGGATAATTTACCG 1608  
Db 1561 ACAATATATTAGATAAAATCACTCAAAATTCGGCCGGTTAAATGTTGGGATAATTTACCG 1620  
QY 1609 TTTGTTCCAGTGTAAAGACACAGGACATACAGGAGGGGATTTATTACAGTATAATAGA 1668  
Db 1621 TTTGTTCCAGTGTAAAGACACAGGACATACAGGAGGGGATTTATTACAGTATAATAGA 1680  
QY 1669 AGTACTGTTCTGTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAAGCA 1728  
Db 1681 AGTACTGTTCTGTAGGAACCTTATTTCTAGCTCGATATGCGCTAGCATTTAGAAAAAGCA 1740  
QY 1729 GCGAATATCGTGTAGACTGAGATATGCTACTGATCGAGATATTGTATGCAATGTAAC 1788  
Db 1741 GCGAATATCGTGTAGACTGAGATATGCTACTGATCGAGATATTGTATGCAATGTAAC 1800  
QY 1789 GATGCTCAGATTGATGCGCAAAACCAATGAACCCAGCTGAGGATCTGACATCTAAACT 1848  
Db 1801 GATGCTCAGATTGATGCGCAAAACCAATGAACCCAGCTGAGGATCTGACATCTAAACT 1860  
QY 1849 TTTAAAGTTGAGATGCTATCACAACTAAATTTAGCAACAGATAGTTCGCTAGCATTTG 1908  
Db 1861 TTTAAAGTTGAGATGCTATCACAACTAAATTTAGCAACAGATAGTTCGCTAGCATTTG 1920  
QY 1909 AAACATAATTTAGTGAGACCTTAATTCACATTAATCTGATATAGTTTACGTTGACCGA 1968  
Db 1921 AAACATAATTTAGTGAGACCTTAATTCACATTAATCTGATATAGTTTACGTTGACCGA 1980  
QY 1969 ATCGAATTCATCCCGTAGATGAGACATATGAGCGCAACAA 2010  
Db 1981 ATCGAATTCATCCCGTAGATGAGACATATGAGCGCAACAA 2022

## RESULT 10

ABK87244

ID ABK87244 standard; DNA; 2022 BP.

XX AC ABK87244;

XX DT 07-OCT-2002 (first entry)

XX DE Bacillus thuringiensis LKMS.N1218-1 mutant gene sequence.

XX KW Pesticidal; spraying; dusting; broad casting; seed coating; insect pest;  
XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;  
XX KW insect target range; endotoxin; Cry1218; gene; mutant; ds.  
XX OS Bacillus thuringiensis.  
XX OS Synthetic.

XX PN WO200234774-A2.

XX PD 02-MAY-2002.

XX PF 24-OCT-2001; 2001WO-US45468.

XX PR 24-OCT-2000; 2000US-242838P.

XX PR 23-OCT-2001; 2001US-0032717.

XX PA (DUPO ) DU PONT DE NEMOURS &amp; CO E I.

XX PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;

XX

DR WPI; 2002-519178/55.

XX P-PSDB; AAU99265.

XX New isolated pesticidal polypeptide useful for impacting insect pest  
PT e.g. Colorado potato beetle -

XX

PS Claim 23; Page 135-138; 176pp; English.

XX

CC The present invention relates to a new pesticidal polypeptide. The  
CC invention is useful for impacting an insect pest by applying the  
CC the molecules of the invention to the environment of the insect pest by  
CC spraying, dusting, broad casting, or seed coating, where the insect pest  
CC is selected from Colorado potato beetle, western corn rootworm or  
CC southern corn rootworm. The invention is also useful for increasing  
CC insect target range and for producing transgenic microorganisms and  
CC plants that express the pesticidal polypeptide. The invention is also  
CC useful for producing transformed plants and in transforming any organism  
CC to produce the pesticidal polypeptide of the invention. The present  
CC nucleic acid sequence encodes a *Bacillus thuringiensis* mutant Cry1218  
CC endotoxin protein.

XX

SQ Sequence 2022 BP; 695 A; 349 C; 395 G; 583 T; 0 other;

## Query Match

Best Local Similarity 54.9%; Score 1986.4; DB 24; Length 2022;

Matches 2009; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY

1 ATGAGTCCAAATATCAAAATGAATATGAAATTTATAGATCGGACACCTTCTACTTCTGTA 60  
Db 1 ATGAGTCCAAATATCAAAATGAATATGAAATTTATAGATCGGACACCTTCTACTTCTGTA 60

QY

61 TCCAATGATTTCAACAGATACCCCTTTTGGCAATGAGCCCAAAATGCGTACAAAATATG 120  
Db 61 TCCAATGATTTCAACAGATACCCCTTTTGGCAATGAGCCCAAAATGCGTACAAAATATG 120

QY

121 GATTATAAAGATTTATTAATAATGTTCTGGGGAAATGCTAGTGAATACCCCTGGTTCACT 180  
Db 121 GATTATAAAGATTTATTAATAATGTTCTGGGGAAATGCTAGTGAATACCCCTGGTTCACT 180

QY

181 GAAGTACTTGTAGCGGACAAGATGAGCTAAGCGGCAATTCATATAGTAGTAAATTA 240  
Db 181 GAAGTACTTGTAGCGGACAAGATGAGCTAAGCGGCAATTCATATAGTAGTAAATTA 240

QY

241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTGGTCTTTATCTCAACTTATT 300  
Db 241 CTATCAGGTTTAGGGTCCCATTTGTTGGCCGATAGTGGTCTTTATCTCAACTTATT 300

QY

301 GATATTTCTGTGGCTTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360  
Db 301 GATATTTCTGTGGCTTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360

QY

361 GAATCATTAATCAAAAAATAGCAGAAATATGCAAGGAATAAAGCGCTTTCGGAATTAAGAA 420  
Db 361 GAATCATTAATCAAAAAATAGCAGAAATATGCAAGGAATAAAGCGCTTTCGGAATTAAGAA 420

QY

421 GGATTAGGTAATTAATTAACCAATTTATCTAATCTGCTTGAAGAAATGGGAGAAATCCA 480  
Db 421 GGATTAGGTAATTAATTAACCAATTTATCTAATCTGCTTGAAGAAATGGGAGAAATCCA 480

QY

481 -----AATGTTTCAAGAGCGCTTACGAGATGTGCAAAATCGATTGAAATCCTG 528  
Db 481 TTAABAAATGCTAATGTTTCAAGAGCGCTTACGAGATGTGCAAAATCGATTGAAATCCTG 540

QY

529 GATAGTTTATTAACGCAATATATGCCATCTTTTAGAGTGAACAAATTTTGAAGTACCATT 588  
Db 541 GATAGTTTATTAACGCAATATATGCCATCTTTTAGAGTGAACAAATTTTGAAGTACCATT 600

QY

589 CTTACTGTATATGCATGGCAGCAACCTTCATTCTTCTTATTAAGGACGGTCAATT 648  
Db 601 CTTACTGTATATGCATGGCAGCAACCTTCATTCTTCTTATTAAGGACGGTCAATT 660

QY

649 TTTGGAGAAATGGGATGGTCAACAACTACTATTATTAATCTATTATGATCGTCAATG 708

Db 661 TTTGGAGAAGATGGGATGTCACAACTACTATTATAACTATTATGATCGTCAAAATG 720  
Qy 709 AAACCTTACTGAGATATTTCTGATCAGCTGTGTAAAGTGGTATGAAGCTGGTTAGCAAAA 768  
Db 721 AAACCTTACTGAGATATTTCTGATCAGCTGTGTAAAGTGGTATGAAGCTGGTTAGCAAAA 780  
Qy 769 TTTAAAGGACAGAGCGCTAAACAAATGGGTGTGACTATAACCAATTCGGTAGAGAAATGACA 828  
Db 781 TTTAAAGGACAGAGCGCTAAACAAATGGGTGTGACTATAACCAATTCGGTAGAGAAATGACA 840  
Qy 829 CTGCGGTTTTAGATGTTGTGTCATTTATCCCAAAATATGACACAGCGGTACCCAATG 888  
Db 841 CTGCGGTTTTAGATGTTGTGTCATTTATCCCAAAATATGACACAGCGGTACCCAATG 900  
Qy 889 GAAACGAAAGCACAACTAACCAAGGAGATATATACAGATCCACTGGGCGCGGTAAACGTG 948  
Db 901 GAAACGAAAGCACAACTAACCAAGGAGATATATACAGATCCACTGGGCGCGGTAAACGTG 960  
Qy 949 TCTTCAATTTGGTTCCTGATGACAAAGCACCTTCTTTCGGAGTGATAGAAATCATCCGTT 1008  
Db 961 TCTTCAATTTGGTTCCTGATGACAAAGCACCTTCTTTCGGAGTGATAGAAATCATCCGTT 1020  
Qy 1009 ATTCGACACACCCCAATGATTTGATTTATATAACGGGACTCACAGTGTATACAAATCAAGA 1068  
Db 1021 ATTCGACACACCCCAATGATTTGATTTATATAACGGGACTCACAGTGTATACAAATCAAGA 1080  
Qy 1069 AGCATTTCTTCGGTCTGATATAGACATTTGGGCTGGTTCATCAATTAAGCTACCATCGT 1128  
Db 1081 AGCATTTCTTCGGTCTGATATAGACATTTGGGCTGGTTCATCAATTAAGCTACCATCGT 1140  
Qy 1129 GTCAGTAGGGTAGTAATCTTCAACAAATGATGAACCTTAATCAAAATCTACACAGCACT 1188  
Db 1141 GTCAGTAGGGTAGTAATCTTCAACAAATGATGAACCTTAATCAAAATCTACACAGCACT 1200  
Qy 1189 AGTACCTTTGATTTTACGAATTTATGATTTTACAGACTCTATCAAGAGTTCATCGACTC 1248  
Db 1201 AGTACCTTTGATTTTACGAATTTATGATTTTACAGACTCTATCAAGAGTTCATCGACTC 1260  
Qy 1249 CTTGATATTTTACCCCTGGTTATAGTATATATTTTTTGGGATGCCAGAGTCCAGTTT 1308  
Db 1261 CTTGATATTTTACCCCTGGTTATAGTATATATTTTTTGGGATGCCAGAGTCCAGTTT 1320  
Qy 1309 TTTATGTTAAACCAATTTGAATTAATACCAGAAAGCTTTAAAGTATAATCCAGTTTCCAAA 1368  
Db 1321 TTTATGTTAAACCAATTTGAATTAATACCAGAAAGCTTTAAAGTATAATCCAGTTTCCAAA 1380  
Qy 1369 GATATTTATAGCGAGTACAGAGATTTCCGAATTTAGAAATTTACCTCCAGAAATTTAGATCAA 1428  
Db 1381 GATATTTATAGCGAGTACAGAGATTTCCGAATTTAGAAATTTACCTCCAGAAATTTAGATCAA 1440  
Qy 1429 CCAATTTATAGTATATAGCATAGATTTATGTCATATACAGATTTCCCGCGAGGGT 1488  
Db 1441 CCAATTTATAGTATATAGCATAGATTTATGTCATATACAGATTTCCCGCGAGGGT 1500  
Qy 1489 AACCTACCGGATTTAGTACTGCTGATTTCTTCGGACACATCCGAAGTGCAGATTTAAACAT 1548  
Db 1501 AACCTACCGGATTTAGTACTGCTGATTTCTTCGGACACATCCGAAGTGCAGATTTAAACAT 1560  
Qy 1549 ACAATATATTCAGATAAAATCACTCAAATTCGGCGGTTAAATGTTGGGATTAATTTACCG 1608  
Db 1561 ACAATATATTCAGATAAAATCACTCAAATTCGGCGGTTAAATGTTGGGATTAATTTACCG 1620  
Qy 1609 TTTGTTCCAGTGTAAAGGACAGACATACAGAGGGGATTTATACAGTATATATAGA 1668  
Db 1621 TTTGTTCCAGTGTAAAGGACAGACATACAGAGGGGATTTATACAGTATATATAGA 1680  
Qy 1669 AGTACTGTTCTGTAGGACCTTATTTCTAGCTCCGATATGGCTAGCATTTAGAAAAGCA 1728  
Db 1681 AGTACTGTTCTGTAGGACCTTATTTCTAGCTCCGATATGGCTAGCATTTAGAAAAGCA 1740  
Qy 1729 GGGAAATATCGTGTAGACTGAGATATGCTACTGATGAGATTTGTTATGATGTAAAC 1788

Db 1741 GGGAAATATCGTGTAGACTGAGATATGCTACTGATGACAGATATTTGATTCATGTAAAC 1800  
Qy 1789 GATGCTCAGATTTGAGTCCCAAAAACAAATGAACCCAGGTGAGGATCTGACATCTTAAACT 1848  
Db 1801 GATGCTCAGATTTGAGTCCCAAAAACAAATGAACCCAGGTGAGGATCTGACATCTTAAACT 1860  
Qy 1849 TTTAAAGTTCAGATGCTATACAAATTAATTAATTTAGCAACAGATGTTGCTAGCAATTG 1908  
Db 1861 TTTAAAGTTCAGATGCTATACAAATTAATTAATTTAGCAACAGATGTTGCTAGCAATTG 1920  
Qy 1909 AAACATATTTAGTGAAGACCCCTTAATTCACATTTCTGGTATAGTTTAGTTGACCGA 1968  
Db 1921 AAACATATTTAGTGAAGACCCCTTAATTCACATTTCTGGTATAGTTTAGTTGACCGA 1980  
Qy 1969 ATCGAATTCATCCAGTAGATGAGACATATGAAGCGGAACAA 2010  
Db 1981 ATCGAATTCATCCAGTAGATGAGACATATGAAGCGGAATTA 2022

## RESULT 11

ABK87256

ID ABK87256 standard; DNA; 2022 BP.

XX ABK87256;

DT 07-OCT-2002 (first entry)

DE Bacillus thuringiensis LRNS.N1218-1 mutant gene sequence.

XX Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest;  
KW Colorado potato beetle; western corn rootworm; southern corn rootworm;  
KW insect target range; endotoxin; Cry1218; gene; mutant; ds.  
XX Bacillus thuringiensis.

OS Synthetic.

PN WO200234774-A2.  
XX 02-MAY-2002.

XX 24-OCT-2001; 2001WO-US45468.

PF 24-OCT-2000; 2000US-242838P.

PR 23-OCT-2001; 2001US-0032717.

PA (DUPO ) DU PONT DE NEMOURS &amp; CO E I.

XX Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;

PI WPI; 2002-519178/55.

XX P-PSDB; AAU99271.

XX New isolated pesticidal polypeptide useful for impacting insect pest  
PT e.g. Colorado potato beetle -  
XX Claim 23; Page 160-162; 176pp; English.

PS The present invention relates to a new pesticidal polypeptide. The

XX invention is useful for impacting an insect pest by applying the  
CC the molecules of the invention to the environment of the insect pest by  
CC spraying, dusting, broadcasting, or seed coating, where the insect pest  
CC is selected from Colorado potato beetle, western corn rootworm or  
CC southern corn rootworm. The invention is also useful for increasing  
CC insect target range and for producing transgenic microorganisms and  
CC plants that express the pesticidal polypeptide. The invention is also  
CC useful for producing transformed plants and in transforming any organism  
CC to produce the pesticidal polypeptide of the invention. The present  
CC nucleic acid sequence encodes a Bacillus thuringiensis mutant Cry1218  
XX endotoxin protein.

SQ Sequence 2022 BP; 694 A; 349 C; 396 G; 583 T; 0 other;

Query Match 54.9%; Score 1986.4; DB 24; Length 2022;



07-OCT-2002 (first entry)  
 Bacillus thuringiensis LRMS.R1218-1 mutant gene sequence.  
 Pesticidal; spraying; dusting; broadcasing; seed coating; insect pest;  
 Colorado potato beetle; western corn rootworm; southern corn rootworm;  
 insect target range; endotoxin; Cry1218; gene; mutant; ds.  
 Bacillus thuringiensis.  
 Synthetic.  
 WO200234774-A2.  
 02-MAY-2002.  
 24-OCT-2001; 2001WO-US45468.  
 24-OCT-2000; 2000US-242838P.  
 23-OCT-2001; 2001US-0032717.  
 (DUPO) DU PONT DE NEMOURS & CO E I.  
 Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;  
 WPI; 2002-519178/55.  
 P-PSDB; RAU99273.  
 New isolated pesticidal polypeptide useful for impacting insect pest  
 e.g. Colorado potato beetle -  
 Claim 23; Page 168-170; 176pp; English.  
 The present invention relates to a new pesticidal polypeptide. The  
 invention is useful for impacting an insect pest by applying the  
 molecules of the invention to the environment of the insect pest by  
 spraying, dusting, broadcasing, or seed coating, where the insect pest  
 is selected from Colorado potato beetle, western corn rootworm or  
 southern corn rootworm. The invention is also useful for increasing  
 insect target range and for producing transgenic microorganisms and  
 plants that express the pesticidal polypeptide. The invention is also  
 useful for producing transformed plants and in transforming any organism  
 to produce the pesticidal polypeptide of the invention. The present  
 nucleic acid sequence encodes a Bacillus thuringiensis mutant Cry1218  
 endotoxin protein.  
 Sequence 2013 BP; 691 A; 348 C; 394 G; 580 T; 0 other;  
 Query Match 54.8%; Score 1985.8; DB 24; Length 2013;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 2003; Conservative 0; Mismatches 7; Indels 3; Gaps 1;  
 1 ATGAGTCCAAATTAATCAAAATGAATGAAATATAGATGCGACACCTTCTACTTCTGTA 60  
 1 ATGAGTCCAAATTAATCAAAATGAATGAAATATAGATGCGACACCTTCTACTTCTGTA 60  
 61 TCCAAATGATTTCAACAGATACCTTTTGGGATGAGCCAAACAAATGCGCTACAAATATG 120  
 61 TCCAAATGATTTCAACAGATACCTTTTGGGATGAGCCAAACAAATGCGCTACAAATATG 120  
 121 GATTATAAAGATTATTTAAAAATGTCGCGGAAATGCTAGTGAATACCTGGTTCACT 180  
 121 GATTATAAAGATTATTTAAAAATGTCGCGGAAATGCTAGTGAATACCTGGTTCACT 180  
 181 GAAGTACTGTTAGCGGCAAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 240  
 181 GAAGTACTGTTAGCGGCAAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 240  
 241 CTATCAGGTTTATAGGCTCCCATTTGTTGGCCGATAGTGAAGTGAAGTGAAGTGAAGT 300  
 241 CTATCAGGTTTATAGGCTCCCATTTGTTGGCCGATAGTGAAGTGAAGTGAAGTGAAGT 300  
 301 GATATTCTGTGCTTACAGGGAAGAGTCAATGGGAAATTTTATGGAAACAAAGTAGAA 360  
 |||||

Db 301 GATATTCTGTGGCTTCAGGGGAAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAA 360  
 Qy 361 GAACTCATTAAATCAAAAATAGCAGAAATATGCAAGGAATTAAGCGCTTTCGGAATTAGAA 420  
 Db 361 GAACTCATTAAATCAAAAATAGCAGAAATATGCAAGGAATTAAGCGCTTTCGGAATTAGAA 420  
 Qy 421 GGATTAGTAAATTAATCAATTAATCTAACTCGCTTGAAGAAATGGGAAAGAAATCC- 479  
 Db 421 GGATTAGTAAATTAATCAATTAATCTAACTCGCTTGAAGAAATGGGAAAGAAATCCA 480  
 Qy 480 --AAATGGTTCAAGAGCTTACGAGATGTCGAAATCGATTTGAAATCCTCGATAGTTTA 537  
 Db 481 TTAAGAAATGCTAGAGCTTACGAGATGTCGAAATCGATTTGAAATCCTCGATAGTTTA 540  
 Qy 538 TTTAGGCAATATATGCGCATCTTTTAGAGTGAACAAATTTGAAGTACCAATCTCCTACTGTA 597  
 Db 541 TTTAGGCAATATATGCGCATCTTTTAGAGTGAACAAATTTGAAGTACCAATCTCCTACTGTA 600  
 Qy 598 TATGCAATGGCAGCAACCTTCAATTTACTGTTATTAAGGACGCGTCAATTTTGGAGAA 657  
 Db 601 TATGCAATGGCAGCAACCTTCAATTTACTGTTATTAAGGACGCGTCAATTTTGGAGAA 660  
 Qy 658 GAATGGGGATGTCACAACTACTATTAATTAATCTATTAATGATGTCGAATGAAATCTTACT 717  
 Db 661 GAATGGGGATGTCACAACTACTATTAATTAATCTATTAATGATGTCGAATGAAATCTTACT 720  
 Qy 718 GCAGAAATATCTGATCACTGTGTAAGTGGTATGAACCTGTTTAGCAAAATTTAAAGGC 777  
 Db 721 GCAGAAATATCTGATCACTGTGTAAGTGGTATGAACCTGTTTAGCAAAATTTAAAGGC 780  
 Qy 778 ACAGCGCTAAACAAATGGTGTGACTATAACCAATTTCCGTAGAGAAATGACACTGCGGTT 837  
 Db 781 ACAGCGCTAAACAAATGGTGTGACTATAACCAATTTCCGTAGAGAAATGACACTGCGGTT 840  
 Qy 838 TTAGATGTTGTCATTAATTTCCCAATTAATGACACACGACGTCCTCAATGAAACGAAA 897  
 Db 841 TTAGATGTTGTCATTAATTTCCCAATTAATGACACACGACGTCCTCAATGAAACGAAA 900  
 Qy 898 GCACAACTAAACAGGAGTATATACAGATCCATCGGCGGCTAAACGTCCTCAATTT 957  
 Db 901 GCACAACTAAACAGGAGTATATACAGATCCATCGGCGGCTAAACGTCCTCAATTT 960  
 Qy 958 GGTTCCTGCTATGACAAAGCACCTTCTTTGGAGTGTAGTAATCATCGGTTATTCGACCA 1017  
 Db 961 GGTTCCTGCTATGACAAAGCACCTTCTTTGGAGTGTAGTAATCATCGGTTATTCGACCA 1020  
 Qy 1018 CCCATGTTATTTGATTAATAACGGGACTCACAGTGTATACAAATCAAGAACGATTTCT 1077  
 Db 1021 CCCATGTTATTTGATTAATAACGGGACTCACAGTGTATACAAATCAAGAACGATTTCT 1080  
 Qy 1078 TCCGCTCGCTATATAAGACATTTGGCTGTCATCAATAAGCTACCATCGTGTCTAGTAGG 1137  
 Db 1081 TCCGCTCGCTATATAAGACATTTGGCTGTCATCAATAAGCTACCATCGTGTCTAGTAGG 1140  
 Qy 1138 GGTAGTAAATCTTCAACAAATGTATGGAATCAATCAAAATCTACACAGCACTAGTACCTTT 1197  
 Db 1141 GGTAGTAAATCTTCAACAAATGTATGGAATCAATCAAAATCTACACAGCACTAGTACCTTT 1200  
 Qy 1198 GATTTTACGAATTAATGATTTTACAAAGTCTATCAAAAGGATGAGTACTCTCTGATATT 1257  
 Db 1201 GATTTTACGAATTAATGATTTTACAAAGTCTATCAAAAGGATGAGTACTCTCTGATATT 1260  
 Qy 1258 GTTTTACCTGCTATACGTTATATATTTTGGAAATGCGAGAGTGGTGTTCATGTA 1317  
 Db 1261 GTTTTACCTGCTATACGTTATATATTTTGGAAATGCGAGAGTGGTGTTCATGTA 1320  
 Qy 1318 AACCAATTAATTAATACCAAGAAAGCGTTAAAGTATATATCCAGTTTCCAAAGATATTATA 1377  
 Db 1321 AACCAATTAATTAATACCAAGAAAGCGTTAAAGTATATATCCAGTTTCCAAAGATATTATA 1380  
 Qy 1378 GCGAGTACAAGAGATTTCGGAATTTAGAAATTAATCTCAGAAATCTTCAGATCAACCAATATT 1437  
 Db 1381 GCGAGTACAAGAGATTTCGGAATTTAGAAATTAATCTCAGAAATCTTCAGATCAACCAATATT 1440  
 |||||





Qy 862 AATTATGACACGACGCTACCAATGGAACCGAAGACCAACTAAACGGAAGTATAT 921  
Db 730 AATTATGACACGACGCTACCAATGGAACCGAAGACCAACTAAACGGAAGTATAT 789  
Qy 922 ACAGATCCACTGGCGCGGTAAACGCTTCTTCAATTTGGTTCCTGGTATGACAAACACCT 981  
Db 790 ACAGATCCACTGGCGCGGTAAACGCTTCTTCAATTTGGTTCCTGGTATGACAAACACCT 849  
Qy 982 TCTTTTCGGAGTATAGAAATCATCCGTTATTCGACACCCCATCTTATGATTTATATAAG 1041  
Db 850 TCTTTTCGGAGTATAGAAATCATCCGTTATTCGACACCCCATCTTATGATTTATATAAG 909  
Qy 1042 GGACTCACAGTGTATACAAATCAAGCAATTTCTTCGGCTCGCTATATAAGCAATTCG 1101  
Db 910 GGACTCACAGTGTATACAAATCAAGCAATTTCTTCGGCTCGCTATATAAGCAATTCG 969  
Qy 1102 GCTGTCTATCAATTAAGCTACCATCTGTGTCAGTAGGGGTAGTAATCTTCAACAAATGTAT 1161  
Db 970 GCTGTCTATCAATTAAGCTACCATCTGTGTCAGTAGGGGTAGTAATCTTCAACAAATGTAT 1029  
Qy 1162 GGAACTTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATATGATTTTAC 1221  
Db 1030 GGAACTTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATATGATTTTAC 1089  
Qy 1222 AAGACTCTATCAAGGATGCACTCTTGTATTTTACCTCGTGTATAGTATATA 1281  
Db 1090 AAGACTCTATCAAGGATGCACTCTTGTATTTTACCTCGTGTATAGTATATA 1149  
Qy 1282 TTTTITGGAAATGCCAGAAATCGAGTTTTCATGTTTAAACCAATGTAATATACCAAGAG 1341  
Db 1150 TTTTITGGAAATGCCAGAAATCGAGTTTTCATGTTTAAACCAATGTAATATACCAAGAG 1209  
Qy 1342 AGTTTAAAGTATATTCAGTTTCCAAAGATATTTATGCGAGTACAGAGATTCGGATTA 1401  
Db 1210 AGTTTAAAGTATATTCAGTTTCCAAAGATATTTATGCGAGTACAGAGATTCGGATTA 1269  
Qy 1402 GAATTAACCTCCAGAAATCTCAGATCAACCAATTTATGAGTCATATAGCCATAGATTATGT 1461  
Db 1270 GAATTAACCTCCAGAAATCTCAGATCAACCAATTTATGAGTCATATAGCCATAGATTATGT 1329  
Qy 1462 CATATCACAAATGTTCCGCGAGGTTACACTACCTACCGGATAGTACTGTATTTCTTGG 1521  
Db 1330 CATATCACAAATGTTCCGCGAGGTTACACTACCTACCGGATAGTACTGTATTTCTTGG 1389  
Qy 1522 ACACATCGAAGTGCAGATTTTAAACATCAATATTTTCAATTAATCTCAAAATTCGG 1581  
Db 1390 ACACATCGAAGTGCAGATTTTAAACATCAATATTTTCAATTAATCTCAAAATTCGG 1449  
Qy 1582 GCCGTTAAATGTTGGGATAATTTACCGTTTGTTCAGTGTAAAGGACCAAGACATACA 1641  
Db 1450 GCCGTTAAATGTTGGGATAATTTACCGTTTGTTCAGTGTAAAGGACCAAGACATACA 1509  
Qy 1642 GGAGGGATTTATACAGTATATAAGAGTACGTTGTTGTAGGAACCTTATTTCTAGCT 1701  
Db 1510 GGAGGGATTTATACAGTATATAAGAGTACGTTGTTGTAGGAACCTTATTTCTAGCT 1569  
Qy 1702 CGATATGGCTAGCATTTAGAAAGCAGGGAATATTCGTGTAGAGCTGAGATATGCTACT 1761  
Db 1570 CGATATGGCTAGCATTTAGAAAGCAGGGAATATTCGTGTAGAGCTGAGATATGCTACT 1629  
Qy 1762 GATGAGATATTTGATTTGATGTAAACGATGCTCAGATTCAGATGCAAAACCAATGAAC 1821  
Db 1630 GATGAGATATTTGATTTGATGTAAACGATGCTCAGATTCAGATGCAAAACCAATGAAC 1689  
Qy 1822 CCAGGTGAGGATCTGACATCTTAAACCTTTTAAAGTTGCGAGATGCTATCAACATTAAT 1881  
Db 1690 CCAGGTGAGGATCTGACATCTTAAACCTTTTAAAGTTGCGAGATGCTATCAACATTAAT 1749  
Qy 1882 TTAGCAACAGATGTTGCTAGCTTGAACATATTTTAGTGAAGCCCTTAATTCACA 1941  
Db 1750 TTAGCAACAGATGTTGCTAGCTTGAACATATTTTAGTGAAGCCCTTAATTCACA 1809  
Qy 1942 TTATCTGGTATAGTTTACGTTGACCGAATTCGAATTCATCCAGTAGATGA 1991

Db 1810 TTATCTGTGTATAGTTTACGTTGACCGAATTCGAATTCATCCAGTAGATTA 1859

## RESULT 14

ABK87251

ID ABK87251 standard; DNA; 1854 BP.

XX

AC ABK87251;

XX

DT 07-OCT-2002 (first entry)

XX

DE Bacillus thuringiensis LKMS.R49PDV mutant gene sequence.

XX

KW Pesticidal; spraying; dusting; broadcasing; seed coating; insect pest;

KW Colorado potato beetle; western corn rootworm; southern corn rootworm;

KW insect target range; endotoxin; Cry1218; gene; mutant; ds.

XX

OS Bacillus thuringiensis.

XX

PN WO200234774-A2.

XX

PD 02-MAY-2002.

XX

PF 24-OCT-2001; 2001WO-US45468.

XX

PR 24-OCT-2000; 2000US-242838P.

XX

PR 23-OCT-2001; 2001US-0032717.

XX

PA (DUPO ) DU PONT DE NEMOURS &amp; CO E I.

XX

PI Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LB;

XX

DR WPI; 2002-519178/55.

XX

DR P-PSDB; AAU99270.

XX

PT New isolated pesticidal polypeptide useful for impacting insect pest

XX

PT e.g. Colorado potato beetle -

XX

PS Claim 27; Page 155-157; 176pp; English.

XX

The present invention relates to a new pesticidal polypeptide. The invention is useful for impacting an insect pest by applying the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasing, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm. The invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present nucleic acid sequence encodes a Bacillus thuringiensis mutant Cry1218 endotoxin protein.

XX

SQ Sequence 1854 BP; 627 A; 322 C; 368 G; 537 T; 0 other;

Query Match

Best Local Similarity 50.5%; Score 1827.4; DB 24; Length 1854;

Matches 1844; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

Qy 142 ATGTCTCGGGGAATGCTAGTGAATACCTGCTTCCACCTGAAGTACTTCTTAGCGGACAA 201

Db

1 ATGTCTCGGGGAATGCTAGTGAATACCTGCTTCCACCTGAAGTACTTCTTAGCGGACAA 60

Qy

202 GATGAGCTTAAGCGCGCAATTCATATAGTAGTAATTAATCTATCAGTTTAGGGTCCCA 261

Db

61 GATGAGCTTAAGCGCGCAATTCATATAGTAGTAATTAATCTATCAGTTTAGGGTCCCA 120

Qy

262 TTTGTTGGCCGATAGTGTCTTTTATCTCACTTATTTGATTTCTGTGGCCCTCAGGG 321

Db

121 TTTGTTGGCCGATAGTGTCTTTTATCTCACTTATTTGATTTCTGTGGCCCTCAGGG 180

QY 322 CAAAAGAGTCATGGGAAATTTTATGGAAACAAGTAGAAGAACTCATTAATCAAAAATA 381  
DB 181 GAAAGAGTCAATGGGAAATTTTATGGAAACAAGTAGAAGAACTCATTAATCAAAAATA 240  
QY 382 GCAGATATGCAAGGAATAAGCGCTTTTCGGAATTAGAAGGATAGGTATAATTCGAA 441  
DB 241 GCAGATATGCAAGGAATAAGCGCTTTTCGGAATTAGAAGGATAGGTATAATTCGAA 300  
QY 442 TTATATCTAACTCGCTTGAAGATGGGAAGAAATCC--AAATGGTTCAAGAGCCTTA 498  
DB 301 TTATATCTAACTCGCTTGAAGATGGGAAGAAATCCATTAATAATGCTAGAGCCTTA 360  
QY 499 CGAGATGCGGAATCGATTGAAATCTCGATAGTTTATTTACGAAATATATGCCATCT 558  
DB 361 CGAGATGCGGAATCGATTGAAATCTCGATAGTTTATTTACGCAATATATGCCATCT 420  
QY 559 TTTAGAGTGCAAAATTTTGAAGTACCATTCTCTACTGTATATGCAATGGCGCAACCTT 618  
DB 421 TTTAGAGTGCAAAATTTTGAAGTACCATTCTCTACTGTATATGCAATGGCGCAACCTT 480  
QY 619 CATTTACTGTTTATAAGGACGGCTCAATTTTGGAGAAGAAATGGGATGGTCAACCACT 678  
DB 481 CATTTACTGTTTATAAGGACGGCTCAATTTTGGAGAAGAAATGGGATGGTCAACCACT 540  
QY 679 ACTATTAACTATATGATCGTCAATGAACTTACTGCAAGATATCTGATCACTGT 738  
DB 541 ACTATTAACTATATGATCGTCAATGAACTTACTGCAAGATATCTGATCACTGT 600  
QY 739 GTAAAGTGTATGAACTGCTTTAGCAAAATTAAGGCGACGCGCTAAACATGGGTT 798  
DB 601 GTAAAGTGTATGAACTGCTTTAGCAAAATTAAGGCGACGCGCTAAACATGGGTT 660  
QY 799 GACTATAACCAATTCGTAGAGAAATGACACTGGCGGTTTTAGATGTTTGTCAATATTC 858  
DB 661 GACTATAACCAATTCGTAGAGAAATGACACTGGCGGTTTTAGATGTTTGTCAATATTC 720  
QY 859 CCAATTTAGACACACGACGTACCCAAATGGAAGCAACCACTTAAAGGGAAGTA 918  
DB 721 CCAATTTAGACACACGACGTACCCAAATGGAAGCAACCACTTAAAGGGAAGTA 780  
QY 919 TATACAGATCCACTGGGCGGGTAAAGTGTCTTCAATGGTTCCTGTTATGACAAGCA 978  
DB 781 TATACAGATCCACTGGGCGGGTAAAGTGTCTTCAATGGTTCCTGTTATGACAAGCA 840  
QY 979 CCTTCTTTGGAGTGATAGAAATCATCGTTATTGACACACCCCATGTTTGTATTATATA 1038  
DB 841 CCTTCTTTGGAGTGATAGAAATCATCGTTATTGACACACCCCATGTTTGTATTATATA 900  
QY 1039 ACGGACTCACAGTGATACACAATCAAGAACGCAATTTCTTCGCTCGCTATATAAGACAT 1098  
DB 901 ACGGACTCACAGTGATACACAATCAAGAACGCAATTTCTTCGCTCGCTATATAAGACAT 960  
QY 1099 TGGGCTGGTCAATCAATAGCTACCATCGTGTGAGTAGGGGTAGTATCTTCAACAAATG 1158  
DB 961 TGGGCTGGTCAATCAATAGCTACCATCGTGTGAGTAGGGGTAGTATCTTCAACAAATG 1020  
QY 1159 TATGGAATCAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATTTATGATTT 1218  
DB 1021 TATGGAATCAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAATTTATGATTT 1080  
QY 1219 TACAAGCTCTATCAAGAGTACGATCTCTTGTATATGTTTACCTCGTGTATACGTAT 1278  
DB 1081 TACAAGCTCTATCAAGAGTACGATCTCTTGTATATGTTTACCTCGTGTATACGTAT 1140  
QY 1279 ATATTTTGGATGCGAGAGTGGAGTTTTCATGTGTAAACCAATTTGAATATATACAGA 1338  
DB 1141 ATATTTTGGATGCGAGAGTGGAGTTTTCATGTGTAAACCAATTTGAATATATACAGA 1200  
QY 1339 AAGACGTTAAAGTATATCCAGTTTCCAAAGATATATAGCGAGTACAGAGATTCGGAA 1398  
DB 1201 AAGACGTTAAAGTATATCCAGTTTCCAAAGATATATAGCGAGTACAGAGATTCGGAA 1260  
QY 1399 TTAGAAATTAACCTCCAGAAACTTCAGATCAACCAATTTATGATCATATAGCCATAGATTA 1458

DB 1261 TTAGAATTAACCTCCAGAACTTCAGATCAACCAATTTATGAGTCATATAGCCATAGATTA 1320  
QY 1459 TGTCAATATCAACAGTATTCGCGGAGGGGTAAACACTACCGGATTAGTACCTGTTTCT 1518  
DB 1321 TGTCAATATCAACAGTATTCGCGGAGGGGTAAACACTACCGGATTAGTACCTGTTTCT 1380  
QY 1519 TGGACACATCGAAGTGCAGATTTTAAACAATAACAATATATTCAGATAAAATCACTCAAAAT 1578  
DB 1381 TGGACACATCGAAGTGCAGATTTTAAACAATAACAATATATTCAGATAAAATCACTCAAAAT 1440  
QY 1579 CCGCGCTTAAATGTTGGGATAATTTACCGTTTGTTCAGTGGTAAAGGACCGAGACAT 1638  
DB 1441 CCGCGCTTAAATGTTGGGATAATTTACCGTTTGTTCAGTGGTAAAGGACCGAGACAT 1500  
QY 1639 ACAGGAGGGGATTTATACAGTATATAGAACTACTGGTTCTGTAGGAACCTTATTCTTA 1698  
DB 1501 ACAGGAGGGGATTTATACAGTATATAGAACTACTGGTTCTGTAGGAACCTTATTCTTA 1560  
QY 1699 GCTCGATATGGCTAGCATTTAGAAAAAGCAGGGAATATCGTGTAAAGCTGAGATATGCT 1758  
DB 1561 GCTCGATATGGCTAGCATTTAGAAAAAGCAGGGAATATCGTGTAAAGCTGAGATATGCT 1620  
QY 1759 ACTGATGCGAGATATGATTTGCATGTAAACGATGCTCAGATTCAGATGCGCAAAACAATG 1818  
DB 1621 ACTGATGCGAGATATGATTTGCATGTAAACGATGCTCAGATTCAGATGCGCAAAACAATG 1680  
QY 1819 AACCCAGGTGAGGATCTGACATCTTAAACCTTTTAAAGTTGCAGATGCTATCACAACATTA 1878  
DB 1681 AACCCAGGTGAGGATCTGACATCTTAAACCTTTTAAAGTTGCAGATGCTATCACAACATTA 1740  
QY 1879 AATTTAGCAACAGATAGTTGCTAGCATTTGAAACATAATTTAGGTGAAGACCTTAATTC 1938  
DB 1741 AATTTAGCAACAGATAGTTGCTAGCATTTGAAACATAATTTAGGTGAAGACCTTAATTC 1800  
QY 1939 ACATTAATCTGTTAGTATGTTACGTTGACCGAATCGAATTCATCCAGTAGATGA 1991  
DB 1801 ACATTAATCTGTTAGTATGTTACGTTGACCGAATCGAATTCATCCAGTAGATGA 1853

## RESULT 15

ABK87249  
ID ABK87249 standard; DNA; 1863 BP.

XX ABK87249;

XX AC ABK87249;

XX DT 07-OCT-2002 (first entry)

XX DE Bacillus thuringiensis NGSR.N49PDV mutant gene sequence.

XX DE Pesticidal; spraying; dusting; broadcasing; seed coating; insect pest;

XX KW Colorado potato beetle; western corn rootworm; southern corn rootworm;

XX KW insect target range; endotoxin; Cry1218; gene; mutant; ds.

XX OS Bacillus thuringiensis.

XX OS Synthetic.

XX PN WO200234774-A2.

XX XX 02-MAY-2002.

XX XX 24-OCT-2001; 2001WO-US45468.

XX XX 24-OCT-2000; 2000US-242838P.

XX XX 23-OCT-2001; 2001US-0032717.

XX XX (DUFO) DU PONT DE NEMOURS & CO E I.

XX XX Abad AR, Duck NB, Feng X, Flannagan RD, Kahn TW, Sims LE;

XX XX WPI; 2002-519178/55.

XX XX P-P8DB; AAU99268.

XX XX

PT New isolated pesticidal polypeptide useful for impacting insect pest  
PT e.g. Colorado potato beetle -

PS Claim 27; Page 147-150; 176pp; English.

XX The present invention relates to a new pesticidal polypeptide. The  
CC invention is useful for impacting an insect pest by applying the  
CC the molecules of the invention to the environment of the insect pest by  
CC spraying, dusting, broadcasting, or seed coating, where the insect pest  
CC is selected from Colorado potato beetle, western corn rootworm or  
CC southern corn rootworm. The invention is also useful for increasing  
CC insect target range and for producing transgenic microorganisms and  
CC plants that express the pesticidal polypeptide. The invention is also  
CC useful for producing transformed plants and in transforming any organism  
CC to produce the pesticidal polypeptide of the invention. The present  
CC nucleic acid sequence encodes a *Bacillus thuringiensis* mutant Cry1218  
CC endotoxin protein.

XX Sequence 1863 BP; 627 A; 325 C; 373 G; 538 T; 0 other;

Query Match 50.4%; Score 1826.4; DB 24; Length 1863;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 1849; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

|    |     |   |     |
|----|-----|---|-----|
| QY | 142 | ATGTCGCGGAAATGCTAGTCAATACCTCGTTCACCTGAAGTACTTGTAGCGGACAA        | 201 |
| DB | 1   | ATGTCGCGGAAATGCTAGTCAATACCTCGTTCACCTGAAGTACTTGTAGCGGACAA        | 60  |
| QY | 202 | GATCAGCTAAGCGCGCAATTTGATATAGTAAATTTACTATCAGGTTTAGGGTCCCA        | 261 |
| DB | 61  | GATCAGCTAAGCGCGCAATTTGATATAGTAAATTTACTATCAGGTTTAGGGTCCCA        | 120 |
| QY | 262 | TTTCTGGCGGATAGTGAGCTTTTATCTCAACTTTATGATTTCTGTGGCTTCAGGG         | 321 |
| DB | 121 | TTTCTGGCGGATAGTGAGCTTTTATCTCAACTTTATGATTTCTGTGGCTTCAGGG         | 180 |
| QY | 322 | GAAGAAGTCAATGGGAAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAATA       | 381 |
| DB | 181 | GAAGAAGTCAATGGGAAATTTTATGGAACAAGTAGAAGAACTCATTAATCAAAAATA       | 240 |
| QY | 382 | GCAGAAATGCAAGGAATAAAGCGCTTTTCGGAATTTAGGAAGTATAGGTAATTAACAA      | 441 |
| DB | 241 | GCAGAAATGCAAGGAATAAAGCGCTTTTCGGAATTTAGGAAGTATAGGTAATTAACAA      | 300 |
| QY | 442 | TTATATCTAAGTGGCTTTGAAGATGGAAGAAATCCAAATGGTTCAAGAAATGGTTCC       | 492 |
| DB | 301 | TTATATCTAAGTGGCTTTGAAGATGGAAGAAATCCAAATGGTTCAAGAAATGGTTCC       | 360 |
| QY | 493 | ---GCCTTACGAGATGTCGGAATTCGATTTGAAATCCTGGATAGTTTATTTACGCAATAT    | 549 |
| DB | 361 | CGGCGCTTACGAGATGTCGGAATTCGATTTGAAATCCTGGATAGTTTATTTACGCAATAT    | 420 |
| QY | 550 | ATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTTCTTACTGTATATGCAATGGCA    | 609 |
| DB | 421 | ATGCCATCTTTTAGAGTGACAAATTTTGAAGTACCATTTCTTACTGTATATGCAATGGCA    | 480 |
| QY | 610 | GCCAACTCTTACTGTTTATTAAGACGCGTCAATTTTGGAGAGAATGGGGTGG            | 669 |
| DB | 481 | GCCAACTCTTACTGTTTATTAAGACGCGTCAATTTTGGAGAGAATGGGGTGG            | 540 |
| QY | 670 | TCAACAACCTACTATTAAATCTATTATGATCGTCAAAATGAACTTACTGCGAATATTCT     | 729 |
| DB | 541 | TCAACAACCTACTATTAAATCTATTATGATCGTCAAAATGAACTTACTGCGAATATTCT     | 600 |
| QY | 730 | GATCACTGTGTAAGTGTATGAATCTGGTTTGTAGCAAAATTAAGGACGCGCTAAA         | 789 |
| DB | 601 | GATCACTGTGTAAGTGTATGAATCTGGTTTGTAGCAAAATTAAGGACGCGCTAAA         | 660 |
| QY | 790 | CAATGGGTTGACTATACCAATTCCTAGAGAAATGACACTGGCGGTTTGTAGTGTGTT       | 849 |
| DB | 661 | CAATGGGTTGACTATACCAATTCCTAGAGAAATGACACTGGCGGTTTGTAGTGTGTT       | 720 |
| QY | 850 | GCATTTATCCCAAAATTTATGACACACGCGTACCCCAATGGAATCGAAATTCATCCAGTAGAT | 909 |

|    |      |  |      |
|----|------|--|------|
| DB | 721  | GCATTTATCCCAAAATTTATGACACACGCGCTACCCCAATGGAACGAAAGCACAACTAACCA   | 780  |
| QY | 910  | AGGAGATATATACAGATCCACTGGGCGGTAAGAGTGTCTTCAATTTGCTTCTCGGTAT       | 969  |
| DB | 781  | AGGAGATATATACAGATCCACTGGGCGGTAAGAGTGTCTTCAATTTGCTTCTCGGTAT       | 840  |
| QY | 970  | GACAAAGCACCTTCTTTGGAGTGATAGAAATCATCCGTTATTTCGACCAACCCCAATGATTT   | 1029 |
| DB | 841  | GACAAAGCACCTTCTTTGGAGTGATAGAAATCATCCGTTATTTCGACCAACCCCAATGATTT   | 900  |
| QY | 1030 | GATTATATAACGGGACTCAGAGTGATATACAAATCAAGAAGCAATTTCTTCGGTTCGCTAT    | 1089 |
| DB | 901  | GATTATATAACGGGACTCAGAGTGATATACAAATCAAGAAGCAATTTCTTCGGTTCGCTAT    | 960  |
| QY | 1090 | ATAAGCAATTTGGCTGCTCATCAATTAAGCTACCATCGTCTCAGTAGGGGTAGTAATCTT     | 1149 |
| DB | 961  | ATAAGCAATTTGGCTGCTCATCAATTAAGCTACCATCGTCTCAGTAGGGGTAGTAATCTT     | 1020 |
| QY | 1150 | CAACAAATGTATGGAACCTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAAT    | 1209 |
| DB | 1021 | CAACAAATGTATGGAACCTAATCAAAATCTACACAGCACTAGTACCTTTGATTTTACGAAT    | 1080 |
| QY | 1210 | TATGATATTTCAAGACTCTATCAAGGATGCGAGTCTCTTGATATTTGTTTACCCCTGGT      | 1269 |
| DB | 1081 | TATGATATTTCAAGACTCTATCAAGGATGCGAGTCTCTTGATATTTGTTTACCCCTGGT      | 1140 |
| QY | 1270 | TATACGTATATTTTTTGGAAATGCGAGAGTCTGAGTTTTTTCATGGTAAACCAATTTGAAT    | 1329 |
| DB | 1141 | TATACGTATATTTTTTGGAAATGCGAGAGTCTGAGTTTTTTCATGGTAAACCAATTTGAAT    | 1200 |
| QY | 1330 | AATACCAAGAAGAGCTTTAAAGTATAATCCAGTTTCCAAAGATATTTATAGCGAGTACAA     | 1389 |
| DB | 1201 | AATACCAAGAAGAGCTTTAAAGTATAATCCAGTTTCCAAAGATATTTATAGCGAGTACAA     | 1260 |
| QY | 1390 | GATTCGGAATTTAGAAATTTACCTCCAGAAATTTTCAGATCAACCAATTTATAGTCAATATAGC | 1449 |
| DB | 1261 | GATTCGGAATTTAGAAATTTACCTCCAGAAATTTTCAGATCAACCAATTTATAGTCAATATAGC | 1320 |
| QY | 1450 | CATGATATTTGATATATCAAGTATTTCCGCGACGGGTAACTACCGGATTTAGTACCT        | 1509 |
| DB | 1321 | CATGATATTTGATATATCAAGTATTTCCGCGACGGGTAACTACCGGATTTAGTACCT        | 1380 |
| QY | 1510 | GTATTTTCTTGGACACATCGAAGTGCAGATTTTAAACAATCAATATATTCAGATAAATC      | 1569 |
| DB | 1381 | GTATTTTCTTGGACACATCGAAGTGCAGATTTTAAACAATCAATATATTCAGATAAATC      | 1440 |
| QY | 1570 | ACTCAAAATTCGCGCGTTAAATTTGGGATAATTTTACCGTTTGTTCAGTGGTAAAGGA       | 1629 |
| DB | 1441 | ACTCAAAATTCGCGCGTTAAATTTGGGATAATTTTACCGTTTGTTCAGTGGTAAAGGA       | 1500 |
| QY | 1630 | CCAGGACATACAGAGGGGATTTTATTCAGTATATTAAGAGTACTGGTCTCTGTAGGAAC      | 1689 |
| DB | 1501 | CCAGGACATACAGAGGGGATTTTATTCAGTATATTAAGAGTACTGGTCTCTGTAGGAAC      | 1560 |
| QY | 1690 | TTATTTCTAGCTGATATGGCTAGCAATTAAGAAAACGAGGAAATATCTGTAGAACTG        | 1749 |
| DB | 1561 | TTATTTCTAGCTGATATGGCTAGCAATTAAGAAAACGAGGAAATATCTGTAGAACTG        | 1620 |
| QY | 1750 | AGATATCTACTGATGAGGATAATTTGATTTGATGCAATGTAACGATGCTCAGATTTAGATGCA  | 1809 |
| DB | 1621 | AGATATCTACTGATGAGGATAATTTGATTTGATGCAATGTAACGATGCTCAGATTTAGATGCA  | 1680 |
| QY | 1810 | AAAAAATGAACCCAGGTAGGATCTGACATCTTAAACCTTTTAAAGTTGCGAGTGTATC       | 1869 |
| DB | 1681 | AAAAAATGAACCCAGGTAGGATCTGACATCTTAAACCTTTTAAAGTTGCGAGTGTATC       | 1740 |
| QY | 1870 | ACAACTTTAAATTTAGCAACAGATAGTTTCGTAGCTTGAACCAATATTTTAGGTGAAGAC     | 1929 |
| DB | 1741 | ACAACTTTAAATTTAGCAACAGATAGTTTCGTAGCTTGAACCAATATTTTAGGTGAAGAC     | 1800 |
| QY | 1930 | CCTAATTTCAACATTTATCTGGTATAGTTTACGTTTGACCGAATTCGAAATTCATCCAGTAGAT | 1989 |

Db 1801 CCTAATTCACATTATCTGGTATAGTTTACGTTGACCGAATCGAATTCATCCAGTAGAT 1860

Qy 1990 GA 1991

Db 1861 TA 1862

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